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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such
5 polynucleotides, along with uses for these polynucleotides and proteins, for example in
therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as
10 lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured
rapidly over the past decade. The now routine hybridization cloning and expression cloning
techniques clone novel polynucleotides "directly" in the sense that they rely on information
directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in
the case of hybridization cloning; activity of the protein in the case of expression cloning). More
15 recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA
sequences based on the presence of a now well-recognized secretory leader sequence motif, as
well as various PCR-based or low stringency hybridization-based cloning techniques, have
advanced the state of the art by making available large numbers of DNA/amino acid sequences
for proteins that are known to have biological activity, for example, by virtue of their secreted
20 nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of
PCR-based techniques, or by virtue of structural similarity to other genes of known biological
activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for
example, diagnostics, forensics, gene mapping; identification of mutations responsible for
25 genetic disorders or other traits, to assess biodiversity, and to produce many other types of data
and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel
30 isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules,
cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic
variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more
epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

5 The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-8051. The polypeptides sequences are designated SEQ
10 ID NO: 8052-16102. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that
15 hybridize to the complement of SEQ ID NO: 1-8051 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-8051. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ
20 ID NO: 1-8051 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-8051. The sequence information can be a segment of any one of SEQ ID NO: 1-8051 that uniquely identifies or represents the sequence
25 information of SEQ ID NO: 1-8051.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed
30 to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their
35 reverse or direct complements) according to the invention have numerous applications in a variety

of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

5 In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-8051 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-8051 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath
10 et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-8051; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-8051;
15 and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-8051. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-8051; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing
20 (*e.g.*, SEQ ID NO: 8052-16102); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.* orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

25 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-8051; or (b) polynucleotides that hybridize to the complement of the
30 polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably

produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the
5 polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of
10 interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex
15 and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and
20 monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds
25 that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a
30 polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the
35 administration of the polynucleotides or polypeptides of the invention to individuals exhibiting

symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100

nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can
5 be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-8051.

10 Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in
15 Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence
20 information from the nucleic acid sequences of SEQ ID NO: 1-8051. The sequence information can be a segment of any one of SEQ ID NO: 1-8051 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-8051. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set
25 of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also
30 approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the
35 increased probability for mismatch at each nucleotide position (3×25). The probability that an

eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

5 The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic
10 elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

15 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino
20 acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that
25 have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

30 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue
35 may be removed from the protein during processing in the cell. The peptide may be produced

synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

10 The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 15 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural

or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*,

washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be

disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

5 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction
10 of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the
15 suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the
20 context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the
25 nucleotide sequences of SEQ ID NO: 1-8051; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 8052-16102; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 8052-16102. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of
30 the nucleotides sequences of SEQ ID NO: 1-8051; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 8052-16102.
35 Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in

receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-8051 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-8051 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-8051 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-8051, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most

preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-8051, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-8051 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-8051 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the

polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-8051, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-8051 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-8051 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example.

Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia).

- 5 Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-8051, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 8052-16102 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-8051 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-8051), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of
10 an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified
15 such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the
20 control of a strong pol II or pol III promoter are preferred.

 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The
25 antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

30 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit
35 translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-8051). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-8051 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and
5 Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical
10 structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or
15 solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral
20 backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For
25 example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or
30 primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug
35 delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

25

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 8052-16102 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-8051 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-8051 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 8052-16102 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 8052-16102 or the corresponding full length or mature protein; and

5 "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity.

10 Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 8052-16102.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

15

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where

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25 proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

30 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

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A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

5 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either
10 cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 8052-16102.

15 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or
20 deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the
25 molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved
30 systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to
35 retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

5 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present
10 invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification
15 of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

20 Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen,
25 respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other
30 aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*,
5 by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and
10 PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard
15 selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to
20 replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or
25 protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene
30 under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally
35 occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

- 5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in
10 Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,
15 Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse
25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1
30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in
35 Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

- Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce
5 autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and
10 identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be
15 used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In
20 addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated
25 cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al.,
30 Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention
35 exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the
10 growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.
15 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A
25 protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More
30 specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

5 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected
10 cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

 A polypeptide of the present invention may provide the necessary stimulation signal to T
15 cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain
20 protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as
25 the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

 The activity of a protein of the invention may, among other means, be measured by the
30 following methods:

 Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;
35 Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

- 5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1
10 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3,
15 In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:
20 Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation
25 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research
30 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

5 A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention,
10 alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as
15 a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

20 The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci.
25 USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils,
30 T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other
35 trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines
15 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

20 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events
25 in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

Therapeutic compositions of the invention can be used in the following:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

35 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, *e.g.* reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D,

5 Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate
10 (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

15 In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

20 *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30
25 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,
30 *e.g.* from American Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the
35 invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

10 The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

20 By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

25 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

35 This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

5 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
10 of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or
15 chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid
20 arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

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4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia,
30 acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

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4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- 10 (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord
15 infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- 20 (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the
25 nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to
30 diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or
35 injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit
5 any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*,
10 choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may
15 be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron
20 conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect
25 neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

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4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing
35 or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or
5 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other
10 than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or
15 entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis
20 and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes
25 possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the
30 polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately
35 adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified
5 nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*,
10 by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model
15 system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, *Science*, 219:56, or by B. Waksman et al., 1963, *Int. Arch. Allergy Appl. Immunol.*, 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed *Mycobacterium tuberculosis* in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant
20 mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed *Mycobacterium tuberculosis* in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and
25 24 days after injection of *Mycobacterium* CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

30 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

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4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance
5 the activity of the protein or other active ingredient or complement its activity or use in
treatment. Such additional factors and/or agents may be included in the pharmaceutical
composition to produce a synergistic effect with protein or other active ingredient of the
invention, or to minimize side effects. Conversely, protein or other active ingredient of the
present invention may be included in formulations of the particular clotting factor, cytokine,
10 lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-
inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other
hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as
IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein
of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or
15 complexes with itself or other proteins. As a result, pharmaceutical compositions of the
invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention
including a first protein, a second protein or a therapeutic agent may be concurrently
administered with the first protein (*e.g.*, at the same time, or at differing times provided that
20 therapeutic concentrations of the combination of agents is achieved at the treatment site).
Techniques for formulation and administration of the compounds of the instant application may
be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest
edition. A therapeutically effective dose further refers to that amount of the compound sufficient
to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the
25 relevant medical condition, or an increase in rate of treatment, healing, prevention or
amelioration of such conditions. When applied to an individual active ingredient, administered
alone, a therapeutically effective dose refers to that ingredient alone. When applied to a
combination, a therapeutically effective dose refers to combined amounts of the active
ingredients that result in the therapeutic effect, whether administered in combination, serially or
30 simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically
effective amount of protein or other active ingredient of the present invention is administered to
a mammal having a condition to be treated. Protein or other active ingredient of the present
invention may be administered in accordance with the method of the invention either alone or in
35 combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with
5 an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds
10 may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which
15 increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other
20 glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as
25 sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v
30 polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the
35 co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue

5 regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution

10 and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

15 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of

20 proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include

25 compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in

30 the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (*i.e.*, the concentration of

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of any of the full length proteins of the invention, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention, *e.g.*, a hydrophilic

region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be
5 generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments,
10 analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or
15 monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

20 5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic
25 protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an
30 adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified; for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

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5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

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5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab)}_2$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

5 Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the
10 recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct
15 bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion
20 preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable
25 host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the
30 CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for
35 increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain F_v (sF_v) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptopbutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.13.8 Immunoconjugates

5 The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been
10 described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin,
15 mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP),
20 iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a
25 ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such
30 streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

35 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-8051 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-8051 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

5 In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see 10 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA 15 molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

20 The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise 25 contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed 30 polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a 35 polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

5 Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard,
10 T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the
15 present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a
20 sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present
25 invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to
30 another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which
35 contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-8051, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see
5 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into
10 polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the
15 present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid
20 hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-8051. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-8051 can be used as an indicator of the presence of RNA of cell type of such a tissue
25 in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The
30 probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes
35 *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

- 5 Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic
10 strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader
15 aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon
20 consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

25 5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The
30 inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid
5 Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from
10 a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-8051 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases
15 (i.e., Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score
20 greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-8051) of the present invention are incorporated in the attached Sequence Listing. A subset of the predicted polypeptide sequences contain an unknown amino acid; a stop codon; a possible nucleotide deletion; or a possible nucleotide insertion. These sequences have also been
25 shown in their entirety in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-8051. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers
30

to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-8051 were obtained by a BLASTX
5 version 2.0a1 19MP-WashU search against Genpept release 123 and Geneseq release 200110 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-8051. The nearest neighbor results for SEQ ID NO: 1-8051, having identifiable function(s) are incorporated in the attached Sequence Listing.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J.
10 Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the polypeptide sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provides the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide
15 sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1)
pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by pFam analysis for each polypeptide, namely: the name of
20 the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-8051. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each
25 in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/577,408.

TABLE 1

| Tissue Origin | Tissue/ RNA Source | Library Name | SEQ ID NO: |
|---------------|--------------------------|--------------|---|
| adult brain | GIBCO | AB3001 | 53-57 119-121 205-206 229-232 311-314 318-320 328-331 340-341 360-361 382-383 398 400 433 444 448-449 455 461-465 467-468 476-479 488 501-504 506 508-513 522-526 533-535 541-542 559- 560 562 637-640 649 654-655 658 679-683 751-752 755 757-764 766 771 780-782 841-849 857 867-869 872-874 879 884-885 890 915-917 945 969 1006-1009 1031-1035 1101-1103 1110 1112 1115 1120-1121 1123 1131 1185-1190 1252 1299-1301 1303-1304 1314- 1316 1338 1355-1359 1361-1363 1382-1387 1395-1399 1447 1458- 1460 1473-1477 1479-1481 1484-1485 1489-1493 1495-1496 1498 1515 1517 1534-1535 1565-1566 1601 1603 1612 1614-1619 1621- 1622 1626 1642-1644 1646 1679 1690-1693 1695-1696 1698-1704 1706-1715 1717-1718 1726 1728-1737 1739-1748 1751-1760 1762- 1763 1768-1771 1782 1843 1847 1862-1863 1877-1880 1882-1886 1895-1901 1904-1905 1922 1976-1991 2023 2034 2171-2174 2182- 2184 2200-2203 2220-2223 2232-2233 2250 2332-2339 2347-2350 2352-2356 2359-2361 2371-2372 2375 2380 2383-2384 2386-2388 2466-2469 2485-2489 2533 2547-2550 2575 2585-2586 2588-2589 2602 2682-2686 2688 2714-2715 2737 2739-2741 2744-2745 2789- 2791 2798-2802 2839-2841 2899 2910-2918 2920-2922 2924 2952- 2955 3043-3050 3095-3096 3101-3102 3104-3105 3109-3110 3116- 3117 3134-3135 3179-3180 3223-3224 3236-3237 3260-3261 3265 3271-3272 3280-3282 3311 3325 3349-3350 3354 3393-3395 3397- 3400 3491-3493 3499-3503 3517-3519 3521-3523 3560 3581-3582 3588-3589 3592-3596 3617-3619 3631 3683 3696 3698-3702 3762- 3763 3801 3805 3834-3835 3837-3838 3850-3855 3866 3944 3955 3967 3979-3985 3990 4017-4020 4081 4098 4100-4103 4126-4127 4189-4190 4193 4226 4266-4269 4271-4272 4298-4301 4303 4320- 4323 4325 4341 4344-4345 4347-4349 4427-4428 4436 4454 4537- 4541 4543 4549-4550 4552-4554 4564-4567 4576 4580-4591 4599 4610 4698 4710 4806-4808 4810 4812 4833 4847-4853 4884-4885 4910 4940-4941 4943-4944 4952 4954-4958 4972 5033-5038 5040- 5044 5056-5060 5062 5105 5116 5137 5141 5158-5161 5163 5166- 5167 5226-5227 5229-5233 5236-5238 5240-5249 5252-5261 5263- 5267 5272 5274 5340-5341 5478-5480 5525 5546-5547 5566-5570 5581 5628-5634 5644 5760 5771 5782 5872 5881-5887 5904 5911 5971-5976 6003 6007 6037-6038 6074 6124-6128 6189 6191-6194 6198 6231-6233 6249-6250 6339-6340 6360 6413-6414 6553-6556 6586-6587 6656 6681 6722-6727 6729-6736 6771 6782 6794 6805 6903 6906 6939-6942 7044-7051 7053 7055-7056 7087-7089 7116 7131 7254-7255 7294 7340 7377-7379 7662 7677 7686 7697 7730 7732-7734 7741 7744-7760 7763 7775 7808-7810 7835-7836 7847 7942 8025 |
| adult brain | GIBCO | ABD003 | 4-5 28-29 44 47 205-206 211-212 229-232 246-248 250-259 261- 266 282-284 318-320 323-328 338-341 349-354 356-359 368-375 382-383 385-386 397-398 400 404-409 426-427 433 444-449 455 476-479 486-489 492-493 495-497 500-504 506 508-515 517 522- 526 528-529 555-556 584-592 602-604 606-614 616 622 624 627- 633 635-640 649 658 666 668 672-676 679-683 686-688 690-692 704-707 722-723 726 768-769 771 782 841-843 846-849 857 867- 869 872-874 876-881 884-885 890 893-895 900 902 911-917 919- 921 923-927 929 945 960-962 969 973 979-985 991-993 995-1000 1006-1009 1020 1031-1035 1037-1040 1042-1043 1056-1057 1063 1070-1072 1083 1086-1094 1100-1109 1111 1113 1115 1119-1123 1129 1131 1137-1148 1165 1174-1175 1183 1185-1197 1204 1210- 1212 1221-1225 1227-1232 1236-1237 1241-1242 1250 1253 1264- 1265 1267-1270 1272 1279-1281 1286 1291-1293 1303-1306 1308- 1309 1314-1316 1334-1336 1338-1344 1355-1359 1361-1363 1365- 1368 1370 1372-1375 1382-1390 1392-1400 1411-1413 1423 1438- 1439 1442-1445 1447-1449 1451-1456 1476-1477 1484-1485 1489- 1493 1495-1496 1500 1503-1504 1506-1507 1515 1523-1524 1534- 1536 1538 1549 1560 1564-1571 1576-1578 1595-1601 1603 1610 1621-1622 1626 1640-1641 1644 1646 1648-1652 1674 1676-1680 1691-1693 1695-1696 1698-1700 1703-1704 1706 1711-1713 1718 1732-1736 1741-1745 1747-1748 1751-1754 1764 1768-1779 1781- 1790 1792-1805 1807-1819 1821-1826 1828-1837 1839-1844 1850 |

| Tissue Origin | Tissue/ RNA Source | Library Name | SEQ ID NO: |
|---------------|--------------------------|--------------|---|
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| adult brain | Invitrogen | ABR016 | 28-29 56 1534-1536 1538 1612 1614 1642-1643 1755-1760 1762 1946 1948-1951 2010-2011 2013 2016-2022 2137 2204-2205 2207-2208 2835 2837 2853-2854 2857-2858 2955 3039-3040 3071-3077 3463 3853-3854 3990 4554 4565 4576 4737-4739 5272 5274 5298 6195-6196 6353 6356-6358 6424-6427 6761 6851-6854 |
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| WO 01/88088 Origin | | PCT/US01/14827 | |
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| adult kidney | Invitrogen | AKT002 | 18 44 69-72 80-87 89-98 100-109 112-117 123-124 133 168-169 265-266 268 270-273 318-320 323-325 328 335-337 340-341 385- 387 389-397 426-427 431 434-435 450-454 456 486-487 489 501- 504 506 514-515 517 584-593 595-596 602 607-614 616-620 627- 633 635-640 654-655 663-664 670-671 679-681 722-723 747 780- 781 823-825 844-845 876-877 883-885 900 902 915-917 949-950 959 963-965 967-970 979 1006-1009 1019 1024-1028 1056-1057 1087-1088 1090-1094 1101-1103 1115-1121 1123 1127-1128 1165 1192-1193 1195-1196 1202-1203 1205-1207 1211-1214 1216-1218 1228-1230 1241-1242 1257 1269 1294-1295 1297-1301 1303-1304 1314-1316 1323-1325 1341-1344 1355-1359 1361-1363 1388-1390 1405-1406 1424-1426 1438-1439 1442-1445 1447 1450 1461 1472 1498 1503-1504 1506-1507 1521-1522 1529-1533 1536 1538 1543- 1547 1562 1565-1566 1576-1579 1581-1582 1625 1648-1652 1657- 1663 1690-1693 1695-1696 1703-1704 1706 1711-1713 1746 1765- 1767 1773 1775-1777 1783-1790 1792-1794 1806 1825-1826 1828- 1831 1843 1845 1866-1869 1895-1901 1904-1905 1915-1918 1922 1938-1945 1952-1957 1960-1961 1963 1976-1978 1980-1989 1991 2010-2011 2013 2016-2023 2027-2036 2039-2041 2052 2106-2108 |

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| adult lung | GIBCO | ALG001 | 19 28-29 44 74-76 78-79 123-124 178-179 205-206 229-232 246- 248 250-259 261-264 282-284 318-320 344 355 366 368-374 377 385-386 388 397-400 404-407 426-427 433 444 448-456 466 476- 479 484-485 488 492-493 500 508-515 517-526 541-542 545-546 552-554 593 595-596 602-604 606 658 704-707 744-745 769 782 836 844-845 851 859-862 876-877 880-881 892 900 902 911-912 914 923-927 930 935-936 938 969-970 973 999-1000 1006-1009 1024-1028 1058-1061 1063 1068-1069 1072 1083 1089 1096-1103 1111 1113 1115-1118 1122 1124-1126 1129 1140 1146-1148 1156- 1160 1165 1174-1175 1185-1190 1221-1225 1227 1267-1268 1282 1299-1301 1303-1304 1317 1319 1323-1325 1341-1348 1350-1354 1371 1380 1391 1402 1410-1413 1424-1426 1438-1439 1442-1446 1489-1493 1495-1496 1503-1504 1506-1507 1541-1542 1612 1614- 1619 1644 1646 1648-1652 1681-1684 1690 1698-1699 1703-1704 1706 1711-1713 1730-1731 1747-1748 1751-1754 1775-1777 1782- 1789 1799-1804 1836-1837 1839-1842 1858-1860 1871-1876 1887 1904-1905 1911-1913 1922 1946 1948-1951 1977-1978 1980-1989 1991 1996-2000 2010-2011 2013 2016-2022 2039-2040 2081-2083 2102 2105 2124-2127 2136 2143 2181 2185-2186 2188-2195 2197- 2199 2204-2205 2207-2208 2216 2218 2225-2227 2229 2332-2339 2345-2350 2359-2361 2387-2388 2425-2428 2430-2432 2439-2444 2455-2458 2496-2502 2510 2517 2528 2533 2539 2545 2556 2563 2567 2575 2579-2583 2595-2597 2599-2601 2629-2631 2679-2682 2690-2693 2699-2704 2714-2715 2744-2745 2763 2766 2787 2789- 2791 2803-2804 2806-2807 2813-2820 2838 2915-2917 2922 2924 2943-2944 3011-3012 3014 3018-3019 3043-3050 3078-3080 3082- 3091 3093 3095 3127-3132 3183 3192 3212 3218 3222-3224 3226 3233-3235 3355 3436-3438 3463 3499-3501 3506 3521-3523 3560 3563-3564 3581-3582 3592-3596 3610-3612 3615-3616 3626 3631 3679 3691 3696 3698-3702 3713-3714 3732 3745 3762 3764-3765 3788-3790 3805 3832-3833 3855 3892 3903 3911 3922 3937-3940 |

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| lymph node | Clontech | ALN001 | 20-21 28-29 34-35 37 40-42 80-87 89-98 100-109 112-117 282-284 335-337 349-351 365 367 387 389-396 432 448-454 456 476-479 488 500-504 506 518-524 536-538 540 552-554 603-604 606 618-620 645 649 747 753 769 846-849 856 923-927 939-943 954 973 979 999-1000 1019 1021 1029-1030 1041 1052 1056-1057 1063 1070-1072 1083 1089 1100 1111 1115-1118 1122 1124-1125 1129 1131 1133-1135 1140 1167-1172 1310-1313 1427 1447 1473-1475 1498 1576-1578 1595 1604-1606 1648-1652 1680 1768-1771 1775-1777 1782 1843 1845 1850 1861 1870 1887 1935 2137 2143 2162-2163 2200 2216 2218 2232-2233 2289-2294 2319 2322-2327 2345-2346 2350 2352-2356 2359-2361 2363-2365 2387-2388 2425-2427 2449 2466-2469 2490-2491 2563 2575 2590-2594 2607-2611 2632-2634 2682 2694 2744-2745 2750-2753 2763 2787 2795 2803-2804 2856 2865 2876 2910-2914 2955 2977 2982-2987 3010 3020-3022 3039-3040 3043-3050 3095 3116-3117 3127-3132 3218-3219 3260-3264 3311 3412-3415 3417 3419 3439 3499-3501 3521-3523 3575-3576 3579-3580 3592-3596 3600 3677 3679 3713-3714 3717-3718 3720-3722 3760 3769 3774 3776 3786 3797 3799 3913-3915 3937-3940 3944 3955 3967 4102-4103 4106-4108 4114-4120 4250-4258 4316 4357 4368 4379 4411 4436 4478 4575 4577-4579 4587 4599 4610 4616-4617 4633-4642 4644-4649 4677-4679 4688-4689 4745 4870-4871 4904 4978-4980 5020 5075-5076 5078-5081 5105 5107-5120 5224 5265-5266 5292-5294 5312-5313 5356 5486-5489 5531-5533 5563 5573 5594 5605 5616 5627 5645-5648 5653-5656 5667-5671 5841-5845 5875-5878 5962-5963 5987-5988 6005-6007 6022 6025-6029 6073 6104-6106 6148-6152 6179 6260-6265 6267-6274 6283-6285 6399 6410 6508 6553-6554 6615 6619-6621 6679 6778 6780-6781 6803 6920-6921 6984-6987 6998 7069-7070 7098-7107 7109 7231 7241 7252 7257-7258 7270 7314-7316 7356 7377-7379 7453-7460 7508 7587-7589 7688 7708 7719 7801-7803 7820 7839 7895-7897 7969-7973 8044-8046 |
| young liver | GIBCO | ALV001 | 16-17 28-29 118-121 192-193 223-232 268 270-273 282-284 295-301 318-320 326-328 335-337 352-354 356-359 368-374 376 378-381 387 389-397 431 433-435 444 455 477 488 492-493 501-504 506 508-515 517 536-537 540 547-549 551-554 557-558 574-580 586-593 595-596 602 613-614 616 627-629 637-644 650-655 666 668 689 700 708-709 720 722-723 731 742 782 844-845 851 863 872-874 884-885 893-895 900 902 923-927 945 969 973 1006-1009 1037-1040 1042-1043 1101-1103 1110 1112 1115 1124-1125 1136 1165 1177-1179 1191 1213-1214 1216-1218 1226 1228-1230 1236-1237 1246 1264-1265 1267-1268 1279-1281 1294-1295 1297-1301 1339-1340 1346-1348 1350-1359 1361-1363 1365-1369 1374-1375 1416-1418 1424-1426 1447 1450 1458-1461 1472 1476-1477 1486-1493 1495-1496 1498 1514 1523-1524 1570 1589-1590 1592-1594 1601 1603 1612 1614-1619 1640-1643 1690 1698-1699 1703-1704 1706 1715 1717-1718 1782-1789 1798 1809 1823-1824 1845-1846 1862-1863 1867 1874-1876 1881 1891-1901 1907-1909 1935 1938-1940 1992-1995 2039-2040 2105 2114-2118 2120-2127 2143 2177- |

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| adult liver | Clontech | ALV003 | 55 299-301 641-644 649-653 872-874 1941-1945 2136 2285-2286 2641-2642 3171-3172 3468-3469 4063 4067-4068 4104-4105 5233 7186 7197 7808-7810 7849 |
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| adult placenta | Clontech | APL001 | 71-72 223-228 246-248 250-259 261-264 268 270-273 368-373 387 389-396 431-432 434-441 476 478-479 500 538 618-620 645 686- 688 690-691 753 856 900 902 954 1005 1031-1035 1087-1088 1090- 1094 1276-1278 1328-1331 1526 1782 1952-1957 1960-1961 2124- 2127 2143 2359-2361 2412-2417 2419-2423 2464-2469 2564-2565 2682 2708 2777 2784 2796 2898 2909 3026-3034 3036-3038 3328 3330 3433-3434 3575-3576 3579-3580 3585-3586 3969-3971 3990 3996 4017-4020 4091-4097 4155-4156 4298-4301 4303 4512 4571- 4574 4743 4754 4820 4847-4853 4919 4981-4984 4986-4989 5027 5078-5081 5139 5197-5202 5250 5312 5329-5330 5360 5471 5582 5587-5588 5641-5642 5674 5693 5802 5961 6022 6025-6032 6039 6235-6237 6319-6320 6322-6331 6341-6342 6344 6404 6408-6409 6519 6525-6529 6583-6584 6901 7043 7079-7080 7273 7275 7692- 7695 7702 7815 |
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| Genomic DNA from BAC 63118 | Research Genetics (CITB BAC Library) | BAC001 | 2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876 7944-7947 |
| Genomic DNA from BAC 39316 | Research Genetics (CITB BAC Library) | BAC002 | 2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 5056-5060 5062 |
| Genomic DNA from BAC 39316 | Research Genetics (CITB BAC Library) | BAC003 | 2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876 7944-7947 |
| adult bladder | Invitrogen | BLD001 | 40-42 123-124 329-331 476 478-479 552-554 571 573 682-683 708 710-719 782 816 818 935-936 963-965 967-968 973 1070-1071 1113 1115-1118 1120-1121 1123 1156-1160 1165 1198-1201 1264-1265 1341-1344 1355-1359 1361-1363 1395-1399 1470-1471 1478 1640-1641 1686-1689 1779 1781 1795 1895-1901 1915-1918 1965-1967 1977-1978 1980-1989 1991 2002-2008 2039-2040 2114-2117 2188-2195 2197-2199 2220-2223 2234-2238 2240-2242 2276 2345-2349 2464-2469 2690-2694 2764 2767-2768 2787 2789-2791 2835 2837 2842-2843 2849-2850 2853-2854 2857-2858 2910-2914 2975-2976 3073-3077 3141-3142 3217 3385 3396 3669 3678 3688 3766 3937-3940 3996 4035-4039 4044 4172-4173 4176 4218 4220 4295 4377 4380-4382 4488 4806-4808 4810 4827-4831 4837 4847-4853 5138 5270-5271 5376-5380 5470 5654-5656 5873-5874 5918-5919 6201 6245 6560-6561 6836 6851-6854 6919 6978-6979 7054 7300-7301 7393-7395 7462-7465 7491 7760 |
| bone | Clontech | BMD001 | 1 22-23 28-29 39-42 44 52 55-56 61-65 67 71-72 74-76 80-98 100- |

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| marrow | | | 109 112-117 155 166 176 178-187 189-190 223-233 237-239 246- 248 250-259 261-266 268 270-273 282-284 291 302 310 315-320 322-328 335-337 344 352-359 363-364 366 368-374 377 385-386 388 398-400 426-427 432-433 444-456 460-468 476-479 483-489 495-504 506-515 517-526 538 541-542 545-546 552-554 567-570 584-585 593 595-596 602-604 606 613-614 616 618-620 622 624 627-629 637-640 645 647-649 654-655 657-658 666 668 670-671 679-681 686-688 690-691 703 708 722-723 726-730 732-741 743- 745 747-749 753 757-764 766-771 782 844-845 851 854-858 867- 869 876-877 879-881 890 900 902 910 923-927 938-943 954 957- 959 969-970 973-976 978-979 990 998-1000 1006-1013 1019 1023- 1029 1031-1035 1037-1040 1042-1046 1050-1051 1056-1061 1063 1068-1080 1083 1089 1095-1103 1111 1115 1120-1125 1127-1131 1136-1145 1151 1156-1160 1174-1175 1177-1179 1181-1184 1191 1194 1197 1204 1213-1214 1216-1218 1221-1225 1227-1230 1236- 1237 1241-1242 1250 1253 1258 1261 1264-1265 1267-1268 1284- 1286 1291-1293 1303-1304 1310-1317 1319 1322 1334-1336 1341- 1344 1355-1359 1361-1363 1371 1380 1385-1387 1391 1395-1399 1401-1403 1410-1413 1423-1427 1438-1439 1442-1445 1447 1458- 1460 1462-1465 1473-1477 1479-1481 1498 1500 1503-1504 1506- 1507 1510-1513 1515 1517 1529-1533 1536 1538 1540 1543-1547 1550-1559 1561 1565-1566 1587-1588 1595-1600 1604-1606 1615- 1619 1625 1627 1648-1652 1674 1676-1678 1680 1686-1690 1701- 1704 1706 1718 1741-1745 1755-1760 1762-1763 1765-1773 1782- 1790 1792-1794 1796-1797 1825-1826 1828-1831 1843 1845 1866 1874-1887 1892 1904-1905 1911-1913 1922 1930 1935 1946 1948- 1957 1959-1961 1977-1978 1980-1989 1991-2000 2010-2011 2013- 2023 2027-2040 2081-2083 2085-2086 2088-2093 2103-2108 2124- 2127 2135-2137 2143 2155-2156 2158-2159 2162-2163 2171-2174 2177-2178 2180-2181 2188-2195 2197-2205 2207-2214 2216 2218 2225-2226 2230-2238 2240-2242 2282-2283 2285-2286 2317 2319- 2327 2332-2339 2341-2346 2350 2352-2361 2363-2365 2368 2371- 2372 2375 2381-2382 2387-2390 2401-2406 2408-2410 2425-2428 2430-2436 2438-2447 2449-2458 2460 2464-2469 2480 2494 2500- 2503 2505-2506 2533 2547-2548 2553-2554 2563-2565 2575 2585- 2589 2595-2599 2602 2607-2612 2621-2626 2628 2632-2634 2638 2664-2665 2667 2674-2677 2682-2686 2688 2695-2697 2699-2704 2708 2714-2717 2730-2733 2744-2745 2764-2765 2767-2768 2774- 2776 2778-2779 2781-2783 2785-2787 2789-2791 2803-2804 2806- 2807 2814-2820 2822 2898 2909 2933 2955-2960 2962-2971 2978- 2979 2981-2987 3016-3017 3020-3022 3039-3040 3055 3078-3080 3082-3091 3093 3095 3112-3113 3115-3117 3179-3180 3185-3190 3192 3212 3218-3219 3222 3233-3235 3238-3242 3249-3250 3262- 3264 3289-3295 3297 3299-3302 3325 3347 3355 3398-3400 3407- 3408 3412-3415 3418 3429 3433-3434 3440 3451 3453 3462 3467- 3469 3473-3474 3491-3493 3499-3501 3508-3509 3514 3516-3519 3521-3525 3527-3529 3560-3561 3563-3564 3574-3577 3579-3580 3585-3586 3588-3591 3597 3614 3668 3675 3679-3680 3683-3685 3695 3697 3708 3713-3714 3717-3718 3720-3722 3732 3749 3773- 3775 3783-3785 3788-3790 3802 3805 3816 3832-3833 3879-3880 3882-3883 3909-3910 3912 3951-3953 3979-3985 3990 4041 4053 4066 4075-4076 4078-4080 4091-4097 4102-4103 4122-4124 4133 4178-4185 4187-4196 4215 4218 4220 4231 4243 4248 4256-4258 4264 4285-4286 4295 4307-4308 4320-4323 4325 4329-4330 4332- 4333 4357 4368-4371 4377 4379 4385-4386 4389 4392-4395 4400 4424 4462-4464 4466-4467 4470 4473 4516-4519 4521-4522 4529 4537-4539 4554 4565 4571-4574 4576 4582-4585 4587 4598-4599 4610 4625 4628-4631 4633-4642 4644-4649 4651-4657 4702-4703 4705 4709 4726-4727 4740-4742 4745 4777 4781-4784 4802 4814- 4815 4837 4847-4853 4872-4873 4884-4885 4889-4897 4899 4906 4911 4927-4930 4932-4936 4945 4948-4951 4978-4980 5020 5051- 5052 5064 5075-5076 5087 5090-5093 5095 5099-5101 5107-5115 5117 5121-5123 5125-5126 5128-5130 5137 5141 5144-5146 5176- 5178 5197-5202 5210-5211 5265-5266 5272 5274 5276 5298 5329- 5330 5339-5352 5361 5372 5376-5380 5383 5385-5387 5391-5393 5395-5396 5399 5409 5443 5450-5454 5458 5462-5463 5468-5469 5482 5484-5485 5512-5513 5528 5534-5537 5539 5560 5566-5569 |

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| bone marrow | Clontech | BMD002 | 28-29 123-124 191 223-232 237-239 246-248 250-259 261-264 318-320 326-327 340-341 344 355 366 368-374 377 385-386 388 398-400 404-407 432 450-454 456 477 484-485 488 500 514-515 517 538 545-546 586-592 602-604 606-612 618-620 645 649 654-655 667 678 722-723 747 753 757-764 766-767 773 784 795 806 841-843 856 887-889 891 900 902 939-943 946-950 954 959 963-965 967-968 973 979 999-1000 1036-1040 1042-1043 1056-1057 1095 1115 1156-1160 1181 1191 1264-1265 1279-1281 1299-1301 1334-1336 1341-1344 1355-1359 1361-1363 1371 1377-1380 1391-1394 1402 1410 1424-1426 1432-1437 1447 1473-1475 1541-1542 1552-1558 1604-1606 1611 1628-1633 1635 1642-1643 1648-1652 1664 1690 1701-1704 1706 1718 1782-1789 1798 1809 1867 1881 1887 1892 1907-1909 1911-1913 1915-1918 1922 1938-1940 1992-1995 2016-2022 2037 2081-2083 2106-2108 2135-2137 2143 2155-2156 2158-2159 2185-2186 2188-2195 2197-2199 2201-2205 2207-2208 2232-2238 2240-2242 2246 2285-2286 2289-2294 2322-2327 2345-2346 2352-2356 2363-2365 2381-2382 2391-2394 2412-2417 2419-2423 2425-2427 2449 2454-2458 2460 2466-2469 2494 2496-2497 2503 2505-2506 2553-2554 2558-2562 2595-2597 2599 2617-2620 2625-2626 2628 2682 2699-2704 2744-2745 2764 2767-2768 2771 2803-2804 2822 2828 2836 2853-2854 2857-2858 2898 2909-2914 2982-2987 3003-3008 3010 3039-3040 3043-3050 3055-3063 3087-3091 3093 3116-3117 3179-3180 3209-3211 3213-3215 3223-3224 3262-3264 3358-3359 3416 3448 3473 3577 3728 3730 3732 3743 3893-3898 3913-3915 3937-3940 3954 3992 4003-4005 4016 4048-4049 4053 4066 4174 4191 4207 4209 4218 4220 4282 4316 4320-4323 4325 4329-4330 4336-4340 4392-4395 4516 4582-4585 4604-4605 4696 4814-4815 4847-4853 4872-4873 4884-4885 4892 4899 4928-4929 4940-4941 4943-4944 4948-4951 4978-4980 4985 4996 5010-5013 5069-5070 5099-5101 5107-5115 5117 5333-5335 5401-5404 5406-5407 5410 5531-5533 5645-5648 5654-5656 5667-5670 5694 5705 5752-5754 5807-5810 5841-5846 5848-5850 5861 5875-5878 5934-5935 5937-5938 6131-6132 6177 6181-6182 6198-6200 6206-6211 6231-6233 6256 6311-6313 6337-6338 6545-6546 6567 6698-6700 6709 6735 6849 6903 6906 6915 6917-6918 6920-6923 7002 7007-7010 7031 7098-7107 7109 7118 7121-7122 7231 7241 7251-7252 7321-7322 7377-7379 7393-7395 7440 7443-7445 7453-7460 7462-7465 7469 7479-7480 7517 7542 7659 7664-7665 7708 7719 7771-7772 7774 7808-7810 7821 7893-7894 7987 8024 8034-8035 |
| bone marrow | Clontech | BMD004 | 7 9-11 178-179 722-723 747 973 2136 2341-2344 2389-2390 2455-2458 2955 4053 4066 4183-4185 4892 5818-5820 6922-6923 7377-7379 7808-7810 7893-7894 |

| Tissue Origin | Tissue/ RNA Source | Library Name | SEQ ID NO: |
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| bone marrow | Clontech | BMD007 | 28-29 363-364 460 474-475 552-554 1540 2106-2108 2136 2425-2427 2672-2673 2677 2682 2765 2822 4053 4066 5137 5141 5980 5991 6002 6012 6024 6922-6923 7186 7197 7453-7460 7469 8034-8035 |
| adult colon | Invitrogen | CLN001 | 66 77 311-314 323-327 404-407 476 478-479 484-485 663-664 823-825 844-845 872-874 969 979 1036 1110 1112 1177-1179 1213-1214 1216-1218 1279-1281 1371 1380 1391 1395-1399 1402 1410 1523-1524 1528 1565-1566 1628-1633 1635 1642-1643 1657-1663 1705 1715-1717 1727 1747-1748 1751-1754 1867 1895-1901 1923-1924 1926-1929 1974 2039-2040 2081-2083 2102 2162-2163 2389-2390 2428 2430-2432 2466-2469 2699-2704 2710 2712 2792 2795 2808-2812 2900-2908 2955 3081 3092 3103 3114 3179-3180 3278-3279 3310 3732 3741-3742 3840-3842 3979-3985 4238 4336-4340 4369-4371 4436 4537-4539 4571-4574 4618-4619 4726-4729 4734-4735 4737-4739 4777 4805-4808 4810 4837 4976-4977 5155 5212-5215 5225 5298 5401-5404 5406-5407 5531-5533 5631-5632 5638 5696-5699 5761-5763 5789-5790 5918-5919 5952-5954 6022 6025-6029 6163 6171-6173 6181-6182 6235-6237 6284 6331 6333-6335 6353 6356-6358 6450-6451 6453 6525-6529 6578-6579 6681 6687-6688 6721 6973-6977 6988-6989 7087-7089 7340 7453-7460 7587-7589 7790 7942 7989-7990 |
| mixture of 16 tissues-mRNAs* | various vendors* | CTL016 | 297-298 426-427 477 488 528-529 552-554 658 722-723 988 994 1037-1040 1042-1043 1124-1125 1146-1148 1904-1905 2284-2286 2563 3039-3040 4526-4527 4659-4663 4952 4954-4958 5594 5605 5616 5627 6755-6758 7377-7379 7808-7810 |
| mixture of 16 tissues-mRNAs* | various vendors* | CTL021 | 7 28-29 294 376 378-381 436-441 476 478-479 484-485 533-535 552-554 844-845 852-853 1299-1301 1585-1586 2016-2022 2136-2137 2185-2186 2204-2205 2207-2208 2284 2377-2378 2535-2538 2540-2543 3171-3172 3234-3235 3548 3560 4256-4258 4892 4952 4954-4958 5107-5115 5117 5599-5602 5694 5705 6109 6260-6265 6267-6274 6420 6422 6574 6585 6915 6917-6918 6939-6942 7377-7379 7453-7460 7808-7810 7841-7842 |
| mixture of 16 tissues-mRNAs* | various vendors* | CTL028 | 4017-4020 7808-7810 |
| adult cervix | BioChain | CVX001 | 9-11 21 28-29 40-44 55-56 66 77 80-87 89-98 100-109 112-117 122-124 178-179 181-183 202-203 215-217 229-232 246-248 250-259 261-264 268 270-273 311-314 318-320 323-325 333 335-339 360-361 374 382-383 398 400 404-409 432 442-443 445-454 456 466 476 478-479 486-487 489 492-493 501-504 506 514-515 517 522-524 538-539 541-542 550 555-556 571 573-582 586-593 595-596 602 607-612 630-633 635-636 645 647-649 658-662 666 668 670-671 704-706 708 722-725 727-728 747 753 768-769 771-772 774-775 780-781 785 816 818 820-821 837 854-856 858-863 867 869 880-881 884-885 905-909 911-912 915-917 923-927 937 939-943 954 959 969-970 973 979 990-993 995-997 1019 1021 1030-1035 1041 1052 1056-1057 1063 1068-1072 1083 1089 1096-1103 1111 1114-1118 1122 1124-1125 1129-1130 1140 1165 1167-1172 1174-1176 1183 1185-1190 1194 1204 1211-1212 1221-1225 1227-1230 1236-1237 1254-1256 1267-1268 1286-1287 1289 1291-1293 1303-1304 1314-1316 1328-1331 1334-1336 1341-1344 1355-1359 1361-1363 1369-1370 1372-1373 1377-1379 1382-1390 1395-1399 1408 1416-1418 1423-1426 1428 1430 1446 1457-1460 1462-1465 1470-1471 1473-1478 1503-1504 1506-1507 1515 1534-1535 1543-1547 1549 1560 1564-1566 1572-1575 1580 1591 1595 1621-1623 1640-1643 1657-1663 1674 1676-1678 1690-1693 1695-1696 1698-1699 1703-1709 1716 1718 1727 1755-1760 1762-1763 1768-1771 1773-1774 1782-1789 1799-1804 1820 1825-1831 1836-1837 1839-1843 1845 1847-1848 1850-1851 1861-1867 1870 1874-1880 1882-1890 1895-1901 1907-1909 1931-1934 1946 1948-1951 1974 2010-2011 2013 2016-2022 2039-2040 2076 2085-2086 2088-2093 2105-2108 2110-2112 2124-2127 2137 2147-2156 2158-2159 2162-2166 2169-2174 2177-2178 2180 2188-2195 2197-2200 2204-2205 2207-2208 2216 2218 2230-2238 2240-2242 2284 2322-2327 2341-2344 2347-2350 2352-2356 2359-2361 2401-2406 2408-2410 2412-2417 2419-2423 2428 2430-2434 2452-2458 2480 2494-2499 2503 2505-2506 2515-2516 2518-2527 2533 2551-2552 2555 2557-2565 2569-2571 |

| Tissue Origin | Tissue/ RNA Source | Library Name | SEQ ID NO: |
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| diaphragm | BioChain | DIA002 | 229-232 335-337 385-386 436-441 708 923-927 1006-1009 1211- 1212 1299-1301 1498 1541-1542 2806-2807 3560 4250-4255 4884- 4885 6763 7289-7290 7987 |
| endothelial cells | Stratagene | EDT001 | 9-11 21 24-25 28-29 36 40-45 47 49-51 55-56 66 77-79 168-169 178-179 191-195 215-217 229-233 237-239 246-248 250-259 261- 266 268 270-273 282-284 311-320 323-325 329-331 335-337 340- 341 344 349-361 365-373 375 377 387-400 404-409 423 426-431 433-449 455 461-465 467-468 477 486-489 492-493 500 508-515 517-524 528-529 545-546 552-554 567-570 574-580 584-585 593 595-600 602-604 606-614 616 618-620 622 624 627-629 637-640 |

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| Genomic clones from the short arm of chromosome 8 | Genomic DNA from Genetics Research | EPM001 | 2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876 |
| Genomic clones from the short arm of chromosome 8 | Genomic DNA from Genetics Research | EPM003 | 2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3628-3629 3916-3921 3923-3932 3934-3936 |
| Genomic clones from the short arm of chromosome 8 | Genomic DNA from Genetics Research | EPM004 | 2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3628-3629 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876 5928' 7023 |
| esophagus | BioChain | ESO002 | 28-29 40-42 164-165 477 488 622 624 1110 1112 1115 2232-2233 3567 5752-5754 5918-5919 7289-7290 7808-7810 8024 |
| fetal brain | Clontech | FBR001 | 178-179 323-325 1116-1118 1202-1203 1205-1207 1395-1399 1409 1428 1430 1486-1488 1694 1697 1701-1702 1737 1739-1740 1782 2024-2026 2147-2152 2710 2712 2899 2919 3023 3025 3087-3091 3093 3116-3117 3150 3322 3585-3586 3717-3718 3720-3722 3732 3867-3870 4021 4329-4330 4341 4805 4884-4885 4906 5641-5642 5760 5771 5782 6702-6703 6934-6937 7587-7589 7790 |
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| fetal brain | Clontech | FBR006 | 2 16-17 55 110 144 164-165 180 211-212 221 229-232 246-248 250-259 261-264 321 335-337 360-361 365 367 387 389-396 428-430 432 436-441 448-449 466 495-497 528-529 536-540 550 552-556 559-560 562 567-570 574-580 603-604 606-612 622 624 637-640 645 654-655 663-664 670-671 685-688 690-691 722-723 732-741 743-745 753 757-764 766 841-843 856-857 868 872-874 879-881 883-885 890 896-900 902 905-909 919-921 929 954 969 988 994 999-1000 1006-1009 1073-1080 1101-1110 1112 1137-1139 1141-1145 1156-1160 1167-1172 1177-1179 1181 1191-1193 1195-1196 1211-1212 1221-1225 1227 1231-1232 1251 1264-1265 1299-1301 1337 1355-1359 1361-1363 1365-1368 1420 1428 1430 1440 1462-1465 1473-1475 1486-1488 1499 1541-1542 1548 1559 1561 1604-1606 1611 1628-1633 1635 1640-1643 1653 1680 1686-1690 1698-1699 1701-1704 1706 1790 1792-1794 1823-1826 1828-1831 1838 1845 1872-1873 1895-1901 1904-1905 1911-1914 1923-1934 1936 1946-1951 1992-1995 2001 2012 2024-2026 2064 2085-2086 2088-2091 2097 2099-2100 2103-2104 2106-2108 2114-2117 2128-2129 2131-2134 2153-2154 2171-2174 2177-2178 2180-2181 2188-2195 2197-2200 2209-2214 2230-2231 2234-2238 2240-2242 2289-2294 2319 2347-2349 2352-2356 2359-2361 2380-2382 2425-2428 2430-2432 2435 2466-2469 2515-2516 2518-2527 2558-2562 2595-2597 2617-2620 2625-2626 2628 2632-2636 2639-2640 2643-2644 2682-2686 2688 2698 2705 2710 2712 2729 2738 2744-2746 2750-2753 2757 2761 2764 2767-2768 2774-2776 2808-2812 2814-2820 2835 2837 2842-2843 2853-2854 2857-2858 2898 2900-2909 2915-2917 2943-2944 2955-2960 2982-2987 3003-3008 3011-3012 3014 3039-3040 3056-3063 3070-3077 3087-3091 3093 3100-3102 3104-3105 3116-3117 3123-3125 3127-3132 3151-3158 3179-3180 3218 3223-3224 3230 3234-3235 3260-3261 3310 3331 3349 3363 3374 3431-3432 3439 3454-3456 3462 3470 3474 3592-3596 3623 3696 3698-3702 3732 3772 3775 3796 3806-3807 3809-3810 3861 3867-3871 3878 3881 3893-3898 3937-3940 3944 3955 3967 4002-4005 4015 4017-4020 4030-4031 4033 4048-4049 4083-4085 4102-4103 4128 4134 4183-4185 4260-4263 4309-4310 4326-4328 4336-4340 4352-4354 4357 4363-4366 4368-4371 4379 4391 4433 4443 4464 4466-4467 4486 4516 4560 4564 4566-4568 4659-4663 4675 4781-4784 4789 4796-4797 4814-4815 4837-4841 4847-4853 4884-4885 4920 4931 4948-4958 4985 4995-4996 5048-5049 5099-5101 5125-5126 5128-5130 5149 5193-5194 5196-5202 5319-5322 5401-5404 5406-5407 5411 5482 5484-5485 5800-5801 5841-5845 5875-5878 5894 5895 5913 5934-5935 5937-5938 5941-5942 6022 6025-6029 6037-6038 6052-6054 6107 6112 6133 6136 6153-6154 6157 6195-6196 6198 6242-6243 6306-6309 6333-6335 6353 6356-6358 6394 6494 6505 6560-6561 6624-6625 6781 6804 6806 6837 6839-6848 6890-6892 6903 6906 6946-6947 6966 6982 6984-6987 7007-7010 7012-7014 7016 7027 7113-7115 7119 7168 7185 7187 7230 7340 7428-7429 7431-7434 7474-7475 7616 7644 7655 7694 7696 7698-7700 7794 7805 7847 7871-7872 7882-7883 7886 7921 7941-7942 7976 7981-7982 7989-7995 8034-8037 8044-8046 |
| fetal brain | Clontech | FBRs03 | 1400 1690 2638 3042 5149 6198 7366 7377-7379 7808-7810 |
| fetal brain | Invitrogen | FBT002 | 40-42 47 60 69-73 178-179 210-212 237-239 265-266 311-314 335-337 360-361 374 387 389-397 466 477 486-489 500 541-542 603-604 606-614 616 627-629 654-655 744-745 826-827 841-845 872-874 900 902 969 973 979 999-1000 1087-1088 1090-1094 1110 1112 1119 1156-1162 1164 1174-1175 1191-1193 1195-1196 1221-1225 1227 1241-1242 1264-1265 1305-1306 1308-1309 1314-1317 1319 1338 1346-1348 1350-1359 1361-1363 1369 1376-1379 1381 1395-1399 1405-1406 1415 1428 1430 1432-1439 1442-1445 1479-1481 1484-1485 1523-1524 1528 1534-1535 1552-1558 1562-1563 1601 1603 1612 1614-1619 1638-1641 1686-1693 1695-1696 1700 1703-1704 1706 1718 1730-1731 1763 1765-1767 1790 1792-1794 1823-1824 1844 1874-1876 1895-1901 1904-1905 1911-1913 1930-1934 1938-1940 1962 1996-2000 2010-2011 2013 2024-2033 2035-2036 2041 2052 2094-2097 2099-2100 2106-2108 2128-2129 2131-2134 2147-2152 2164-2166 2169-2174 2177-2178 2180-2181 2234-2238 2240-2242 2289-2294 2322-2327 2374 2381-2382 2385 2395-2400 2407 2418 2429 2437 2448 2459 2463 2466-2470 2480 2482 |

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| fetal lung | Clontech | FLG004 | 265-266 476 478-479 552-554 1056-1057 1165 1365-1368 1424-1426 1552-1558 1690 2699-2704 3260-3261 7118 7121 |
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| fetal liver- spleen | Columbia University | FLS003 | 7 28-29 223-228 268 270-273 299-301 376 378-383 557-558 844- 845 923-927 1355-1359 1361-1363 2136 2284 2584 2699-2704 2795 3123-3125 3468-3469 3560 3562 4053 4066 4091-4097 4183-4185 6364-6365 6367 7116 7186 7197 7263 7274 7850 7852-7861 7893- 7894 |
| fetal liver | Invitrogen | FLV001 | 7 49-51 55 78-79 223-228 237-239 265-266 282-284 295-301 309 311-314 335-337 363-364 375-376 378-383 387 389-397 433 444 455 460 474-475 480-482 495-497 536-537 540-542 586-592 613- 614 616 650-655 666 668 679-681 707-708 724-725 744-745 757- 764 766 816 818 822-825 840-845 872-874 900 902 919-921 945 963-969 979 999-1000 1011-1013 1047-1048 1051 1110 1112 1151- 1152 1163 1174-1175 1177-1179 1191-1193 1195-1196 1211-1214 1216-1218 1299-1301 1338-1340 1346-1348 1350-1359 1361-1363 1381 1405-1406 1514 1552-1559 1561 1585-1586 1589-1590 1592- 1594 1601 1603 1628-1633 1635 1642-1643 1698-1699 1703-1704 1706 1747-1748 1751-1754 1763 1775-1777 1850 1861 1870 1895- 1901 1904-1905 1923-1924 1926-1929 1938-1940 1962 1977-1978 1980-1989 1991 2063 2106-2108 2124-2127 2136 2177-2178 2180 2185-2186 2284-2286 2380-2382 2389-2395 2397-2400 2425-2428 2430-2432 2435 2476-2478 2480 2494 2503 2505-2507 2528 2533 2539 2545 2556 2567 2600-2601 2682 2730-2733 2787 2994-2997 3015 3039-3040 3043-3050 3052 3100 3151-3155 3173-3177 3244 3256 3266-3267 3274 3285 3296 3299-3302 3355 3436-3437 3449- 3450 3452 3468-3469 3506 3562 3610-3612 3620-3622 3743 3745 3829 3849 3944 3955 3967 4053 4064 4066 4087 4089-4097 4104- 4105 4138-4142 4144-4146 4150-4153 4172-4173 4176 4183-4185 4234-4235 4326-4328 4357 4368 4379 4445 4459 4491-4493 4516 4533-4539 4544-4546 4659-4663 4693 4728-4729 4806-4808 4810 4814-4815 4847-4853 4874-4875 4877-4880 4953 4981-4984 4986- 4989 5010-5013 5073-5074 5144-5146 5189-5190 5197-5202 5204- 5205 5207 5216 5218-5221 5270-5272 5274 5401-5404 5406-5407 5416 5427 5531-5533 5677 5703-5704 5747-5748 5760 5771 5782 5934-5935 5937-5938 5961 5987-5988 6030-6032 6104-6106 6145 6199-6200 6300-6303 6333-6335 6339-6340 6377 6388 6399 6410 6412 6420 6422 6450-6451 6453-6454 6470-6471 6499-6501 6607 6618 6654 6656 6704-6705 6755-6758 6765 6869 6872-6875 6922- 6923 6959 6968 6973-6977 6982 6984-6987 7012-7013 7016 7063 7069-7070 7118 7121 7186 7194-7195 7197 7262-7263 7274 7310- 7311 7393-7395 7427 7462-7465 7467-7468 7543-7544 7677 7686 7697 7771-7772 7795-7796 7808-7810 7837-7838 7847 7874-7879 7949-7952 7963 7993-7995 8041 |
| fetal liver | Clontech | FLV002 | 432 538 645 753 852-853 856 954 1654 1749 1849 2412-2417 2419- 2423 2898 2909 3118-3119 3575-3576 3579-3580 3837 |
| fetal liver | Clontech | FLV004 | 28-29 61-65 78-79 184-187 189-190 299-301 385-386 547-549 551 602 650-653 658 722-723 748-749 939-943 999-1000 1006-1009 1124-1125 1589-1590 1592-1594 1596-1600 1698-1699 1701-1704 1706 1782 1938-1945 2027-2033 2035-2036 2136 2177-2178 2180 2200 2204-2205 2207-2208 2215 2220-2223 2234-2238 2240-2242 2285-2286 2332-2339 2380-2382 2391-2394 2584 2600-2601 2714- 2715 2803-2804 2925-2929 2938-2939 2941-2942 2982-2987 3116- 3117 3122 3133 3171-3172 3506 3937-3940 4060-4062 4104-4105 |

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| fetal muscle | Invitrogen | FMS001 | 237-239 246-248 250-259 261-264 318-320 323-325 332 334-337 363-364 382-383 476 478-479 518-524 555-556 571 573 654-655 666 668 674-676 710-719 724-725 744-745 757-764 766 782 876-878 887-889 891 903-909 930 963-965 967-968 1058-1061 1073-1080 1087-1088 1090-1094 1104-1109 1115 1119 1165 1177-1179 1202-1203 1205-1207 1213-1214 1216-1218 1266 1287 1289 1303-1306 1308-1309 1339-1340 1355-1359 1361-1363 1374-1375 1381 1448-1449 1451-1456 1462-1465 1484-1485 1529-1533 1563 1595 1671-1672 1705 1714 1716 1718 1727 1747-1748 1751-1754 1765-1767 1850 1857-1861 1870 1888-1890 1910-1913 1930 1959 1974 1977-1978 1980-1989 1991 2016-2022 2063 2092-2093 2137 2164-2166 2169-2170 2224 2284 2289-2294 2425-2427 2533 2682 2694 2708-2709 2726-2728 2750-2753 2762 2787 2795 2852-2854 2857-2858 2900-2908 2910-2914 2930-2931 2973-2974 2998-3001 3039-3040 3052 3134-3135 3156-3158 3212 3222 3233 3288 3356-3357 3385 3396 3431-3432 3444 3499-3501 3506 3548 3560 3588-3589 3683 3745 3788-3790 3836 3993-3994 4063-4064 4067-4068 4083-4085 4133 4336-4340 4357 4368 4379 4436 4486 4491-4493 4526-4527 4532 4571-4575 4577-4579 4616-4617 4761 4827-4831 4837 4847-4853 4892 4969-4971 5056-5060 5062 5078-5081 5125-5126 5128-5130 5137 5141 5149 5155 5228 5239 5282-5283 5285 5436 5478-5480 5537-5539 5566-5569 5671 5684-5692 5694 5705 5752-5754 5821 5854-5857 5900-5901 5908-5909 5998-6001 6030-6032 6083-6084 6143-6144 6181-6182 6294 6420 6422 6440 6442-6446 6454 6605 6681 6763 6851-6854 6872-6875 6939-6942 6948 7007-7010 7087-7089 7191 7194-7195 7256 7289-7290 7298 7358-7359 7377-7379 7551-7553 7587-7589 7664-7665 7673-7675 7771-7772 7808-7810 7899-7900 7943 7987 8024 |
| fetal muscle | Invitrogen | FMS002 | 4-5 477 488 666 668 887-889 891 923-927 929 1056-1057 1266 1299-1301 1305-1306 1308-1309 1428 1430 1686-1689 1782 2063 2204-2205 2207-2208 2232-2233 2284 2425-2427 2956-2960 3052 4064 4508 5752-5754 7771-7772 7808-7810 |
| fetal skin | Invitrogen | FSK001 | 7 9-11 16-17 40-42 55 66 77-79 123-124 136-143 145-163 166 178-179 237-239 246-248 250-259 261-264 309 311-314 323-325 335-339 368-374 376 378-383 387 389-396 404-407 423 432-433 444 450-456 476-482 488 501-504 506 514-515 517 522-526 538 552-556 559-560 562 574-580 584-585 607-612 622 624 645 647-649 654-655 658 666 668 684 686-688 690-691 704-706 708 710-719 722-723 753 767 771 780-782 785 829-832 840-845 856 864-867 869 872-874 887-889 891-892 900 902 911-912 923-927 935-936 945-948 954 963-965 967-969 979-985 988 994 1015-1017 1022 1031-1035 1051 1056-1061 1063 1072-1080 1083 1089 1100 1110-1112 1114-1119 1122 1129 1132 1140 1151 1161-1162 1164-1165 1177-1179 1211-1212 1221-1225 1227-1230 1264-1265 1287 1289 1305-1306 1308-1309 1317 1319 1328-1331 1355-1359 1361-1363 1374-1375 1381 1395-1399 1428 1430 1447 1458-1460 1470-1471 1484-1485 1489-1493 1495-1496 1514 1539 1541-1542 1550-1558 1572-1578 1580 1591 1601 1603 1621-1622 1625 1644-1646 1655 1657-1663 1665-1666 1674 1676-1678 1681-1684 1690-1693 1695-1696 1701-1709 1716 1727 1738 1746-1748 1750-1754 1765-1767 1782 1790 1792-1797 1843 1845 1857-1860 1866 1874-1876 1888-1890 1895-1901 1904-1905 1910 1922 1931-1934 1937 1964 1974 1977-1978 1980-1989 1991-1995 2002-2008 2010-2011 2013 2023 2027-2036 2039-2040 2063 2081-2083 2085-2086 2088-2093 2109 2114-2118 2120-2123 2137 2141 2146-2152 2157 2164-2166 2168-2170 2177-2180 2187-2199 2204-2208 2216-2218 2224-2226 2228 2234-2242 2244 2253 2265 2282-2284 2319 2331 2352-2356 2359-2361 2380-2382 2387-2388 2450-2451 2463 2480 2494 2498-2499 2528 2533 2539 2545 2556 2564-2565 2567 2599 2613-2615 2627 2629-2631 2639-2640 2646-2654 2656-2663 2679-2686 2688 2706-2709 2729 2738 2746 2750-2760 2762 2774-2777 2784 2792 2794 2806-2812 2822 2846 2849-2850 2855 2859-2860 2938-2939 2941- |

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| fetal spleen | BioChain | FSP001 | 28-29 385-386 450-454 456 552-554 593 595-596 649 730 1056- 1057 1264-1265 1498 2185-2186 2232-2233 2345-2346 4516 4554 4565 4576 5416 5427 6161-6162 6735 7231 7241 7252 7808-7810 7966 |
| umbilical cord | BioChain | FUC001 | 7 28-29 40-42 55 71-72 123-124 155 166 178-179 194-195 223-232 237-239 246-248 250-259 261-266 302 309 323-325 329-331 335- 337 363-365 367 382-383 387 389-397 404-409 411-420 422 432- 433 442-444 455 460-465 467-468 476-479 488 500 514-515 517 522-524 538 571 573 584-592 597-600 602-604 606 618-620 627- 633 635-640 645 647-649 654-655 658-662 666 668 686-692 700 707-709 720 731 742 753 757-764 766 771 833-835 841-843 856 859-862 867 869 872-874 880-881 892-895 905-909 911-913 923- 927 929-930 935-936 954 963-965 967-969 973 979 987-988 994 |

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| infant brain | Columbia University | IB2002 | 4-5 9-11 39-45 55 66 71-72 77 126-130 205-206 213-220 229-233 237-239 246-248 250-259 261-266 309 323-328 335-337 340-341 344 355 360-361 366 368-373 377 382-383 387-397 399 428-432 434-441 448-454 456-459 461-465 467-468 476-482 488 495-497 514-515 517 528-529 538 541-542 552-554 571 573-580 586-592 607-612 618-620 622 624 627-633 635-636 645 649 654-655 658 665-666 668 674-676 685-692 695-702 709 720 722-725 731-743 753 771 773 780-782 784 795 806 823-825 829-832 844-849 852- 863 868 872-874 879-881 883-885 890 900 902 911-912 915-917 919-921 923-927 930 945-950 954 969-970 979-985 1006-1009 1015-1017 1020 1022 1031-1035 1037-1040 1042-1043 1049 1056- 1057 1070-1071 1073-1081 1086 1096-1099 1113 1116-1121 1123 1146-1148 1152 1161-1165 1177-1179 1181-1182 1184 1202-1203 1205-1207 1213-1214 1216-1218 1231-1232 1236-1238 1241-1242 1264-1265 1279-1281 1283 1286-1287 1289 1291-1293 1299-1301 1303-1309 1314-1316 1322 1334-1336 1341-1344 1346-1348 1350- 1359 1361-1363 1374-1375 1382-1390 1395-1399 1409 1411-1413 1415 1419 1424-1426 1438-1439 1442-1445 1447 1458-1460 1462- 1465 1470-1471 1479-1481 1486-1493 1495-1496 1521-1522 1534- 1535 1552-1559 1561 1567-1569 1571 1601 1603 1615-1619 1621- 1622 1628-1633 1635 1638-1641 1644 1646 1648-1653 1656-1663 1665-1672 1681-1684 1690-1700 1703-1704 1706 1711-1713 1718 1732-1736 1747-1748 1751-1754 1761 1763 1774 1782 1790 1792- 1794 1796-1798 1806 1809 1823-1826 1828-1831 1836-1837 1839- 1843 1846-1847 1856 1862-1865 1868-1869 1895-1901 1904-1905 1911-1913 1923-1924 1926-1929 1935 1941-1945 1977-1978 1980- 1989 1991 2024-2033 2035-2036 2039-2040 2097 2099-2100 2105 2114-2118 2120-2123 2128-2129 2131-2134 2137-2138 2141 2143 2145-2152 2155-2160 2164-2166 2168-2174 2177-2180 2185-2187 2196 2200 2204-2208 2216-2218 2220-2223 2225-2226 2228 2234- 2263 2265-2281 2284 2296 2307 2318 2329 2332-2340 2345-2346 2350-2356 2359-2361 2369-2370 2374 2380-2388 2396 2407 2412- 2427 2429 2437 2448 2454 2459 2466-2470 2480 2482 2485-2491 2500-2502 2515-2516 2518-2527 2529-2531 2533 2569-2571 2575 2584-2598 2600-2602 2606 2629-2631 2641-2642 2674-2676 2679- 2686 2688 2695-2697 2699-2704 2706-2707 2714-2715 2718-2721 2723-2725 2762 2764 2767-2768 2772 2774-2776 2781-2783 2785- 2786 2792 2798-2802 2808-2812 2814-2820 2827 2829 2834 2838- 2843 2853-2854 2857-2858 2899-2908 2921 2930-2932 2943-2948 2951 2955 2962-2971 2977-2979 2981-2987 3013 3054 3064-3067 3070 3081 3092 3095-3096 3100-3105 3107 3111 3114 3120-3122 |

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| infant brain | Columbia University | IB2003 | 9-11 40-42 71-72 126-130 229-232 237-239 323-325 360-361 398 400 428-430 436-441 445-447 457-459 476-479 488 552-554 574- 580 584-592 630-633 635-640 649 658 663-664 666 668 686-688 690-691 757-764 766 771 780-782 816 818 840-843 846-849 880- 881 884-885 900 902 930 969-970 999-1000 1006-1009 1015-1017 1022 1056-1057 1104-1109 1119-1121 1123 1177-1179 1183 1194 1198-1201 1204 1211-1212 1236-1237 1287 1289 1299-1301 1303- 1304 1307 1334-1336 1341-1344 1355-1359 1361-1363 1365-1368 1374-1375 1395-1399 1409 1415-1418 1529-1533 1567-1569 1571- 1575 1601 1603 1615-1619 1628-1633 1635 1648-1652 1657-1663 1686-1689 1703-1704 1706-1709 1711-1714 1718 1763 1780 1791 1825-1826 1828-1831 1846 1850 1861 1870 1887 1895-1901 1904- 1905 1923-1924 1926-1929 1996-2000 2010-2011 2013 2024-2033 2035-2036 2039-2040 2081-2083 2087 2114-2117 2137 2164-2166 2169-2170 2177-2178 2180 2185-2186 2204-2205 2207-2208 2225- 2226 2234-2238 2240-2243 2250 2296 2307 2318 2328-2340 2350- |

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| leukocyte | Clontech | LUC003 | 8-11 25 36 40-42 52 55 66 71-72 77 80-87 89-98 100-109 112-117 223-228 246-248 250-259 261-264 274-277 282-284 368-373 385-386 398 400 433 444 455 466 476 478-479 483 486-487 489 492-493 500 552-554 627-629 685 704-706 732-741 743 844-845 1005 1056-1057 1070-1071 1082 1115-1118 1133-1136 1146-1148 1156-1160 1185-1190 1236-1237 1291-1295 1297-1298 1355-1359 1361-1363 1385-1387 1395-1399 1424-1426 1458-1460 1499-1502 1517 1549 1560 1783-1789 1848 1851 1922 1977-1978 1980-1989 1991 1996-2000 2010-2011 2013-2015 2106-2108 2114-2117 2136-2137 2171-2174 2185-2186 2204-2205 2207-2208 2345-2346 2359-2361 2428 2430-2434 2445-2447 2460 2498-2499 2533 2564-2565 2580-2583 2595-2597 2632-2634 2638 2763 2898 2909 2982-2987 3039-3040 3070 3298 3355 3407 3411 3418 3429 3463 3499-3501 3521-3523 3575-3576 3579-3580 3610-3612 3713-3714 3763 3799 3845-3846 3909-3910 3912 3979-3985 4048-4049 4060-4062 4102-4103 4286 4357 4368 4379 4389 4400 4436 4484-4485 4568 4633-4642 4644-4649 4654 4688-4689 4734-4735 4777 4814-4815 4884-4885 4910 5087 5136-5137 5141 5342-5349 5351-5352 5462-5463 5560 5562 5571 5645-5648 5671 5675-5676 5812-5813 5815 5920 5962-5963 5987-5988 5998-6001 6022 6025-6029 6079 6090 6110 6120-6122 6153-6154 6181-6182 6260-6265 6267-6274 6441 6550 6552 6765 6795 6800 7011-7013 7016 7244 7261 7377-7379 7668 7670-7675 7771-7772 7808-7810 7817 7819 7969-7973 7984-7986 7988-7990 8044-8046 |
| melanoma from cell line ATCC #CRL 1424 | Clontech | MEL004 | 9-11 25 28-29 36 60-65 178-180 233 267 315-320 404-409 428-430 433 442-444 450-456 461-465 467-468 500 514-515 517-521 541-542 552-554 571 573 584-585 603-604 606 618-620 637-640 666 668 670-671 726 732-741 743 757-764 766 833-835 851 915-917 969 973 987-988 991-997 1018-1019 1058-1062 1120-1121 1123-1125 1131 1136 1167-1172 1176 1185-1190 1250 1253 1288 1355-1359 1361-1363 1377-1379 1381 1395-1399 1424-1426 1428 1430 1448-1449 1451-1456 1484-1485 1489-1493 1495-1496 1517 1541-1542 1572-1575 1648-1652 1657-1663 1680 1686-1689 1765-1767 1772 1782-1790 1792-1794 1843 1845 1868-1869 1877-1880 1882-1886 1903-1905 1922 1968-1969 1971-1972 2010-2011 2013 2038-2040 2081-2083 2085-2086 2088-2091 2105 2143 2162-2163 2181 2234-2238 2240-2242 2289-2294 2345-2346 2350 2359-2361 2381-2382 2425-2427 2433-2434 2450-2451 2503 2505-2506 2564-2565 2580-2583 2638 2646-2654 2656-2665 2667 2674-2676 2682 2744-2745 2781-2783 2785-2787 2795 2798-2802 2827 2829 2856 2865 2876 2982-2987 3043-3050 3071-3077 3081 3087-3093 3103 3111 3114 3116-3117 3123-3125 3212 3218 3220 3222-3224 3233-3235 3286 3342 3416-3417 3419 3439 3454-3456 3458-3459 3499-3501 3560 3600 3683 3713-3714 3717-3718 3720-3722 3743 3796 3802 3821-3822 3867-3870 3887 3891 3899 3954 4015 4133 4183-4185 4286 4309-4310 4336-4340 4344-4345 4347-4349 4357 4368 4372 4379 4415 4425 4440 4465 4488 4561 4628-4631 4671-4672 4702 4781-4784 4813 4817 4838-4841 4904 4907-4908 4910 4973 5014-5017 5056-5060 5062 5131-5132 5136-5137 5141 5303 5336 5520-5522 5577 5594 5605 5616 5627 5657-5659 5661-5663 5677-5680 5694 5705 5715 5717-5718 5814 5823 5825 5836 5847 5851-5852 5858 5873-5874 5914 6088 6143-6144 6153-6154 6260-6265 6267-6274 6336 6420 6422 6450-6451 6453 6479 6506-6507 6509 6583-6584 6586-6587 6643 6702-6703 6727 6755-6758 6804 6806 6851-6855 7108 7116 7120 7168 7194-7195 7408 7419 7461-7465 7472 |

| Tissue Origin | Tissue/ RNA Source | Library Name | SEQ ID NO: |
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| induced neuron cells | Stratagene | NTD001 | 40-42 246-248 250-259 261-266 335-337 411-420 422 428-430 555- 556 567-570 613-614 616 703 771 854-855 858 872-874 915-917 969 1006-1009 1018 1056-1057 1063 1072 1083-1085 1089 1100 1111 1122 1129 1140 1264-1265 1291-1293 1382-1384 1395-1399 1529-1535 1615-1619 1657-1663 1701-1702 1718 1772 1783-1790 1792-1794 1843 1847 1864-1865 1996-2000 2016-2022 2024-2026 2081-2083 2105-2108 2204-2205 2207-2208 2220-2223 2322-2327 2332-2339 2345-2346 2350 2363-2365 2369-2370 2575 2625-2626 2628 2638 2641-2642 2672-2673 2679-2682 2742-2743 2792 2798- 2802 2835 2837 2919 2938-2939 2941-2942 3011-3012 3014 3039- 3040 3056-3063 3096 3116-3117 3123-3125 3134-3135 3150-3155 3230 3354 3395 3560 3617 3889 3958-3964 3977 3990 4017-4020 4087 4089-4090 4256-4258 4289 4329-4330 4406 4446-4449 4547- 4548 4571-4574 4623-4624 4664 4666 4781-4784 4802 4811 4827- 4831 5137 5141 5272 5274 5448 5563 5566-5569 5631-5632 5644 5654-5656 5694 5705 5791-5792 5794-5799 5908-5909 6022 6025- 6029 6092 6186-6188 6191 6198 6260-6265 6267-6274 6294 6360 6413-6414 6424-6427 6658-6660 6662-6666 6727 6883 7049-7051 7130 7146 7328 7375 7377-7379 7386 7441 7641-7643 7790 7808- 7810 7996 |
| retinoic acid- induced neuronal cells | Stratagene | NTR001 | 9-11 28-29 178-179 323-325 431 434-441 477 486-489 559-560 562 666 668 844-845 949-950 969 1070-1071 1146-1148 1174-1175 1264-1265 1299-1301 1355-1359 1361-1363 1783-1789 1843 2200 2345-2346 4102-4103 4748 4791 5272 5274 7291-7293 7771-7772 7808-7810 |
| neuronal cells | Stratagene | NTU001 | 28-29 71-72 80-87 89-98 100-109 112-118 340-341 368-373 477 488 501-504 506 552-554 584-592 666 668 686-688 690-691 707 826-827 841-845 854-855 858 872-874 900 902 911-912 919-921 949-953 956 963-965 967-968 1006-1009 1011-1013 1015-1018 1056-1057 1124-1125 1156-1160 1243-1245 1264-1265 1299-1301 1303-1304 1346-1348 1350-1359 1361-1363 1438-1439 1442-1445 1458-1460 1552-1558 1572-1575 1587-1588 1601 1603 1621-1622 1703-1704 1706 1747-1748 1751-1754 1845 1862-1863 1895-1901 |

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| pituitary gland | Clontech | PIT004 | 66 77 318-320 382-383 461-465 467-468 518-521 613-614 616 649 666 668 980-985 1056-1057 1165 1202-1203 1205-1207 1228-1230 1257 1284-1285 1303-1304 1576-1578 1648-1652 1654 1701-1702 1711-1713 1749 1783-1789 1849 1857 1977-1978 1980-1989 1991 2002-2008 2039-2040 2106-2108 2234-2238 2240-2242 2345-2346 2350 2533 2553-2554 2563-2565 2575 2629-2631 2638 2682 2787 3096 3151-3155 3212 3218 3222 3233 3422 3499-3501 3521-3523 3560-3561 3602 3613 3732 3788-3790 3867-3870 3902 3976 3996 4024-4025 4035-4039 4391 4445 4549-4550 4552-4553 4625 4664 4666 4668-4669 4703 5125-5126 5128-5130 5136 5203 5452-5454 5478-5480 5681 5987-5988 5998-6001 6130 6183 6220-6221 6862 7062 7186 7197 7790 7871-7872 8044-8046 |
| placenta | Clontech | PLA003 | 205-206 282-284 385-386 552-554 844-845 1124-1125 2124-2127 2204-2205 2207-2208 2955 3026-3034 3036-3038 3732 4091-4097 4326-4328 5654-5656 5841-5845 6319-6320 6322-6330 6450-6451 6453 7808-7810 |
| prostate | Clontech | PRT001 | 40-42 214 233 282-284 318-320 408-409 426-427 436-441 450-454 456 500 518-521 567-570 581-582 584-585 593 595-596 618-620 637-640 647-649 658 672-673 707 726 732-741 743 872-874 969 1005 1031-1035 1037-1040 1042-1046 1056-1057 1086 1101-1103 1115 1165 1167-1172 1191 1221-1225 1227-1230 1258 1261 1305- 1306 1308-1309 1355-1359 1361-1363 1365-1368 1382-1384 1411- 1413 1416-1419 1447 1473-1475 1500 1541-1547 1550-1551 1559 1561 1580 1591 1612 1614-1619 1644 1646 1674 1676-1678 1686- 1689 1737 1739-1740 1775-1777 1783-1789 1823-1826 1828-1831 1843 1862-1863 1887 1904-1905 1910 1922 1941-1945 1968-1969 1971-1972 2010-2011 2013 2084-2086 2088-2091 2118 2120-2123 2136-2137 2144 2201-2203 2216 2218 2345-2346 2350 2359-2361 2389-2390 2425-2428 2430-2432 2450-2451 2464-2465 2480 2495 2500-2502 2533 2544 2546 2549-2552 2558-2562 2584-2586 2588- 2589 2627 2706-2707 2742-2745 2787 2789-2791 2795 2823-2824 2842-2843 2922 2924 2943-2944 2955 2982-2987 3095 3116-3117 3227-3229 3271-3272 3303 3305 3313 3398-3400 3436-3437 3485 3499-3501 3517-3519 3585-3586 3588-3589 3631 3679 3681 3732 3736-3737 3739 3755-3757 3766 3777 3783-3784 3802 3828 3851- 3852 4063 4067-4068 4072-4074 4183-4185 4286-4288 4341 4355- 4356 4358-4360 4387 4392-4395 4401 4404-4405 4433 4443 4464 4466-4467 4473 4505-4508 4628-4631 4650 4699-4701 4703 4753 4755-4756 4774-4775 4937-4939 4959-4962 4997-4998 5002-5006 5008-5009 5056-5060 5062 5090-5093 5095 5137 5141 5171-5172 5174-5175 5399 5420 5435 5457 5526 5573 5583 5610-5611 5949 5962-5963 5966-5967 6004 6007 6069 6198 6202-6203 6235-6237 6292 6333-6335 6443-6446 6479 6612 6687-6688 6735 6771 6782 6794 7087-7089 7238 7248 7284 7286-7287 7377-7379 7462-7465 7482 7499 7624-7627 7667 7738-7739 7928-7930 7932-7933 7987 8001 8034-8035 8044-8046 |
| rectum | Invitrogen. | REC001 | 40-42 123-124 265-266 282-284 323-327 387 389-396 404-409 411- 420 422-423 476 478-482 484-487 489 500 518-521 559-560 562 586-592 617 674-676 744-745 747 823-825 841-843 892 896-899 969 979 990 1022 1036 1115-1118 1120-1121 1123 1213-1214 1216-1218 1447 1479-1481 1563 1572-1575 1580 1591 1604-1606 1612 1614 1640-1643 1657-1663 1679 1686-1697 1703-1704 1706 |

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| salivary gland | Clontech | SAL001 | 2 55 110 178-179 181-183 221 237-239 246-248 250-259 261-264 282-284 321 323-325 328-331 335-337 340-343 345-348 476-479 484-485 488 508-513 545-546 552-554 649 663-664 708 747 773 784 795 806 838 844-845 859-862 872-874 1019 1036 1049 1081 1133-1135 1165 1202-1203 1205-1209 1211-1212 1303-1304 1328-1331 1346-1348 1350-1359 1361-1363 1427 1462-1465 1498 1657-1663 1681-1684 1698-1699 1730-1731 1772 1782 1843 1845 1877-1886 1892 1895-1901 1931-1934 2010-2011 2013 2039-2040 2136 2141 2146 2157 2168 2179 2187 2196 2206 2217 2228 2232-2242 2244 2253 2265 2352-2356 2359-2361 2363-2365 2504 2510 2517 2544 2546 2549-2550 2555 2557 2564-2565 2575 2600-2601 2638 2682 2690-2693 2699-2704 2787 2842-2843 2846 3011-3012 3014 3039-3040 3043-3050 3095 3116-3117 3160-3168 3179-3180 3212 3222 3233 3323 3398-3400 3425-3428 3431-3432 3560 3575-3576 3579-3580 3626 3639-3645 3647-3656 3658-3667 3670-3672 3696 3698-3702 3749 3799 4002 4009 4035-4039 4207 4209 4218 4220 4265 4357 4368 4379-4382 4389 4400 4487 4598 4625 4696 4726-4727 4737-4739 4745 4796-4797 4814-4815 4817 4884-4885 4976-4977 5082 5166-5167 5270-5272 5274 5337 5455 5482 5484-5485 5501-5504 5506-5509 5537 5539 5645-5648 5654-5656 5761-5763 5833-5834 5873-5874 5934-5935 5937-5938 6163 6293 6411 6443-6446 6547-6548 6771 6782 6794 6851-6854 7453-7460 7487-7489 7512 7779-7780 7808-7810 7922-7923 7993-7995 |
| salivary gland | Clontech | SALs03 | 484-485 613-614 616 887-889 891 1355-1359 1361-1363 2510 2517 6684 6695 7377-7379 7580 7590 7601 7612 7622 7633 |
| skin fibroblast | ATCC | SFB001 | 903-904 1355-1359 1361-1363 1874-1876 2533 2638 2682 2744-2745 3212 3222 3233 3260-3261 3417 3419 4526-4527 4561 6198 6260-6265 6267-6274 |
| skin fibroblast | ATCC | SFB002 | 584-585 903-904 1058-1061 1317 1319 1355-1359 1361-1363 1621-1622 2395 2397-2400 2638 3212 3222 3233 4102-4103 4369-4371 4526-4527 4745 5694 5705 6198 6260-6265 6267-6274 |
| skin fibroblast | ATCC | SFB003 | 477 488 584-585 1231-1232 1355-1359 1361-1363 2016-2022 4526-4527 5918-5919 6198 |
| small intestine | Clontech | SIN001 | 80-87 89-98 100-109 112-117 210 476 478-479 484-485 501-504 506 514-515 517 552-554 584-585 617 686-688 690-691 707 722-723 726 732-741 743 747 829-832 841-843 872-874 878 887-889 891 900 902 905-909 915-917 962 969 980-985 1005 1070-1071 1176 1247-1249 1286 1339-1340 1346-1348 1350-1354 1392-1394 1409 1420 1473-1475 1681-1684 1690 1703-1704 1706 1737 1739-1740 1775-1778 1796-1797 1848 1851 1881 1892 1895-1901 1935 2016-2023 2034 2137 2230-2231 2352-2356 2359-2361 2401-2406 2408-2410 2494 2564-2565 2613-2615 2708 2750-2753 2774-2776 2803-2804 2839-2841 2851 2855 2930-2931 2938-2939 2941-2942 2955 3020-3022 3144-3146 3149 3217 3255 3299-3302 3362 3385 3396 3422 3499-3501 3520 3560 3605 3614 3639-3645 3647-3656 3658-3667 3670-3672 3675 3717-3718 3720-3722 3732 3777 3803 3904-3905 3988-3989 4002 4201-4202 4271-4272 4281 4341 4433 4443 4445 4461 4490 4554 4565 4576 4607-4609 4611-4613 4628- |

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| skeletal muscle | Clontech | SKM001 | 7 178-179 229-232 246-248 250-259 261-264 323-325 332 334 404-407 428-430 476-479 488 627-629 744-745 748-749 771 773 784 795 806 863 878 880-881 887-889 891 900 902-904 911-912 919-921 990 1146-1148 1273-1275 1299-1301 1370 1372-1373 1395-1399 1498 1517 1596-1600 1714 1730-1731 1755-1760 1762 1845 1887 1895-1901 2027-2033 2035-2036 2105 2188-2195 2197-2199 2234-2238 2240-2242 2425-2427 2452-2453 2466-2469 2529-2531 2584 2716-2717 2744-2745 2950 2961-2972 2980 2991 3276 3430-3432 3468-3469 3548 3560 3581-3582 3615-3616 3937-3940 4010-4011 4016 4172-4173 4176 4244-4245 4320-4323 4325 4373-4374 4446-4449 4455 4650 4708 4711 4728-4729 4737-4739 4847-4853 4897 4969-4973 5441 5478-5480 5591-5593 5595-5596 5752-5754 6040-6042 6092 6443-6446 6553-6554 6601 6605 6715-6716 6933 7123-7125 7190 7289-7290 7512 7517 7551-7553 7738-7739 7779-7780 7987 8024 |
| skeletal muscle | Clontech | SKM002 | 584-585 887-889 891 903-904 1888-1890 3548 3592-3596 6260-6265 6267-6274 |
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| spinal cord | Clontech | SPC001 | 9-11 40-42 53 66 71-73 77 80-87 89-109 112-117 123-124 133 178-179 194-195 246-248 250-259 261-264 282-284 311-314 328 335-337 375 382-383 397 411-420 422 426-427 433 444-447 455 476-479 488 500 508-515 517 528-529 545-546 552-554 584-585 597-600 602 630-633 635-636 647-648 659-662 666 668 686-688 690-691 708 729 771 780-781 876-877 923-927 929 959-961 969 973 979 988 994 999-1000 1002-1003 1006-1009 1031-1035 1063 1072-1080 1083 1089 1100 1111 1114-1115 1122 1124-1125 1129 1136 1140 1202-1203 1205-1207 1241-1242 1299-1301 1305-1306 1308-1309 1341-1344 1346-1348 1350-1359 1361-1363 1365-1368 1395-1399 1448-1456 1461 1472 1484-1485 1499 1525 1528 1534-1535 1612 1614 1621-1622 1648-1652 1657-1663 1665-1666 1698-1704 1706 1718 1732-1736 1738 1747-1748 1750-1760 1762-1763 1775-1777 1783-1789 1836-1837 1839-1843 1845 1862-1863 1866-1867 1874-1876 1895-1901 1910 1923-1924 1926-1929 1935 1938-1940 1965-1967 1977-1978 1980-1989 1991 1996-2001 2010-2013 2016-2023 2034 2039-2041 2052 2063 2118 2120-2123 2136 2143 2153-2154 2216 2218 2220-2223 2234-2238 2240-2242 2276 2289-2294 2319-2321 2345-2350 2352-2356 2359-2361 2466-2469 2494 2509 2534-2538 2540-2543 2551-2552 2558-2562 2564-2565 2575 2579 2584-2586 2588-2589 2632-2634 2638 2679-2686 2688 2690-2693 2714-2715 2772 2787 2798-2804 2813 2823-2824 2839-2841 2856 2865 2876 2921 2930-2931 2933 2946-2948 2950-2951 2955 2961-2972 2980 2982-2987 2989-2993 3020-3022 3039-3040 3052 3056-3063 3078-3080 3082-3091 3093 3095 3101-3102 3104-3105 3116-3117 3120 3150-3155 3183 3194 3203 3221 3223-3224 3234-3235 3246-3248 3299-3302 3347 3350 3363 3374 3393 3433-3434 3454-3456 3499-3502 3506 3521-3523 3560 3605 3681-3682 3713-3714 3762 3791-3794 3806-3807 3809-3810 3814 3832-3833 3853-3854 3856-3859 3862-3865 3867-3870 3887 3909-3910 3912 3986 3990 3998-3999 4010-4011 4064 4102-4103 4126 4183-4185 4193 4230 4241 4248 4287-4288 4373-4374 4396 4429 4464 4466-4467 4473 4483 4490 4549-4550 4552-4553 4587 4590-4591 4599 4610 4633-4642 4644-4649 4651-4653 4655-4658 4732 4749 4838-4841 4847-4853 4884-4885 4893-4896 4899 4906 4952 4954-4958 4978-4980 5002-5006 5008-5009 5094 5118-5120 5138 5144-5146 5156-5161 5163 5173 5184 5195 5206 5216 5218-5221 5223 5228-5232 5236-5240 5329-5330 5333-5335 5376-5380 5435 5441 5452-5454 5462-5463 5478-5480 5497 5534-5536 5631-5632 5634 5636 5667-5670 5694 5705 5707 5713-5714 5786 5862-5868 5870 5872 5979 5981- |

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| adult spleen | Clontech | SPLc01 | 9-11 55 164-165 233 268 270-273 374 385-386 398 400 426-427 480-482 514-515 517 552-554 603-604 606 658 679-681 722-723 757-764 766 780-781 846-849 876-877 900 902 949-950 1006-1009 1031-1035 1056-1057 1068-1069 1073-1080 1120-1121 1123 1424- 1426 1447 1458-1460 1543-1547 1653 1737 1739-1740 1747-1748 1751-1754 1872-1873 1891 1893-1894 1911-1913 2027-2033 2035- 2036 2143 2185-2186 2204-2205 2207-2208 2225-2226 2289-2294 2528 2539 2545 2553-2554 2556 2567 2587 2598 2682 2781-2783 2785-2786 2934-2935 3116-3117 3385 3396 3717-3718 3720-3722 3732 3750 3893-3898 3904-3905 3979-3985 4072-4074 4102-4103 4195-4196 4250-4255 4600-4601 4688-4689 4699-4701 4709 4847- 4853 4916 5010-5013 5099-5101 5138 5225 5277-5281 5323-5327 5445-5447 5654-5656 5664 5977-5978 6022 6025-6029 6245 6249- 6250 6545-6546 6698-6700 6915 6917-6918 7063 7098-7107 7109 7453-7460 7673-7675 7808-7810 7989-7990 |
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| thalamus | Clontech | THA002 | 168-169 349-354 356-361 374 382-383 432 436-441 476 478-479 528-529 538 581-582 603-604 606 645 666 668 744-745 753 757- 764 766 780-781 816 818 841-843 856-857 868 879 890 945 954 963-965 967-969 979 1073-1080 1120-1121 1123 1165 1185-1190 1202-1203 1205-1209 1290-1293 1305-1306 1308-1309 1374-1375 1385-1387 1395-1399 1478 1628-1633 1635 1640-1641 1665-1666 1691-1693 1695-1696 1703-1704 1706 1730-1731 1746 1763 1790 1792-1794 1796-1797 1845 1881 1892 1904-1905 1923-1924 1926- 1929 1931-1934 1965-1967 1996-2000 2188-2195 2197-2199 2204- 2205 2207-2208 2289-2294 2347-2349 2352-2356 2359-2361 2383- 2384 2386 2425-2427 2535-2538 2540-2543 2564-2565 2575-2577 2682 2690-2693 2716-2717 2737 2739-2741 2772 2781-2783 2785- 2786 2853-2854 2857-2858 3087-3091 3093 3096 3101-3102 3104- 3105 3229 3234-3235 3310 3358-3361 3364-3373 3375-3384 3386- 3388 3449-3450 3452 3491-3493 3495 3499-3501 3513 3601 3603- 3604 3715 3788-3790 3843 3853-3854 4035-4039 4138-4142 4144- 4146 4250-4255 4309-4310 4320-4323 4325 4369-4371 4373-4374 4392-4395 4416-4417 4491-4493 4616-4617 4842 4844 4847-4853 4952 4954-4958 4965 5069-5070 5168-5169 5272-5274 5284 5409 5443 5540-5541 5657-5659 5661-5663 5678-5680 5913 6148-6152 6195-6196 6209-6211 6249-6250 6306-6309 6368-6369 6394 6421 6432 6450-6453 6708 6727 6761 6837 6839-6848 6915 6917-6918 6943-6947 6988-6989 7029-7030 7049-7051 7179-7180 7222 7328 7400-7405 7587-7589 7647 7677 7686 7697 7736 7874-7879 7943 7993-7995 |
| thymus | Clontech | THM001 | 6 9-11 22-23 27 40-42 229-233 246-248 250-259 261-264 282-284 302 323-325 368-373 397 410 423 431-432 434-435 466 476 478- 482 484-485 492-493 495-497 514-515 517-521 538 552-554 630- 633 635-640 645 649 658 708 732-741 743 753 769 780-782 826- |

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| thyroid gland | Clontech | THR001 | 28-29 44-45 55 144 178-179 205-206 229-233 246-267 269 280 318- 320 323-327 332 334-337 340-341 349-354 356-361 365 367 374 376 378-381 385-387 389-398 400 408-409 428-432 434-443 445- 449 461-465 467-468 476 478-479 514-515 517 522-526 528-529 536-540 550 552-554 559-560 562 574-582 586-593 595-596 602 607-612 617 622 624 630-633 635-640 645 647-649 654-655 657- 658 666 668 670-676 685 704-707 710-719 722-723 747 753 768 770-772 774-775 780-782 840-845 851 854-856 858 872-874 878 880-881 884-885 900 902-909 911-912 914-917 923-927 929 938- 943 954 963-965 967-970 973 979 999-1000 1002-1003 1005-1009 1015-1020 1031-1035 1037-1040 1042-1043 1054-1057 1063 1068- 1069 1072 1081 1083 1087-1094 1100-1103 1110-1112 1115 1119- 1123 1129-1130 1136 1140 1165 1167-1173 1176 1183 1192-1196 1204 1210 1213-1214 1216-1218 1228-1230 1236-1237 1246-1249 1257 1283 1291-1293 1303-1304 1314-1317 1319 1322 1328-1331 1341-1344 1349 1355-1359 1361-1363 1370 1372-1375 1382-1390 1395-1399 1404 1411-1413 1415-1419 1424-1426 1446-1449 1451- 1456 1458-1460 1462-1465 1476-1477 1486-1488 1498-1499 1503- 1504 1506-1507 1510-1513 1515 1536 1538 1562 1565-1566 1580 1591 1595 1601 1603 1611 1627 1653 1657-1663 1679 1690-1693 1695-1696 1698-1699 1701-1706 1711-1713 1716 1727 1730-1731 1738 1750 1755-1760 1762-1763 1772-1773 1775-1777 1779 1781- 1790 1792-1794 1796-1797 1820 1825-1831 1843 1845 1857 1871 1877-1880 1882-1887 1895-1901 1904-1905 1911-1918 1922-1929 1931-1935 1962 1974 1992-2000 2002-2008 2010-2011 2013-2022 2024-2033 2035-2036 2039-2040 2081-2083 2085-2086 2088-2091 2102-2109 2114-2117 2136-2138 2143 2147-2156 2158-2159 2162- 2163 2171-2174 2181 2188-2195 2197-2203 2209-2214 2216 2218 2220-2223 2225-2227 2229-2238 2240-2242 2251-2252 2254-2263 2266-2281 2289-2294 2328 2330 2332-2339 2341-2344 2350 2352- 2356 2359-2361 2371-2372 2375 2381-2384 2386 2391-2394 2425- 2428 2430-2432 2435 2439-2444 2449-2454 2464-2465 2476-2478 2480 2490-2491 2507 2512-2514 2529-2531 2533 2535-2538 2540- 2543 2551-2554 2563-2565 2569-2571 2576-2577 2584-2598 2600- 2601 2629-2631 2635-2636 2639-2642 2672-2676 2679-2682 2695- 2697 2708-2709 2716-2717 2750-2756 2758-2760 2763-2764 2767- |

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| trachea | Clontech | TRC001 | 19 54 56 178-179 360-361 365 367 450-454 456 484-485 500 586- 592 603-604 606 613-614 616-617 657-658 663-664 674-676 747 782 837 872-874 893-895 914 938-943 980-985 1070-1071 1101- 1103 1115-1118 1137-1139 1141-1145 1156-1160 1174-1175 1219- 1220 1236-1237 1291-1293 1303-1304 1338 1411-1413 1419 1424- 1427 1450 1461 1472 1604-1606 1621-1622 1694 1697 1796-1797 1845 1856 1990 2010-2011 2013-2015 2102 2118 2120-2123 2136 2155-2156 2158-2159 2220-2223 2289-2294 2345-2346 2350 2363- 2365 2439-2444 2492 2498-2499 2555 2557 2580-2583 2585-2586 2588-2589 2612 2632-2634 2674-2676 2694 2744-2745 2747-2776 2830-2833 2982-2987 3024 3035 3039-3040 3095 3097 3116-3117 3159 3170 3181 3183 3212 3222 3233 3262-3264 3313 3322 3332- 3333 3491-3493 3520 3682 3732 3799 3815 3968 3978 3987 3997 4006 4114-4120 4135 4138-4142 4144-4146 4183-4185 4207 4209 4232 4237 4243 4249 4273 4287-4288 4373-4374 4380-4382 4422 |

| Tissue Origin | Tissue/ RNA Source | Library Name | SEQ ID NO: |
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| uterus | Clontech | UTR001 | 2 30 74-76 110 155 166 213 221 233 318-321 323-325 335-337 411-420 422 477 488 514-515 517 528-529 555-556 584-593 595-596 618-620 647-649 659-662 769 840 854-855 858 880-881 896-900 902 915-917 923-927 973-976 978 1018 1024-1028 1056-1061 1063 1072 1082-1083 1089 1096-1100 1111 1115 1122 1124-1125 1129 1131 1140 1166 1176 1183 1185-1190 1194 1202-1207 1284-1285 1303-1304 1355-1359 1361-1363 1395-1399 1423-1426 1476-1477 1505 1525 1611 1642-1643 1648-1652 1674 1676-1678 1690 1701-1702 1719-1725 1741-1745 1765-1767 1775-1777 1783-1789 1796-1797 1825-1826 1828-1831 1862-1863 1930 1992-1995 2010-2011 2013 2081-2083 2136 2153-2154 2177-2178 2180 2216 2218 2371-2372 2375 2381-2382 2428 2430-2432 2436 2438 2500-2502 2528 2539 2545 2556 2564-2565 2567 2572-2574 2585-2586 2588-2589 2682 2713 2774-2776 2781-2783 2785-2787 2795 2910-2914 3095 3226 3236-3237 3265 3328 3330 3347 3443 3485 3499-3501 3524-3525 3527-3529 3568-3571 3585-3586 3683 3758-3759 3761 3821-3822 3950 4024-4025 4147-4149 4172-4173 4176 4264 4287-4288 4298-4301 4303 4357 4368 4373-4374 4379 4392-4395 4424 4465 4473 4490 4575 4577-4579 4616-4617 4667 4673-4674 4747 4796-4797 4856-4860 4897 4978-4980 5078-5081 5099-5101 5138 5155 5204-5205 5207 5236-5238 5240 5376-5380 5401-5404 5406-5407 5418 5428-5430 5462-5463 5833-5834 5918-5919 6022 6025-6029 6055-6056 6058-6060 6069 6189 6245 6251-6252 6368-6369 6412 6545-6546 6675-6676 6732 6772 6983 7179-7180 7271 7326 7400-7405 7437-7438 7462-7465 7494 7504 7515 7526 7535 7546 7558 7569 7814 7829 7839 8034-8035 |

TABLE 2

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Met h o d | SEQ ID NO: in USSN 09/577,408 | Nucleotide location corresp. to first residue of peptide sequence | Location of first nucleotide of codon corresp. to last residue of peptide sequence | Amino acid sequence (X= Unknown; *=stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|--|---|--------------------|--|--|--|---|
| 1 | 8052 | A | 1 | 2 | 424 | |
| 2 | 8053 | A | 10 | 67 | 373 | FCDCHHFFILMFKSPHIWPGIFSSWLLCF FWACLHHSLSIALLSCTKRYSGLILYFLC SSFEITVSSKSSVSF*RRMVFRNQVLGSR CACCC*GVAAPRPF |
| 3 | 8054 | A | 100 | 404 | 1072 | ARACKIPNTASDRPIIVALQRKRSSPKMT QSAAGTCPTSCMIK/IDSHKCGDDRELFA QAPVDQFPGTAVESVTDSSRYFVIRIEDG NGRRAFIGIGFGRGDADFDFNVALQDHF KWVKQQCEFAKQAQNPDPQPKLDLGF KEGQTIKLNIANMKKKEGAAGNPRVRP ASTGGLSLLPPPPGCKTSTLIPPPGE/PVG CGGIPRPASSCSQFRSTSSQTQPTGW |
| 4 | 8055 | A | 1000 | 2 | 333 | ACPFNKSAEDLLNL/RQGLTAGQLPFLP WWNIVLDS/SLTSIPATSFSTSLATARAR SASEVPIWKITLFCSLSQVRKTTSSGAT KSTVLSTSLTLLH*ILRSISSQ |
| 5 | 8056 | A | 1001 | 292 | 945 | |
| 6 | 8057 | A | 1002 | 46 | 493 | |
| 7 | 8058 | A | 1003 | 2 | 406 | |
| 8 | 8059 | A | 1004 | 192 | 548 | |
| 9 | 8060 | A | 1005 | 1 | 528 | DNELLDYEDDEVETAAGGSMS/EAPAKK DVKGSYFSIHSSGFRDFLLKPELLRAIVD CGFEHPSEVQHECIPQAILGMDFLCQAK SGMGKTAVFVLATLQQLPVTGQVSVL VMCHTRELAFQTR*KTRPFWNVTVCPSG EDTRVGVKETLLPPPLTAPTPWLPSFASP PLLNPHF |
| 10 | 8061 | A | 1006 | 807 | 1034 | |
| 11 | 8062 | A | 1007 | 136 | 1520 | LFTPCFHLFCENPSRSPFPSSPAGPVMMAE NDVDNELLDYER*MRWETAAGGDGAE APAKKDVNGLLCLPSHSSGFRDFLLKPE LLRAIVD\CGFEHPSEVQHECIPQAILGN GMSCARAKSGSGERQAVFVLATLQGLE PVTGQGVCA*GCHTRELAFQISKEYER FSKYMPNVKVAVFFGGLSIKKDEEVLKK NCPHIVVGTPGRILALARNKSLNLKHIKH FILDECCKMLEQLDMRRDVQEIRMTPH EKQVMMFSATLSKEIRPVCRKFMQDPM EIFVDDETCLTLHGLQYYVKLDNEKN RKLFDLLDVLEFNQVVIFVKSQRCIAL AQLLVEQNFPAAIAHRGMPQEERLSRYQ QFKDFQRRILVATNLFGRGMDIERVNI AF NYDMPEDSDTYLHRVARAGRFGTKGLA ITFVSDENDAKILNDVQDRFEVNISELPD EIDISSYIEQTR |
| 12 | 8063 | A | 1008 | 92 | 191 | |
| 13 | 8064 | A | 1009 | 219 | 422 | |
| 14 | 8065 | A | 101 | 2 | 477 | IVSPEVRWAPGVAMEESGYESVLCVKPD VHVYRIPPRATNRGYRAAEWQLDQPSW SGRLRITAKQMAYIKLEDRTSGELFAQ APVDQFPGTAVESVTDSSRYFVIRIEDG NGRRAFI*IGFGDRGDADFDFNVALQDHF KWVKQQCEFAKQAQNPDPQ |
| 15 | 8066 | A | 1010 | 215 | 416 | |
| 16 | 8067 | A | 1011 | 261 | 486 | GFLGKVLQSPATTVVRTLNDRSSIVMGE PISQSSNSQ*FFFKENSRLFLG*CAVE QHFSIFHCVDYII |

| | | | | | | |
|----|------|---|------|------|------|---|
| 17 | 8068 | A | 1012 | 31 | 2697 | |
| 18 | 8069 | A | 1013 | 306 | 439 | |
| 19 | 8070 | A | 1014 | 149 | 404 | |
| 20 | 8071 | A | 1015 | 2 | 343 | |
| 21 | 8072 | A | 1016 | 172 | 341 | |
| 22 | 8073 | A | 1017 | 73 | 408 | |
| 23 | 8074 | A | 1018 | 53 | 237 | |
| 24 | 8075 | A | 1019 | 51 | 480 | |
| 25 | 8076 | B | 102 | 118 | 419 | XLFCVDIDECSIMNGGCETFCNTSEGSYE CSCQPGFALMPDQSRCTDIDECEDNPNIC DGGQCTNIPGEYRCLCYDGFMASEDMK TCVDVNECDLNPNICLX* |
| 26 | 8077 | A | 1020 | 49 | 399 | |
| 27 | 8078 | A | 1021 | 564 | 651 | |
| 28 | 8079 | A | 1022 | 2 | 366 | SLPASDRPPISSPLATSGTIFSAISCFWDLF APFLWLAPSCOPTMSSQIRQNYSTDVEA AVNSLVNLYLQASYTYLSLQDIKKPAED EWGKTPDAMKAAMALEKKLNQALLDL HALGSART |
| 29 | 8080 | A | 1023 | 18 | 781 | EICPSRPKNSARRGGPAGLSLASTVFGRN RSGDWASSLRPPSDFLLRLQPPGPSYRPS PASGTCQHRFLWLAPSCOPTMSSQIRQON YSTDVEAAVNSLVNLYLQASYTYLSLG FYFDRDDVALEGVSHFFRELAEEKREGY *RLMKMQNQRRGGRALFQDIKKPAEDEW GKTPDAMKAAMALEKKLNQALLDLHA LGSARTDPHLCDFLETHFLDEEVKLIK MGDHLTNLHRLGGPEAGLGEYLFERLTL KHD |
| 30 | 8081 | A | 1024 | 217 | 608 | |
| 31 | 8082 | A | 1025 | 147 | 430 | |
| 32 | 8083 | A | 1026 | 489 | 700 | |
| 33 | 8084 | A | 1027 | 899 | 1097 | QPAGPSLTRCATAQALCTTLPPCCLVKQ DGSTIHIRYREPR/QQCWRMPIDLDTLSP EERRARLRKR |
| 34 | 8085 | A | 1028 | 59 | 426 | |
| 35 | 8086 | A | 1029 | 1 | 2148 | |
| 36 | 8087 | A | 103 | 59 | 450 | CLGVTVKDVNQQEFVRALAAFLKKSG KLKVPEWLADTVKLLAKHKELAPYDEN WFY/SREFVRNLASTARHLVLRGGRWG LAPLTKIYGGDVQRKRAFIAPAFSRGWSK SVARRVLQALAEGLKMVEKDQD |
| 37 | 8088 | A | 1030 | 193 | 564 | GDSGGSPWPDEKPKGVKTENNNDHINLK VAGIQDGSVVQFKIKRHTPLSKLMKAY CEARQGLSMRQIRFRI*PGNPIHETDTPAP VGKWKDERYQLMVFFQARPGGVYLKK GTCFFYSKNSVSF |
| 38 | 8089 | A | 1031 | 216 | 372 | |
| 39 | 8090 | A | 1032 | 566 | 787 | |
| 40 | 8091 | A | 1033 | 2 | 401 | |
| 41 | 8092 | C | 1034 | 379 | 453 | |
| 42 | 8093 | A | 1035 | 2465 | 2795 | |
| 43 | 8094 | A | 1036 | 1264 | 1385 | |
| 44 | 8095 | A | 1037 | 1249 | 1457 | |
| 45 | 8096 | A | 1038 | 146 | 438 | |
| 46 | 8097 | A | 1039 | 2 | 2387 | |
| 47 | 8098 | A | 104 | 583 | 1526 | PHLILQVTKAMCPFESGRESFLVVSICIYF KPDSSASFSPDPYSVQC*PQLEPPPHCST SIYFPK/PTLPHIPFPPLTKHPKEDLELA GWTSSGCFYFSLPSTKLGENWSLHPQSH VYRSGDLVGSF*LLSQKLHRNPSICSL KGPPPREGLGNDPVSTNTAPYPRNLP*DL QRTIFSSPSIFYPGPPGAPSGES*NP*ELEG ILEVF*LELCPT/VH*HQPLVFPSPGLF SSFPPQKILTHRLLVQASKPTPLPLRLC PLWSPSHYPSSIAPSSSI.EFGPGSPOKTL |

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| | | | | | | PLWSPSHYPSSLAPSSSLEFGPGSPQKTL E*PPLPKKQTD RHAPGE |
| 48 | 8099 | A | 1040 | 1 | 1329 | |
| 49 | 8100 | A | 1044 | 3 | 581 | |
| 50 | 8101 | A | 1045 | 1 | 741 | PLTRAAGIRHEDSQSVGNSSPEIPVLPEPA YQLGPLCQVLP RRAGSSCLPVMTRTVKL WDKSSRECVHSYCEHGGFVTYVDFHPS GTCIAAAGMDNTVKVWDVRTHRLQHQ YQLHSAAVNGLSFHPSGNYLITASSDSTL KILDLMEGRLLYTLHG HQGPATTVAFSR TGEYFASGGSDEQVMVWKRNF DIGDHG EVTKVPRPPGTLASSMGNLTVSILEQRLT LTEDKLKQCLNQQLIMQRATP |
| 51 | 8102 | A | 1046 | 526 | 1272 | |
| 52 | 8103 | A | 1047 | 57 | 307 | |
| 53 | 8104 | A | 1048 | 1669 | 1820 | |
| 54 | 8105 | A | 1049 | 212 | 547 | |
| 55 | 8106 | A | 105 | 1283 | 1648 | SSGASVAPTSWTSNRFPF*SWVPSSF*RT HGPRPSGPPRERKPRAPGQEPKGT PRES VCLNDLPCPGLLGICRPILQTSP/CHGHH GILSVVNLKGD KPSRSLGLPVFHNH HFRDLSVL |
| 56 | 8107 | A | 1050 | 670 | 1296 | |
| 57 | 8108 | A | 1051 | 243 | 335 | |
| 58 | 8109 | A | 1052 | 1 | 1170 | |
| 59 | 8110 | A | 1053 | 1 | 1122 | |
| 60 | 8111 | A | 1054 | 1 | 392 | |
| 61 | 8112 | A | 1055 | 47 | 296 | |
| 62 | 8113 | A | 1056 | 1 | 315 | |
| 63 | 8114 | A | 1057 | 1 | 579 | |
| 64 | 8115 | A | 1058 | 87 | 507 | |
| 65 | 8116 | A | 1059 | 866 | 1002 | |
| 66 | 8117 | C | 106 | 263 | 304 | MLKLSVRNRETFL* |
| 67 | 8118 | A | 1060 | 385 | 573 | |
| 68 | 8119 | A | 1061 | 328 | 530 | |
| 69 | 8120 | A | 1062 | 6 | 664 | LPGRPTRAPTRPAEHSIVGTRLVSCQLQP SQPNADQGKLTMMRIAVICFLLGITCAI PVKQADSGSSEEKQLYNKY PDAVATWL NPDP SQQNLLAPQTLPSKSNESHDMMD DMDEDDDDHVDSQDSIDSNDSDDVDD TDDSHQSDSHHSDESDELVTDFPTDL PATEVFTPVVPTVD TYDGRGDSV VYGLR SKSKKFRRPDIQY P DATDEDITS |
| 70 | 8121 | A | 1063 | 2 | 613 | PRVRPRVREEAEHSIVGTRLVSGQLQPSQ PNADQGKLTMMRIAVICFLLGITCAIPV KQADSGSSEEKQLYNKY PDAVATWLNP DPSQKQNLLAPQNAVSSEETNDFKQETL PSKSNESHDMMDMDEDDDDHVDSQ DSIDSNDSDDVDDTDDSHQSDSHHSDE SDELVTDFPTDL PATEVFTPVVPTVD TY DGRGDSVG |

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| 71 | 8122 | A | 1064 | 1 | 1073 | TDCRVDPVRPRVRVEHSIVGTRLVSCQ LQPSQPNADQGKLTMMRIA VICFLLGIT CAIPVKQAESGSSEKQLYNKYPDAVA TWLNPDPQSQKQNLAPQITLPSKSNESH DHMDMDDEDDDDHVGTDARDSIGLG TTLDGCRMDTGWIFHQF*WSLHFWME SGWNWSLDFSPRDLAQATEVFQFQFVP TVDTYDGRGDSVVYGLRSKSKFRRPDI QYPDATDEADITSHMESEELNGAYKAIP VGPDPAAPSDWDSRGKDSYETSQDDQ SAETHSHKQSRLYKRKANDESNEHSDVI DSQELSKVSREFHSHEFHSHEDMLVVD KSKEEDKHLKFRISHELDSASSEVN |
| 72 | 8123 | A | 1065 | 1 | 1128 | LETPIDSPRNRPNGNPGATHASGRRQSTAS SGPDSVSGQLQPSQPNADQGKLTMMRIA VICFLLGITCAIPVKQADSGSSEKQLY NKYPDAVATWLKP*PIFRRQNLGPTW LCPLKETNDFKQGGPFPS*GPTERPWT WDDMG*WKVDGWTMWDSDSIDSN SDDVDDTDSSHQSDSHSDEDELVT GFSTDLPADEVFTPVVPTVDTYDGRGDS VVYGLRSKSKFRRPDIQYPDATDEHITS HMESEELNGAYKAIPVAQDLNAPSDWD SRGKDSYETSQDDQSAETHSHKQSRL YKRKANDESNEHSDVIDSQELSKVSREF HSHEFHSHEDMLVVDPKSKEEDKHLKF RISHELDSASSEVN |
| 73 | 8124 | A | 1066 | 514 | 1000 | |
| 74 | 8125 | A | 1067 | 1 | 1098 | |
| 75 | 8126 | A | 1068 | 2388 | 2658 | FYKVTFMWKSKVKSLGDNFVLGSSVPC FLFFFFFLRWSLALLPRLECSGAISAHCI LCLPGSSNS/PASASQVVGITGTCHHAWL IFLYF |
| 76 | 8127 | A | 1069 | 788 | 1000 | |
| 77 | 8128 | A | 107 | 426 | 1519 | AWRRRRSGTSGKATWWCSGLRRASPTP SRRVQSWATAVMWKPSPPSSPASWE/PA LPREPHRAVSEQRQ*GR*PCKPELTAPLC LEPVHRPEGPMGT/YSRCCLSPHRP/PGP VGTFPV/SPEPVHRPQDPWHIPGVPEPVH RPQDPWHIPGVPEPVHRPQDPWHIPGV EPVHRPQDPWHIPGVPEPVHAPTGPVAL ASVGASSRDGLLPAHAAACTLHETAGQ TRTSRLSPS*GLGLPFCSRRSRQPWTPAL GHSKTSGEWRGGARPGCGC*CCMLSPT QQPLPGGHPQARASPRAGEG*TSRAYL AVHAAATLWKLPLPEDPPLLDARISAH RPLCPSGRHRKVSLFLTSLFSISCEARKIG |
| 78 | 8129 | A | 1070 | 306 | 1195 | |
| 79 | 8130 | A | 1071 | 3 | 715 | FVAHTKGVRGLPSMRRSPDCGRMELAA GSFSEEQFWEACAELOQPALAGADWQL LVETSGISYRLLDKKTGLYEYKVFVLE DCSPTLLADIYMDSDYRKQWDQYVKEL YEQECNGETVVYWEVKYFPMSNRDY VYLRQRRDLDMEGRKIHVILARSTSMQ LGERSGVIRVKYKQSLAIESDGKKGSK VFMYYFDNPGGQIPSWLINWAAKNGVP NFLKDMARACQNYLKKT |
| 80 | 8131 | A | 1072 | 1 | 1128 | |
| 81 | 8132 | A | 1073 | 3 | 862 | |
| 82 | 8133 | A | 1074 | 1 | 912 | MTDNILELAQNMDKYTKYEMTTTILSQ PSSSQREQDQGQFQELTVTSEMFRKGK SFCSHPHPEKFLRTFNEIETYLIGNFODLE LESSDDLPRGCTNEKARKTYDPKKLPLP YT/VRPCWILASKLHI*ESYG*RQ*A**CH Q*TPWPRPVVWSLHTEAHEIWCRRSDQ GTSLGRSIPCPVLC*ERSTYDLRPQTD QPSKHLTNLKSASTPPYPNPFITSPHTRS GLQFRSTSSPPAPAQQFTLKKVAEAKGIV KVNAPFSI.SDI.SOISVRI.GSFIKYEKSSPV |

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| | | | | | | KVNAPFSLSDLSQISVRLGSFIKYEKSSPV HGSFGSNPETLYSPRP |
| 83 | 8134 | A | 1075 | 611 | 817 | |
| 84 | 8135 | B | 1076 | 1 | 1500 | MRTREVSITGADFTALLVDIIGNSTSYLT EIFKSTSILSVNQSNESDCIFICVMTGKSG RNLSDFWIEEEKYPIINYFTSGLSGVLAL LLTQSLFGGLFTRTRMKFGAVTRIGGPPL GNQSPSSCSLLHEKDPPTSGPQTDQPKK HLTNFKSGTEEAMNTSLLAPAAEIMAT PGSPSQASPTSGAFTHGTQTPSPTKATAP RYPQTGAQSRPRRFRPPAGAAPKAAA PRHPHPRGTAPPPRRISPESIRPHPPPLDR GPRPPVTPFLIVLGCLILAVLTTFKEYETV SGDWLLETFIFIFGAEFALRIWAAGC CCRYKGWRGRLKFARKPLCMLDIFVLIA SVPVAVGNQGNVLATSLRSLRFLQILR MLRMDRRGGTWKLLGSAICAHSKELITA WYIGFLTILSSFLVYLVEKDVPEVDAQG EEMKEEFETYADALWWGLITLATIGYGD KTPKTWEGRLIAATFSLIGVSFFALPAGIL GSQLALK* |
| 85 | 8136 | A | 1077 | 606 | 1065 | LVARTERLSVSQGFPLPWCTGRIRSHVGL ENECKVLLSGSSSQKMGKPEGRWFSPGV GPPPCLAAPALLRLPWKSPPHPTGGWPA SVPVPVGVLCQRAPLDDQLLVCWPAR VLEKRYWQPPLS*LCPCSAHNMNGYGS GAYVWVLTELTVDFAGFWA |
| 86 | 8137 | A | 1078 | 1 | 822 | MWNAVTLWQQRESCIEESEIGTLETKE THFIRGPKTLAPVDWEGSLPLVFNQCR DASLIHPRFKGFRPRDACLGPSPLAASP AFLGKGQAAPRQAEFGPNSSASAPPY NPFITSPHTWSGLQFHSMTSPPPAQF PLKKVAGAKGIVKRLKTDARLPWKPP DHHRRRASGNSHSGRVQPP/CPAAFVGS C*VSQAFPGARCKLSVDLPFWDLEDARV FMCVRVKRPPNRLCVSNMAVYFTWVQL LQAIWAYTCKSQGMRWLGLGSEA |
| 87 | 8138 | A | 1079 | 38 | 639 | MTLIKSPIVIWTIRSRLKWSQMEMRNLL GTGAKRQRRHVLSVDPKLRWSRTGKA AFPWCLIIAGRPALVLHP*QQVLLSWGR GKI*LTSPSRCTHIEKSCNSWPPL*DKPQP HLQHTRTSKRLNRSGQAFLLQNLQELA TSTRN/PDHQAKECLQPRIPPKPCICAGP HWKLD CSTHLAATPRAPGTLAQGS LTDS FSA |
| 88 | 8139 | A | 108 | 1 | 537 | RRCCCRHTRSPCLALLLEIVSLFSFAVPQ SPDSSPLVFTYFARTHDPDPSLLPLPAQL WQRTMWTMKLLDYER*MRWETAAGG DGAEAPAKKDVKGSYVS/LSHSSGFLDF LLLL*VLPSIVHCAFEHSTHFRHECISQAI LGKDALFPALLDIFLTGVFFLTIFSPVLRV LLRCLFCLS |
| 89 | 8140 | A | 1080 | 1 | 1611 | |

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| 90 | 8141 | A | 1081 | 17 | 1173 | MADSRIKRTWMRMKFGAVTRIGGTSLG RSIPCPALCSVKIHLRPRVLRPTSPRNI SPILN/TARFKRIKACYSPATAWPFKAY KLPLQFPHT/WS*NQTRLTA*FS*KHTCS P*LSSPANLPNPNPFYKTTTFLPRHG**G QILTQELGPRPIAFLSKQLDLTVLTQPS LHAAAAAALILLKALKITKYAQLTYSS HNFQNLFSSSYLMHILSAPWLLQLYSLF VESPTITIVPGTDFNPASHIILDTTPDPHD CISLIHLTFTFPRISSFFVPHPNHIWFIDG SSTRPKCHSPAKAGYAIVSSTSIIEATALP PSTTSQQAELVALTQALTLAKGLCVNIY TDSKYAFHIVHHHARSFLTQKQSSINPS LIKTLNAA |
| 91 | 8142 | A | 1082 | 324 | 548 | SFYHLPSSHVLLTVSFRD*PSPTCPAIYS *KGGWSQRHSQGACYKQKSGHWAKE CPQPRIPPKLRPICVGP |
| 92 | 8143 | A | 1083 | 760 | 1260 | HTDGVLVWMSFLVFSFNSQDPQLQLC WSLEVHSRSCLPYQQWRLSWKCRNH SSSASLTLRAVDWCSYSAILEPRWYCL LYFIQSIILKKHRGRRWIFLMEQRTGGQR IDLPRGGPPI*VTAPNLMHVRVKRPPNRL CVSNKAVYFTSKSGPLSQDVVTVVIH |
| 93 | 8144 | A | 1084 | 908 | 1192 | |
| 94 | 8145 | A | 1085 | 1 | 420 | |
| 95 | 8146 | A | 1086 | 287 | 515 | LFTHVSKELOTSARNLTTRPTAGSPGFL LSHVPSVWDPTANRTVQLTWQPLPEPLE VSGPRLSD*LLPRSSRLSG |
| 96 | 8147 | A | 1087 | 1 | 5127 | |
| 97 | 8148 | A | 1088 | 3 | 721 | |
| 98 | 8149 | A | 1089 | 144 | 408 | |
| 99 | 8150 | A | 109 | 1 | 457 | AGGGCSPKGRPEAKSGQRDWELVAGGP PGISRREGTCCSRFSPRLSQPFRSAQQLQ LAASLPANLSNFCQGSEMPITSRPALDV KGGTSPAKEDARPEKSTLGQ/YSTLLVID NQVSSKTR*PDESANQYYASDTFIILSRT YNRYILVHLSK |
| 100 | 8151 | A | 1090 | 265 | 769 | RQKRHVLSVDPKLRRWSRTGKAAPWC LIIAGRPALVLP*QQVLLSWGRGI*LT SPSRCTIIEKSCNSWPL*DKPQPHLQHTR TSKRLNRSQGAFQNLQELATSTRN/P DHQAKECLQPRIPPKPCICAGPHWKLD CSTHLAATPRAPGTLAQGSLTDSFSA |
| 101 | 8152 | A | 1091 | 69 | 634 | KQKRSTYNLRSSDPPAQETSHQFQIRDK GDTFYLTQNSGAHGLGRQSLDV*S LQGHLSDYSPMFPRCQTMQGRLP*SFTL SGKSRFSGEGASTPQPLLHP*WQVPLFW GRGKYPSTPSSPLVASPAFLGKGQKPPRP SRMPSTFG |
| 102 | 8153 | A | 1092 | 1 | 655 | MGATHPFELLTKMTSQGSDISGDLPWEI NPLSSCSLLHEKDPPTSGPQTDQPKKHL TNFKSETKETHFIRGPKTPVLVTDWEGR LPLVFNHSRDASLIHPRFRGVRPRRDAC LGPSPLAASPAFLEEGQVPQPLLSMSLTP SLLFWRRGKKPSTPSSPLAASPAFLEEGQ VPQPHIS/GA/LDPLFLHPNLL*LCTPTFPF LFWKTVRKYSSNNQKGE |
| 103 | 8154 | A | 1093 | 756 | 878 | LSQWRSDNGPAFISQITQAVSQAPGIQ*N LYIPYHPQSSGK |
| 104 | 8155 | A | 1094 | 781 | 1194 | FPGGGPPI*VIAPNFMVRVRKPPNRLCV SNKAVYFTWVQVGALCRLGA/PAPCIPA APVP/VHGESEPRYNSSRCLAEKLP*ALA ASMWYLSLKALGIESGRVSTAILINISSA RKA/SCVPLGSRILESLMLSTVRALR |
| 105 | 8156 | A | 1095 | 400 | 686 | RQVLLFWGRGKYPSTPSPSPLAASPTFLG QGQELVTSARNLTTRPRNACGPGFLLSH VPSVRDPTGNRTVQLTWQPLPEPLESGP |

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| | | | | | | RLSD*LLLRL |
| 106 | 8157 | A | 1096 | 1 | 883 | MASSAQLLGSSQETYNHSKRQRGGEMS HMAGARRKRERGEMLHTFKQPDLMRW SSVCRKNKEKVGNSRKRRNVRYCFSRK FNGTSKVFEWQVVVVGEINSHVAHTKP VRWSLHTDAHEIWCRDSRRTSLGRSIP CPPVLCMRKIHLQAQVLRPTSPRNISPIL NRRKRHHVLSVDPKLRHRSWTREGSLPL VFNLCDASLIHPGFRGVRPRRDTCLGP SPLAASPTFLGEGARACYKCQKSGHQAK ECLQPRIPPKLCPIWRDPAGNRTVQLTW QPLPKPLELWPKVL |
| 107 | 8158 | A | 1097 | 2 | 551 | CGKVWNFLETFSMALTKMLIMIWTMKF RLRSSQMEMRNLLGTGISLETWCPAS*P L*P*LKGDKIQLRPWLQVRVQGSIGSFQE VLGPWVLRNQELRFGNLCYFAGCMEK PVCPRSLQGGGF/PWYVPAVVGAK VHDVNLHMLSFPSKWKLHTCMKFGAVT WIRGPPLGDQSPVLLLFAP |
| 108 | 8159 | A | 1098 | 1436 | 1699 | |
| 109 | 8160 | A | 1099 | 1099 | 1250 | LVYLKVTGRMEPSWKTLCRILSRRTSPI* QGRPTFRFRKYREHHKDTPRD |
| 110 | 8161 | A | 11 | 366 | 795 | AWVEQSKVLIKEGGIQLLLTIVDTPGFGD AVDNSNCWQPVVIKYFDSKSQDIYLNES QVNRCOMPGNRVHCCLYFIAPSGHGPL HN*RLPPSGRIG*YMFVTTWHCLLLRLK PLDIEFTKHLHEKVNIPLIAKADTLMPPE C |
| 111 | 8162 | A | 110 | 232 | 376 | FPTTKSLG*DSFTSEFCQTFKAELIPILS/R LFQKLEQYVTLPPFYEA |
| 112 | 8163 | A | 1100 | 303 | 1413 | VRRQRSDRERSDARMVRFCNLYM*RKN PFILH*LFR*TLRQTKPDSSA/V*MCQNL MTHSKSTEWKITK/QIFDGDGKTYQNVQ QFIDEGNYTSGDNHTLRDPHYVEDKGH KYLVEANTGTENGYSQSAHLHPGEINS HVAHTKPVWWSLHMDAHEIWCRDSR GTSLGRSIPRPPALCSVRKIHLQPQVLRPT SPRNISPISNPGFCFRNHHQTGFSPAGA NQRGPLAATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFINAAGTT GFPTGKRAVSATQLMDFADFGTTTKQD FRLLGQTSVDRLLQLSQGQAVKGNQLLP VSLVKRKTTLAPNTQTASPRALADSLMQ LARQVSRLESQ |
| 113 | 8164 | A | 1101 | 846 | 1825 | |
| 114 | 8165 | A | 1102 | 2141 | 2384 | AEQWPSVKILRQELATSARNLATRPRNA RSPGFLLSCVPSVWDPTGNQTVQLTWQP LPEPLESGPRLSD*PLPRCSRLSS |
| 115 | 8166 | A | 1103 | 305 | 1148 | |
| 116 | 8167 | A | 1104 | 2779 | 3182 | DKTQPHLLHTGTSKCLNCSGQAFLOQLL LQELATSARNLATRPGNSCSPGFLLSHVP SVDPDTGNRTVQLTWQPLPEPLELWPKV LSRVMDYI*MVY*STIPQNSAIVLTDLLL GVYIPSESKHARPKVVLWAH |
| 117 | 8168 | A | 1105 | 2286 | 4921 | |
| 118 | 8169 | A | 1106 | 1 | 761 | |
| 119 | 8170 | A | 1107 | 1 | 969 | |

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| 120 | 8171 | B | 1108 | 1 | 2175 | MVNPDTGYINYDQLEENARLFHPKLIH GTSCYSRNLEYARLRKIADENGAYLMA DMAHISGLVAAGVVPSPFEHCHVTTTT HKTLRGCRAGMIFYRKGGMAPLGTATL LQALFSLFLSKSRDVPGTGADPGVMYV KRRPRGTDSCGCVLEPRRFLPSGMAFTK EEEEEEEPYNPALPEEYSVPLFPFASQG ANPWSKLSGAKFSRDFILISEFSEQVGPQ PLLTPNDTKVFGTDFLNYFSLRIMSVDY QASFVGHPGSAYPKLNVEDSKVVLGD SKEGAFAYVHHLTYDLEARGFVRPFC MAYISADQHKIMQQFQELSAEFSRASEC LKTGNRKAFAGELEKKLKDLDYTRTVL HTETEIQKKANDKGFYSSQAIEKANELA SVEKSIIEHQDLLKQIRSYPHRKLKGHD CPGEMEHQDQASQASTSNPDESADTD LYTCRPAYTPKLIKAKSTKCFDKKLKTL EELCDTEYFTQTLAQLSHIEHMFRGDLC YLLTSQIDRALLKQQHITNLFEDFVEVD DRMVEKQESIPSKPSQDRPPSSSLEECPI KVLISVGSYKSSVESVLKMEQELGDEEY KEVEVTELSFDPQENLDYLDMDMKGSI SSGESIEGLGTEKSTSVLSKSDSQASLTVP LSPQVVRSKAALLQPHNPTRHRSSTM EYKPDPPHRFSEPWPNEANLSSPAVK DSVTKELOQTARPSREQ* |
| 121 | 8172 | A | 1109 | 2 | 964 | DIPLVMVNPDTGYINYDQLEENARLFHP KLIHAGTSCYSRNLEYARLRKVADENGA YLMADMAHISGLVAAGVVPSPFEHCHV TTTTTHKTLRGCRAGMIFYRKGVKISVG SPRLGKEILYNLESLNSAVFPLQGQPH NHANAGVAVALKQAMTLEFKVYQHQQV VANCRALEALTELGYKIVTGGSDNHLI LVDLRSGKTDGGRAEKVLEACSIACNKN TCPGDRSALRPSGLRLGTPALTSRGLEK DFQKVAHFHRIELTLQIQSDTGVRATL KEFKERLAGDKYQAAVQALREEVESFA SLFPLPLPDF |
| 122 | 8173 | A | 111 | 515 | 909 | LPLFIMNMTVELVWPDTSNLPNSELIS SPTRPNQLFVCLFLGSPSLPRLEYK WYSQ SSL*PQNPGLK*SSPSASYVAKTIDMCH HAWLI FLQTEGL/NYIAQVG/VQTPGF KQSSCLTLPKC*DYRHEPP |
| 123 | 8174 | A | 1110 | 172 | 375 | |
| 124 | 8175 | B | 1111 | 827 | 1276 | MATAAWSSSLEKSYELPDGQVITIGNER FRCPETLFPQSFIMGESAGIHETTYNSIMK CDIDIRKDLANNVLSGGTTMYPGIADR MQKEITALAPSTMKIKIAPPKYSVWI GGSILASLSTFQQMWISKQEYDEAGPSIV HRKCF* |
| 125 | 8176 | A | 1112 | 144 | 261 | |
| 126 | 8177 | C | 1113 | 122 | 253 | MGWVGTATSPHPVAWRTRRPSLSRLPS VRALVVRTERRVPCG* |
| 127 | 8178 | A | 1114 | 50 | 368 | RQAILTAAPRRRAAARA VRSRHGGARA LSPGMEQRRRRRTTWSLLQPRRRRWA ARRPRGRRRAQVARRTARRICPCGRPPV RAPAADPWARRAWSTSRSPAGTE |
| 128 | 8179 | A | 1115 | 336 | 689 | |
| 129 | 8180 | A | 1116 | 164 | 370 | |
| 130 | 8181 | A | 1117 | 974 | 1111 | |
| 131 | 8182 | A | 1118 | 179 | 404 | FSSSIGSLRRQRRGMKTPFGKAAAGQRS RTGAGHGSVSVTMIKRKAHKKHRSRP P/SQPRGNIVGCIIQHGWKDG |
| 132 | 8183 | A | 1119 | 1 | 1698 | |
| 133 | 8184 | A | 112 | 40 | 351 | LKIPMQFLHSGFWFSFFVFFGF*KFGFGP QGGROGGWNTKGEKLPPGSSSLPGPNP QENREKKGPPKTLKFGNLSSSGKTRG |

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| | | | | | | PRGEKNSDPKGTGPGQNPNG |
| 134 | 8185 | A | 1120 | 264 | 799 | |
| 135 | 8186 | A | 1121 | 231 | 351 | |
| 136 | 8187 | A | 1122 | 1 | 3654 | |
| 137 | 8188 | A | 1123 | 1376 | 3462 | TKPKTKTLLSQ*MQKKPLTKFNPNPSC* KLSIN/IVLEVLARAIQKKEIKGIQLGKE EVKLSLFADDMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYTKNRQTE SQIMSELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVG RINIVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQKNKV GGITLPDFKLYYKATVTKTAWYWYQNR VIDQWNRKEPSEITPHTYNYLIFDKPEKN KQWGKDSL FNKWCWENWLAICRKLKL DPFLTPYTKINSRWIKDLNVRPKTIKLE ENLGITIQDIGMGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRVNRQPTT WEKIFTYSSDKGLISRIYNELKQIYKKK TNNPIKKWVKDMNRHFSKEDIYA AKKH MKKCSSLAIREMQIKTTMRYYLTPVRM AIKKSGNNRQTGSGVDLQTPDCLKLR DLTVRRKMKNQKEIASTSTKRTSTPNPT CRSVGPKDCSSLGAMEQSWTENDFDKL TEKKALEENQEEMDKFLDTYTLPRLNQE EVESLNRPI TGSEIEAIDS IPTKKY PGPDG FTAKFYERIKVFCTESLAKWIKWHTKT FIMEFHTIGNAKILQASSFTEVKT KTKTL EHRLESIMALTSQ |
| 138 | 8189 | A | 1124 | 485 | 2347 | TEPKTKTT*LSQ*MQKRPLTKFNNTSC*K LSIN/IVLEVLARAIQKEIKGIQLGKEE VKVSLFADDMIVYLENPTVSAQNLLKLI GNFSKVSGYKINVQKSQAFLYTNNRQTE RQIMSELPFTIASKRIKYLGIQLTRDVKDL FKENNKPLLKEVKEDTNEWKNIPCSWV GRINIVKMAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRACIAKSIFSQKNK AGGITLPDFKLYYKATVTKTAWYWYQNR RDIAQWNRTEPSEIMLHIYNYLIFDKPEK NKQWGKDSL FNKWCWENWLAICRKVK LDPFLTPYTKMNSRWIKDLNVRPKTIKT LEENLGITIQDIGVGKDFMSKTPKAMAT KAKIDKWDLIKLSFCTAKETTIRVNRQP TTWEKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDVNRHFSKEDIYAAK KHMKKCSSLAIREMQIKTTMRYHLPV RMAIKKSGNNRRIQ/GGIWCDRIL*R*TT CRVAKEIQLS*RRI/WKRLQRTL SIPVLDA V*PPMF*ASVIDTMTI*CFEARDTCFTLTL ESFWD MHRCLAASKGIGLLC*PLIWHM SLMGVKSPPFVFSCLWTS AVRPTT |
| 139 | 8190 | A | 1125 | 1 | 2784 | |
| 140 | 8191 | A | 1126 | 1 | 3000 | |
| 141 | 8192 | A | 1127 | 1 | 3045 | |
| 142 | 8193 | A | 1128 | 1 | 2736 | MIISIDAEKAFGKVQQPFMLQTLNKL GID GSYLKJIIRAVYDKPTANITLNGQKLEAFP LKTGTRRGCPSPLLFNIVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKRIKY LGIHLTRDMKDLFKENYKPLLNEIKEDT NKWKNI PCSWVGRINIVKMAILPRFNAI PIKLPMTFFTELEKTTLNFIWN/Q |
| 143 | 8194 | A | 1129 | 1 | 2955 | |

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| 144 | 8195 | A | 113 | 307 | 1429 | CTATQSGWLC LHRPCPAWRCTWRRTTWFCIRYK GEMVKVSRNYFSKLWLLYRYS CIDDSAFERFLPRVWCLLRRYQMMFGVGL LTRGTGLQGFAACMSLRPSTDSLASVSECFASPLNCYFRQYCSAFPDTDGYFGSRGPCLDFAPLSGSFANPPFCEELHGCHGLSL*ETA*ELTGAPVPSSVFIPEWAGNPQHQRSPA WKQ/MPLQTPPVDPACL*A*VPQWLP AHLQEGGNALQGRPOHGALPTE/PTLALPSGRRRLTGCRS*VLPTGSPGP/PATALVLP HRSYLG GPRTGIRGREQGPKPRA SPHLTYSCGEEGAPGVLSDDLGLGPLGQRDPGCH*HMKIMVLPGLSLPVPKSSPQTPSKSHVYRS |
| 145 | 8196 | B | 1130 | 1 | 3105 | MGKKQNRKTGNSKEQSTSPPKCESSSPAREQSWTENDFDELREEGFRRSNYSELW EDIQTGKEVENFEKNLEECITRITNTKKCLKELMELKTKARELREECRNLRSCDQLEERQINETESQQGYPIELSSAPSGPNTHLQNSPPQINRIYIFSAPHHTYSKTDHILGSKALLSKCKRTEIITNYLSDHSAIKLELRINKLTQSRSTTWKLNLLNDYWVHNE MKAEIKMFFETNENKDTTYQNLWDAFK |
| 146 | 8197 | A | 1131 | 1 | 2826 | MEYYAAIKNDEFMSFAGTWMKLGTHILSKLPQGGQTKHHMFSLTAPHHTYSKIDHII GSKALLSKCKRTEIITNYLSDHSAIKLELR IKKLTQNRSTTWKLTNLLNDYWVHNE MKAEIKMFFETYENKDTTYQNLWDAFKAVCRGKFIALNAHKRKQKRSKIDILTSQLEKEKQEQTHSKANRRQEITKIRAELEIETQKTLOKINESRSWFFERINKIDRPLARLIKKKREKNQIDAIKNDKGDITTDPTD |
| 147 | 8198 | A | 1132 | 1709 | 2973 | TEPKTKTT*LSQ*MQKRPLIKFSNASC*KLSIN/IVLDV LARAIQEKEIKGIELGKEEVKLSLFADDMIVYLENPIVSAQNLLKLISNFNKVSGYKINVQKSQAF LHTNNRQTESQITSELPFTIASKRRKYLGIQLTRDMKDLFKDNYKPLLNEIKEDTNKWKNI PCSWVG RINIMKMAILPKATVTETA WYWYQNRDIDQWNRTEPSEIMPRIYHYLIFEKPDKNKQWGKDSL FNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKTIKLEENLGNTIQDIGMGKDFMSKTPKAMATKAKIDKWDLIQLKSFC TAKETTIRVNRQPIEWEKIFANYSSDKGLISRIYNELKQVYKKKTNNPIKKWAKDMNRHFSKEDIYAANRHMKKCSRSLAIREMQIQTMMRYHLTPV |
| 148 | 8199 | A | 1133 | 1 | 2856 | |
| 149 | 8200 | B | 1134 | 1 | 3786 | MVKGSIQQEELTILNIYAPNTGAPRFIKQVLSDLQRDLDSHTLMGDFNNPLSTLDRSMRQKVNKDTQELNSALHQVDLIDIYRTLHHKSTEYRFFSAPHHTYSKIDHILGSKALLSKCKRTEIITNYLSGHSAIKLELKIKNL TQNRSTTWKLNLLNDYWIHNEMKAEIKMFFETNENKDTTYQNLWDAFKAVCRGKFIALNAHKRKQERSKIDTLTSQLEKELEKEQTHSKAGRKKKEITKIRAQLKEIETQ |
| 150 | 8201 | A | 1135 | 1 | 3276 | |
| 151 | 8202 | A | 1136 | 1 | 3042 | |
| 152 | 8203 | A | 1137 | 1 | 3663 | |
| 153 | 8204 | A | 1138 | 1 | 3144 | |

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| 154 | 8205 | B | 1139 | 1 | 3380 | MVKGSIQQEELTILNIYAPNTGAPRFIKQ VLSDLQRDLDSHTLIMGDFNNPLSTLDR SMRQKVNKDTQELNSALHQVDLIDIYRT LHHKSTEYRFFSAPHHTYSKIDHILGSKA LLSKCKRTEIITNYLSGHSIAKLELKIKNL TQNRSTTWKLNLLNDYWIHNEMKAE IKMFFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQLEKE KQEQTHSKASRRINKIDRPLARLIKKKR |
| 155 | 8206 | A | 114 | 161 | 218 | |
| 156 | 8207 | A | 1140 | 1 | 3345 | |
| 157 | 8208 | A | 1141 | 1 | 3429 | |
| 158 | 8209 | A | 1142 | 1 | 3030 | |
| 159 | 8210 | A | 1143 | 1 | 4170 | MNSLEQNPRSKWELLHRGTMELWPTM WADEEEQGLKAVLALSACKFVPGARSK TGLTDCMGVGGGLLPAPPHIPGKRDSH NPLWNITPENQSPTPTVAMERSSSPATEQ SWMENDFDELREEGFRRSNYSELQEEIK TKGKEVKNFEKNLDECITRITNTEKCLKE VMQLKAKARELREECRSLRSRWNLQLEE RVSMEDMNEMKREGKFREKRIKRNE QSLQEIWDYVKRPNLRLIGVPESDGENA TRLENT |
| 160 | 8211 | A | 1144 | 1 | 3921 | |
| 161 | 8212 | A | 1145 | 1 | 2884 | MVKGSIQQEELTILNIHAPNTGAPRFIKQ VLSDLQRDLDSHTLIMGDFNTPSTLDRS MRQKVNKDTQELNSALHQADLIDIYRTL HPKSTEYTFPSLPHHTYSKIDHIVGSKAL LSKCKRTQIITNYLSDHSAIKLELRIKTLT QSRSTTWKLNLLNDYVWHNEMKAEI KMFFETNENKDTTYQNLWDAFKAVCRG KFIALNAHKRKQERSKIDTLTSQLEKEK QEQTHSKASRRQEITKIRAEKETETQ |
| 162 | 8213 | A | 1146 | 1454 | 3917 | |
| 163 | 8214 | A | 1147 | 11537 | 15574 | |
| 164 | 8215 | A | 1148 | 115 | 450 | |
| 165 | 8216 | A | 1149 | 278 | 885 | |
| 166 | 8217 | A | 115 | 116 | 565 | EPTGTASRAATMPNFSGNWKIIRSENFOE LLKVLGVNVMRLKIAVAAASKPAVEIK QEGDTFYIKTSTTVRTTINFKVGEEFEE QTV DGRPCKSLVKWESENKMCVCEQKLL KGEGPKTSWTRELTNDGELILTMTADDV VCTRVYVRE |
| 167 | 8218 | A | 1150 | 2 | 378 | |
| 168 | 8219 | A | 1151 | 172 | 464 | ASHRVGLLQPFNLWPSGCSTVLAKMK SVLVATEGAEVLFYWTDQEFEESSLRLKF GQSENEEEVGLLML*AR*PHPTPPVLS GLNEGKKKSNFIT |
| 169 | 8220 | A | 1152 | 164 | 528 | |
| 170 | 8221 | A | 1153 | 1 | 1122 | |
| 171 | 8222 | A | 1154 | 1 | 558 | |
| 172 | 8223 | A | 1155 | 1 | 495 | |
| 173 | 8224 | A | 1156 | 51 | 579 | LRSSSPATEQSWTENDFDKLEEGFR*SN YSELQEEIQTKGKEVENFEKNLEECITRIT NTEKCLKDLMELKAKARELHEECRSLRS RCDQLEERVSMEDMNEMKREGKFRE KRIKRNEQSLQEIWDYVKRPNLHLIGVPE SDGENGTKLNTLQDIIQENFPNARQA NIQIQ |
| 174 | 8225 | A | 1157 | 286 | 456 | FCHLSSTSWGGADGTCREGGPLGGFMG PSHQ*ESSVPPEAASSFRITFKSSAVSQSPL |

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| 175 | 8226 | A | 1158 | 1 | 1758 | MDDIPQEARQYRHNQAYAYSIQGDGAE DDDERIVRFHTRVTVSDTLASDAARLT CRHGLGNQDRSSSPAMEQSWTENDFDE LTEVGFRRSVITNFSELKEDVRTHRKE HSAIKLELRIKKLIQNLTTTWKLNLLN DYRVNNEMKAEIKMFFETNENKDTTYQ NLCDTFKAVCRGKFIALNAHKRQERSK IDTLTSQLELEKQEQTHSKACRRQETK IQAELKEIETQKTLQKINESRSWFFEKIN IDRPLARLIKKKREKNQIDAINDKGYIT TNPTEIQTIREYYKHL YANKLENLEEM DKFLDTYTLPRLNQEEVESLNRPTGFEIE AIINSLPTEKRPVDPGFTAKFYHSSADCT RSMAPAPASGEALRLLPLMGEGEGETC RDHIAREEAQECSSSPATEQSWMENDFE ELGEEGFRRSVITNFSELKEDVQTHFKEA KNLEKRLDEWLTRINSVEKTLNDLM*LK TVA*ELRDTYTSFNSRFDQVEERVSVIED QMNEEMEREKFRKRV*RNEQS/LQEIW NYVKRPNLHLIGVSEIDRENGTKLENTL QDIFQENFTYLARQANIQIQ |
| 176 | 8227 | A | 1159 | 138 | 324 | |
| 177 | 8228 | A | 116 | 343 | 528 | |
| 178 | 8229 | A | 1160 | 1 | 525 | |
| 179 | 8230 | A | 1161 | 319 | 1035 | EWSSVRRSLVEKRALRRPHQCLCFRMRK TILASNQTCRPFPEAVDITLKGRTVIVKGP /REGTLRRDFNHINVELSLLWKEKKRGF RVDKWWGNRKELATGRD*FVSHVQN MIKGCYT GASGYKMKVLWYAHFPIQRL LFQGELGPSLLKSRNFLGGWKNTSRRVS G*GPGCLLVSVSQGPRKDEINPLKGNDI ELVSKFQRALIQQATTVKNGKURKFFG WVMSMLEKGTVPGLIE |
| 180 | 8231 | A | 1162 | 232 | 338 | |
| 181 | 8232 | A | 1163 | 474 | 647 | |
| 182 | 8233 | A | 1164 | 1 | 413 | |
| 183 | 8234 | A | 1165 | 2 | 2545 | |
| 184 | 8235 | A | 1166 | 1364 | 1618 | SQHSGRPRQADHLRSGVRDQPGQHGEIL SLLKIQKLAGRAGSRL*SQLLERLRLYHR TPA*VTE*DMASKNKKKPHRIQARKYF |
| 185 | 8236 | A | 1167 | 3 | 342 | LTQELPGAEAHACNPSTLGGQGGQIMRS GARDQPGQHSGTPSLLKIQKLAGRGGT HL*SQLLRRLRQENRLNLGSGGCSELRL RHCTPAWVTDSVSKKNELEKESYLIFSSL T |
| 186 | 8237 | A | 1168 | 2 | 232 | WAGRGG SRL*SQHFGRPRRADHERWKN TWELRQLNLGQAPCSRNGMRRYGERRH HPDEPGQPSVEGFLRVLSMCIC |
| 187 | 8238 | A | 1169 | 1294 | 1624 | GQLYEKLGRRGPGAVAHAACNPSTLGG GGWITRSGDRDHPG*HGETPSLLKIQKK LAGRGGGHL*SQLLRRLRQENGVPNGA/ RGCSELRSCTPAWGTEDSVSKKKK K |
| 188 | 8239 | A | 117 | 296 | 629 | FKLTSSRNPPTGPGAVAHAACNPQHFR PRQVDHLRSGV*DQPGQHGETPSLLKIQ KLAGHGGVHL*S*LLRRLRQENRLNLGG GGCSEPRSHCTPAWTTG*DSASKKKK |
| 189 | 8240 | A | 1170 | 427 | 730 | |
| 190 | 8241 | A | 1171 | 6497 | 6788 | SQRFRPGQANCLSSGV*DQPGQYGETL SLLKIQKLGCGGTCL*S*LLGWLRQEN HLNLGDGCGCSEPRMCHCTPPWTEGGS A*KLKKKKKKRKYL |
| 191 | 8242 | A | 1172 | 173 | 395 | |
| 192 | 8243 | A | 1173 | 239 | 404 | |

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| 193 | 8244 | A | 1174 | 126 | 915 | SACVSCNPAALLLALRSAGPPSFLPPHPA RGSAGCVTLSHPTHQPAQHHGWTVKL EVFSLPQCKEDAEWETYPMRREMQUEI LPGULFLGPYSSAMKKQDPSLLAVSSHG QENEFLLPLTRVQSCHGGFYPHDLNLKLI IFQRLHHHILGLPVLQKHGITHICIRQNE ANFIKPNFQQLFSAFVIAIYIMETFGMKY RDAFAYVQERRFCINPNAGFVHQLQEYE AIYLAKLTIQMMSP/LRDRKVIICSFWYH RQFEENT |
| 194 | 8245 | A | 1175 | 1 | 924 | |
| 195 | 8246 | A | 1176 | 441 | 707 | |
| 196 | 8247 | A | 1177 | 109 | 437 | NQRRKWRRSRTQLQTLQEALKAIEIGH QKLAQMKQDPQADL*KQLYELQAKI TALSEKQKRVEQLRKNLIVKQEQPDKF QIQPLQSDNKLRTAQQQPLQQLQQQQ |
| 197 | 8248 | A | 1178 | 343 | 670 | |
| 198 | 8249 | C | 1179 | 130 | 390 | MAEQSLISGGPKPKSVNSLRWINLXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXSWVDK* |
| 199 | 8250 | A | 118 | 74 | 396 | GQILALMPKGGGGGGILTYPNPPLPG*N NFPGLTPRTGINGLGPGRVNFIFKKK GGFPPGARGV*NPGPRGASSPGPKGRG *SPPP/QGPFKPLKRFPDLPIFPR |
| 200 | 8251 | A | 1180 | 238 | 435 | |
| 201 | 8252 | A | 1181 | 615 | 945 | |
| 202 | 8253 | A | 1182 | 232 | 564 | |
| 203 | 8254 | A | 1183 | 3 | 487 | LPNMAQSINITELNLPQLEMLKNQLDQE VEFLSTIAQLKVVTQKYVEAKDCLNVL NKSNEGKELLVPTDGVLCMSPGKLHDV EHLIDVGTGYVVKTAEDAKDFFKR KIDFLTKQMEKIQPALQEKHAMKQAV MEMMSVQKIQQLTALGEAQATAKA |
| 204 | 8255 | A | 1184 | 187 | 423 | |
| 205 | 8256 | A | 1185 | 539 | 871 | |
| 206 | 8257 | A | 1186 | 158 | 1330 | SVDLVIHPLWPPEVLGLQQQPTQFINPET PGYVGFANLPNQVHRKSVKKGFEFTLM VVGESGLGKS/TLS*NSLFLTDLYPERVIP GAAV*FFSRKN*KELVQIEASTVEILRAR GSSLRLASG*DTPGYG*PLFNCRCDF*G QFISYYLMRQF*GGYLHDESGLNRRHHI DNRVHCCFHFISPFHGLQPLDVAFMK AIHNKVNI PVIAKADTLTKERERLKKR ILDEIEHNIKIYHLPDAESDEDEDFKEQT RLKASIPFSVVGSNQIEAKKKVRGRL YPWGVVEVENPEHNDFLKRLTMLITHM QDLQEVTDLHYENFRSERLKRGRKV ENEDMNKDQILLEKEAELRRMQEMIAR MQAQMOMQMQGGDGDGGALGHHV |
| 207 | 8258 | A | 1187 | 405 | 632 | |
| 208 | 8259 | A | 1188 | 111 | 375 | |
| 209 | 8260 | A | 1189 | 428 | 574 | |
| 210 | 8261 | A | 119 | 454 | 777 | ADPMSPSSKSPNMEAVLWIPDTNIVL*SL KVYPSS*TIKSWLGT/CGSRL*COHFRP RRVDHEVKRLRPS*PTWRTPSLL/RTTKIS RAWWHTSVVPATRAEAGESLE |
| 211 | 8262 | C | 1190 | 216 | 458 | MNRDRTSRNRCVCDVFRNAVKGQTVLG RQLFIGRVRVPVRPGEGLPWGFLPVSP WCPSWGLSTHALWWAEAVPGRALVH* |

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| 212 | 8263 | A | 1191 | 1 | 594 | RTRGRTRGLLPSGAPEPEAAGSATAPRG CKNPGAKGGLLAAMAGRQDIFHAIVKA DERFHGEGYREGYEKGSILGVKEGRQHG TLHGAKIGTEIGRYQRFAPAWKCLLHIA PLRRTA*T*RS*HAWIGRIQIFPYDDPTYD KLHEDLDKIRGKFKQVRALCVSSC*EHLI APFPGGAHSGRRCGNGLGLRAPRNC |
| 213 | 8264 | A | 1192 | 482 | 788 | |
| 214 | 8265 | A | 1193 | 572 | 676 | |
| 215 | 8266 | A | 1194 | 1 | 394 | KGGSMHMYAKNFYGGNGIVGAQQQIFE AYNMAALWKLPCIFICENNRYGMGTSV ERAAPSTDYKRGDFIPGLRVDGMDILC VREATRAAAAYCRSGKGPILMELQTYR YHGHSMSDPGVSYRTREEIQE |
| 216 | 8267 | A | 1195 | 641 | 722 | |
| 217 | 8268 | A | 1196 | 354 | 1145 | KQISCINRKLFFVSVTCVMVRKLAVWA WRPASTPQTISSQPTGLTALLSPGAFPSE KFSQSLQDEKEVVLLKGKEDRCTCMPRTS TGAMASWERRCPWAAGIALACKYNGK DEVCLTLYGDGAANQQQIFEAYNMAAL WKLPCIFICENNRYGMGTVERAAASTD YYKRGDFIPGLRVDGMDILCVREATYI GRAYCRSGKGPILMELQTYRYHGHSMS DPGVSYRTREEIQEVRSKSDPIMLLKDR MVNSNLASVEELKGI |
| 218 | 8269 | A | 1197 | 2 | 506 | |
| 219 | 8270 | A | 1198 | 1 | 1455 | |
| 220 | 8271 | A | 1199 | 509 | 839 | |
| 221 | 8272 | A | 12 | 105 | 702 | AGSSVSLGFCPAAAAHKPRGGALRLPVF RRRAQQGPDYALAGVARQPACTCRRRC NRSHCRAEDPQWPTPAAAPAAHSPHMS LGESGLGKLILINSLFLTDLYSPEYGPSQ RIKKPVQVYILVFLIDDKLE*Y*YTQSTC CNFHYASQSWQPAINYIDSKFEDYLNAE SRVNRQMPGNRVQGCIFYIAPSGHGPH HN |
| 222 | 8273 | A | 120 | 133 | 359 | RHCSSGMEJPPTNYPASRADLVAQNYIN YQHGTPHRVFEVHNAYRVIMQDMSG* GHLVSPSSRFFLHSFATSLFE |
| 223 | 8274 | B | 1200 | 109 | 267 | MEETPCRELEEEEEWGSGSEDASKKDGA VESISVPDMVDKNLTCPEEEDTVKV* |
| 224 | 8275 | A | 1201 | 856 | 1030 | VPNLQVGDEKQDSPNGEHWHGQEDST AEPAEVKAMMSVAVV*KNLTPPPLLG RSSV |
| 225 | 8276 | A | 1202 | 67 | 264 | |
| 226 | 8277 | A | 1203 | 3 | 1251 | |
| 227 | 8278 | A | 1204 | 1403 | 3362 | |
| 228 | 8279 | A | 1205 | 388 | 1711 | ACALGMAPQRKRRKQLSMKTGSYSQRS SFQRRKRPQGGRSRNSAPSGATLSLGA LAWHLEWLSVIQLWHYLFITLNSLLTN MAGGDMARVSTYTNAFAFTQFGVLSAP WNGLLMDRLKQKYQKEARKTGSFNIRG PHSLYFPNHHLPHATYRDKAKMKLPLLL ALLFGAVSALHLRSETSTFETPLGAKTL PEDEETPEQEMEETPCRELGGRGREWG LWEVEDASQERWGLFESILQCPDMGGT KTFTCS*GKEGHQLKVGWGPGGCPRPA RYLPG*ESLSRRFSSKLWFFARSCYRG QTWVFHSTTFQY*LSESKCSVLSALMQG QVWIG\GRI\TGSGR\CRRFQWVDGSRW\ NFA\YWG\AHQ\W\SRGGHC\VALC\TRG\ GYW\A\RAH\CLQKNFPFICFPLSWSQPAV QVVSPGQLPPLLCLPSLPPPCNNNGFY |
| 229 | 8280 | A | 1206 | 97 | 441 | |
| 230 | 8281 | A | 1207 | 19 | 432 | |
| 231 | 8282 | A | 1208 | 165 | 257 | |

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| 232 | 8283 | A | 1209 | 80 | 1239 | GAVVGGGRRRRRRITYKCLPKLDPKPK FQEGERVLCFHGPLYEAKCVKVAIKDK QVKYFIHYRGWNKNWDEWVPESVVK YVDTNLQKQRELQKANQEYAEKMR GAAPGKKTSGLQKNVEVTKKNKQK TPAGMGDGGSTSETPQPPRKKRVRDP TVENEETFMNRVEVKVKEELKPWL DDWDALITRIQKQLFYLPKKNVDSILED YANYKKS/RVGNTDNKEYA/VLNEVVAG D*KNTFNVMLGTQLLYKFERPQYAEIL ADHPDAPMSPGVWSAQHLEIHWYRIGA MLAYTPLDEKSLALLNYLHDFLKyla KNSATLFSADYEIVAPPEYHRKAVWKS TLTHLCLDLRKHIFVLSLSPWYKPMCFE DVSV |
| 233 | 8284 | A | 121 | 3 | 1671 | SSGARWRFRAGSMGLFCQRKHSS/SHPV LQKPSVFGNDSDDDDETSSESLQREAA KKQAMKQTKLEIQKALAEDATVYEYDSI YDEMOKKKEENNPKLLGKDRPKYIH NLLKAVEIRKKEQEKREKKIQREME KGEFDDKEAFVTSAYKKKLQERAEER EKRAAALEACLDVTKQKDLSGFYRHLL NQAVGEEVVKCSFREARSGIKEKSRG FSNEVSSKKQNTTREMHSFKLM*K*REN PDADSYFADAKSSPDDK*KKLELTAEGK RS*RPLRMTSSTTGVTTLGHLVKKEGT VPGTTRKDHERREDMRKGKISTSRNPE TKRTITLTVITGKKGILIGTERPVIEPIGR GMNRKINQGRGTKEKEVTEYGKGRKIG RNIPKENKKEIDNKMIRTDPRKERRKR KAKQRKRAYESKGGKVLKLLINTEIEKN ER*VFS/ASERNQDQKQKPKFQGRINF LTNLDFIQNGETWQRTKERNQEKPSNSE SSLGAKHRLTEEGQEKGEQERPPEAVS KFAKRNNEETVMSARDRYLARQMASG |
| 234 | 8285 | A | 1210 | 31 | 1029 | WWNSEVPHGPFMRKAAVLT/APVLFSD G*ARRRHFWQGG*SPRAAWDRVAKDL ATRVPTVLKEQRTETYSQFEGRLRGE NS*TLKLLDNWDSVDLPFSKLRHSF GPC*PRDFLGINLGKRETRGALRQGRLR QRIFGRRLKGPRLQP*LGDDFPRKKLAR KEIGALTRQKGWSRLRARTSKKGARPE LHELARRSLPLGEAVSRPRARPMWDAL RTHLAPYSDEMISQRLGARLGALRENG GARMGQYHAQATEHLSTLSEKAKPAL EDLRQGLLPVLESFKVSFLSALEEYTKK LNTQLRRPPPPYPVLRINVSXVGGKKK KK |
| 235 | 8286 | A | 1211 | 3 | 450 | QTQREPTMVLSPADKTNVKAAGKVG AHAGEYGAEALERMFSLFPTTKTYFPHF DLSHGSAQVKGHGKVVADALNAVAH VDDMPNALSALSDLHAHKLVRDPVNFK LLSHCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR |
| 236 | 8287 | A | 1212 | 9 | 675 | NSARATDSERTHHGARLLPDKTNVKA WGKVGAGHAGEYGAEALERMFSLFPTTK TYFPHFDLASHGSAQG*RAHGKVVADA LTNAVAHVVDMPQTALSALSGPATAH KLVRDPVQLSSS*SHLPCWWTLGRPTSP SEFNPWRLHAFPGTKFPGLLVEAPLLEPS KLPLKGLSLRVGHAFAPLGLPRALLPF PGTRNPVGLLNKILNWGGKKKKKKKIF |
| 237 | 8288 | A | 1213 | 1 | 645 | KIFLSDCLACDSCMTAEKGVQLSQNAK DFRVLN/LNKKCDTSKHKVLVSVCPQ SLPYFAAKFNLSVTDASRRLCGLKSLG VHYVEDTTIAADFS/HWRMLKWQRP PDSRRTCG*GPAAADGRHLR*HPCAASG VQCKRAGAVPGVAGGDQLPQGRGAA YHVPEPGAWHTQPGHQVVKSGQLPAA LGARAKSVVEGGAALSGVKTIKKT |

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| | | | | | | LGARAKSLSVEGGAALSGVLKTLKKT |
| 238 | 8289 | A | 1214 | 193 | 564 | |
| 239 | 8290 | A | 1215 | 211 | 1795 | TPLGRRRRRKTHDKRKPGQGPMPGAEC SKKTKVADDOENVASADAPSPAQENGEGK EFHKLADAKIFLSDCLACDSCMTAEEGV QLSQNAKDFFRVNLNKKCDTSKHKV LVVSVCPSLPYFCWLNFNLSVTDASRR LCGFLKSLGVHYVFDTTIAADFSILAESQ KEFVRRYRQHSEGGNAPCPMLTSACPG L/WVRYAGAGCWGRPITG/HTFLAPPKSP QQVMGSLVKDYFARQQNLASPEKIFPRS LVAPICVYDKKLAEALQKPFPLALHGSR GRLTCVLTSGEICFKLMEQGDLSVRDA AVDTLFGDLKKDKVTRHDGASSNGHLA HIFRHAAKELFN/ERDVEEVTYRTLNRQ RFPQKVTLEEEKRWV*TFVLEPYAFRNI PET*SLKPLKKGKVPFHFVEGSSPCAIG GCLNGKRPKPKIQDGHGDKAPAAGRM EGY/SLDIPVRRPESIAHVQELVQEWL EGINSPKARKVLHTTYQSQERGTHSLG HSSWLKFRPGPSSCSWGQSQEPLSRGRG LP |
| 240 | 8291 | A | 122 | 170 | 339 | IMKLITILFL*CRLLSLTQESQSAEIDLLD NDLFLAEEAIGLYRYIMQIQTNPRI |
| 241 | 8292 | A | 1222 | 1 | 456 | RPRRPQREPTMVLSPADKTNVKAAWGK VGAHAGEYGAEALERMFLSFPTTKTYF PHFDLSHGSSQVKGHGKKVADALTNV GHVDDMPNALSALSDLHAHKLKRVDPVN FKLLSHCLLVTLAAHLPAEFTPAVHAFL DKFLASVSTVLTSKYR |
| 242 | 8293 | A | 1223 | 2 | 435 | QTQREPTMVLSPADKTNVKAAWGKVG AH/AGEYGAEALERMFLSFPTTKTYFPHF DLSHGSAQVKGHGKKVADALTNV/VEH VDDMPNALSALSDLHAHKLKRVDPVNFQ APKATGLLVDPGPAHFPGRVSPRLRQGF LGTKFLGFC |
| 243 | 8294 | A | 1224 | 9 | 390 | NSARATDSERTHHGARLLPDKTNVKA WGKVGGAHAGEYGAEALERMFLSFPTTK TYFPHFDLSHGSAQVKGPTAKKVAER ADQTPWRNVDDMPKRRCP*SDLHAH KLKRVDPVQLSS*SHLPCW |
| 244 | 8295 | A | 1225 | 3 | 452 | |
| 245 | 8296 | A | 1226 | 26 | 636 | NSTDERTHHGARLLPDKTNVKA ^{AWG} KVGGAHAGEYGAEALERMFLSFPTTKTY FPHFDLSHGSAQVKGHGKKVADALT NAVAVDDMPNALSALSDLHAHKLKRV VGPSTFKLLKPLALL*TLGRPPSPAEF QPLGGCKASLGTKFLGFLVEAPLLEPSKL PLKLSLRLAMLSLPLWAFPPAPPLSCT RTPVVFEIKS |
| 246 | 8297 | A | 1227 | 17 | 233 | AFGTRELQCCVFLASMLGVPIPTVQGF QWTLRGTDVETSPFGAPRATSHGVGQM KSCQIPQLKIRMVQNNIIPGETQILLRF TGWESKVNKKQPPVGIKCEPMDQNE QTGGHETDGHRISSVVSAATQECLI*N TIRNVWTQ*TKSNLTRCGPNEELPDPTA LEDKDGQTK |
| 247 | 8298 | A | 1228 | 1 | 433 | |
| 248 | 8299 | C | 1229 | 312 | 443 | MHKRNFRHAGRSQAVQDNWKELNNIYP VSPARLQALLPPAAPC* |

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| 249 | 8300 | A | 123 | 23 | 307 | RQTRWCPVVRLSHYRTLGGCCHLRGR GVA*VRGPQSGTSSVENTPPWRRVSCFP APNITCKDSSGNETHFTGNEVGFFKPISC RNVNGYSYK |
| 250 | 8301 | A | 1230 | 1 | 94 | |
| 251 | 8302 | A | 1231 | 2 | 122 | DLLCPQMG*GWKLTALSQCQLQDGIER SRAKASQCCLSI |
| 252 | 8303 | A | 1232 | 3 | 53 | |
| 253 | 8304 | A | 1233 | 1 | 2679 | SAVGSDHIFHNIPDSTSSATNVSMVVSAG PWSSEKAEMNILEINEKLRPQLAENKQQ FRNLKERCFLTQLAGFLANRQKKYKYE CKDLIKFMLRNERQFKEEKLAELKQAE ELRQYKVLVHSQERELTQLREKLREGD ASRSLNEHLQALLTPDEPKSQGQDLQE QLAEGCRLAQQLVQKLSPENDEDEDED VQVEEDEKVLESSAPREVQKAESKVPE DSLEECAITCSNSHGPCDSNQPHKNITF EEDKVNSTVVDRKSSHDECQDALNILP VPGPTSSATNVSMVVSAGPLSSEKAEMN ILEINEKLRPQLAEKKQQFRSLKEKCFVT QLAGFLAKQQNKYKYECKDLIKSMLR NELQFKEEKLAELKQAEELRQYKVLV HSQERELTQLREKLREGDASRSLNEHL QALLTPDEPKSQGQDLQEQLAEGCRLA QHLVQKLSPENDEDEDEDVQVEEDEKV LESSSPREMOKAESKVPEDSLEECAITC SNSHGPCDSNQPHKNITFEEDKVNSSL VVDRESSHDECQDALNILPVPPTSSATN VSMVVSAGPLSSEKAEMNILEINEKLRP QLAEKKQQFRSLKEKCFVTQVACFLAK QQNKYKYECKDLIKSMLRNELOFKEEK LAELKQAEELRQYKVLVHSQERELTQL REKLREGDASRSLNEHLQALLTPDEPD KSQGQDLQEQLAEGCRLAQHLVQKLS ENDNDDDEDVQVEVAEKVQKSSSPREM QKAEKEVPEDSLEECAITCSNSHGPYDS NQPHRKTITFEEDKV DSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQ ESEEEVPQESWDEGYSTLSIPPERHRW DQVKKEDQEATGPRLSRELLA |
| 254 | 8305 | B | 1234 | 33 | 2996 | MLRNERQFKEEKLAELKQAEELRQYK VLVHAQERELTQLREKLREGDASRSLN EHLQALLTPDEPKSQGQDLQEQLAEGC RLAQHLVQKLSPENDNDDDEDVQVEVA EKVQKSSAPREMOKAEKEVPEDSLEEC AITCSNSHGPYDSNQPHRKTITFEEDKV DSTLIGSSSHVEWEDAVHIIPENESDDEE EEEKGPVSPRNLQSEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQV CM |
| 255 | 8306 | B | 1235 | 16 | 1041 | MVKQNNIIPGETQILVRFTGWESKVNK KQPPVGKCEPMDQYEECKDLIKSMLR NERQFKEEKLAELKQAEELSMVVSAGP WSSEKAEMNILEINEKLRPQLAENKQQF GNLKERCFVTQLAGFLANQQKKYNYEE CKDLIKFMLRNERQFKEEKLAELKQAE ELRQYKVLVHSQERELTQLREKLREGD ASRSLNEHLQALLTLDEPKSQGQDLQE QLAEGCRLAQHLVQKLSPENDEDEDED VQVEEAEKVQKSSAPREVQKTEESKVPE DSLEECAITCSNSHGPCDSNQPHKNITF EEDVNSTLVVDRESSHDECQDALNILP ACMTE* |

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| 256 | 8307 | A | 1236 | 1 | 2219 | MSQSVQDNLKELNNIYPDHSSSPAMEQS RMENDFDELTEVGFRKLVTNFSCLKED VRTHRKEAKNLEKRLDEWPTRMNSVEK TLNDLMELKTMARELRDACTSFSSQFDQ VQETPLKIRMVVKQNNIISAESQILVRFTS WESNVNAKKQLPVGIKCEPMDQECIPGS RACTLLVRFSNGGPPMDPGSERKDLLQL GGELARTSRAVQEAGLGLSTGLWLAESR AKAALEKQALLQAQLEEQLRDKKDLAQ QQMQSDLDKADLSARVTELGLAVKRLQ KQNPEKDQVNTDLTEKLEALVQMLPLES QLPIPTSGTLTPPGYSLVWSPLCVGPGLG SRSGSPIDCVTWGKTDSTMQAHEDAQR EVQRLRSAKELLRRLSGMLMEVEEPEVL QDSLDRCYSTPSMYFELPDSFQHYRSVF YSFEEQHISFALDVE/E*VSYFDGNKSPP GLPDGSHIPTRTAGQARLLHARRRIPQ ERTTTPKVSQLASWVSLG/RQYLHPAGS LRWL*TTLPPTSSSMFPLCPQ/YPSEDSRE AGIKKDQEEEDQGPPCPRLSRELLEAVE PEVLQDSLDRCYSTPSSCLEQPDSCLPYG SSFYALEEKHVGFSLDVGGYLELTDSCQ PYRSAFYILEQQRVGWALDMDIEKYQE VEEDQDPSCPRLSRELLDEKEPEVLQDSL DRCYSTPSGYLELPDLGQPYSAVYSLE EQLGLALDVE/E*VPYDEDETEAQRSE DTGAGSHSW |
| 257 | 8308 | A | 1237 | 3 | 1270 | |
| 258 | 8309 | C | 1238 | 160 | 267 | MGPLTLSSSLHTETFLCPILTQGHQSCQ CENRRL* |
| 259 | 8310 | A | 1239 | 1 | 1233 | |
| 260 | 8311 | C | 124 | 35 | 91 | MSPPQNKGPFPKSPGWF** |
| 261 | 8312 | A | 1240 | 401 | 2582 | |
| 262 | 8313 | A | 1241 | 946 | 2562 | FPLAYSLLFPP/CSRLSRELLEVVEPEVLQ DSLDRCYSTPSSCLEQPDSCQPYGSSFYA LEEKHVGFSLDVGEIEKKGKGRRRGR STKKRRRRGRKEGEEDQNPPCPRLSREL LDEKGPEVLQDSLDRCYSTPSGYLELTD SCQPYRSAFYILEQQRVGWALDMDIEK YQVEEDQDPSCPR*L*AITDA*FCVDTW RCQVQKQECVQFHVFNEG*ITPTDIAV GFHCSRCLGFHFFLPLSFTHLL*VDHTSK AVWQLHGILSKFMENY*AHSFHDHCSLC VPRALTQSVL*PLHQCVTRPIR*AHFLLS LSLPLPVFLFHSFLPGPGLSQHKGNNSLP H*WICPFSF*TVPYVSHEI*LGLCGF*FPL AYSLLFPT/CSRLSRELLDEKEPEVLQDSL DRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEDQGPPCPR LSRELLEVVEPEVLQDSLDRCYSTPSSCL EQPDSCQPYGSSFYALEEKHVGFSLDVG EIEKKGKGRRRGRRSKKKKKGRP |
| 263 | 8314 | A | 1242 | 442 | 5178 | HQELPDPTGPCGRLLSLTIHGVTRIYHA LLWARGPIMSKSQVLGEWEPVQGGKSS ENDKWTMSDPGAEAPTCRAASGV DKE QQGRWQGLWNSHIKPLKIRMVVKQNNIIP GETQILLRFTGWESKVNKKQLPVGIKC EPMQDQENEQTGGHETDGHRIVSVLHFP LISILSYATWGLSLLECIPGSPVCTLLVRF SNVGTRWSLEVRGSPCGFGSNKVCVGM TPEIKMVCVCEGKAGKAVGSGGVEGTK EVST |

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| 264 | 8315 | A | 1243 | 1 | 3242 | MDKPRPGKTTFVIMVSPLPAPYTSPTTH MVTCPAHPRAFLALTHSWDPQVRPAVL NPLPRHGSSFFVVKQPVAKQQLRCLIIYE VALSVMSPTAPSSSRSPWKRPLRPGFE QPGGSREAERLVGSRDGSSRSLHSLHPV REPVPSSLRIRGAAELPLSSDPAFGTG APPGQGSWQYKVLVHAQERELTQLREK LREGRDASRSLNEHLQALLTPDEPKSQ GQDLQEQLAEGCRLAQHLVQKLSPEND NDDD |
| 265 | 8316 | A | 1244 | 148 | 197 | DPLGFL*QKRNNQEDD |
| 266 | 8317 | A | 1245 | 1333 | 2383 | RMKKEHVLHCQFSAWYPFRGVTIKSVI LPLPQNVKDYLLDDGTLVVSGRDDPPTH SQPDSDEAEIQQWSDDENTATLTAFEF P*SLPLKVQGSYQIPLGGQVSFPK*VFGS APRD\AYWIAMNSSLKCKTSLDIFLLFKS SDFITRDFTQPFHCTDDSPDPCIEYELVL EKWCEMIPGGEFRCFVKENKLIGISQRD YTQYYDHISKQKAEIRRCIQDFFK\KHIP VQIL*MKDLVFDIYRDSRGKVWLIDFN PFGEVTDSSLFTWEELISENNFKRRFLV KVDAQEODSPFSVAQTSEVTVQPOLIC SYRL\PKDFVDLSTGEDAHKLIDFLKLK RNQPEGR |
| 267 | 8318 | A | 1248 | 66 | 703 | RRRRLPSVAIMIILPGPSSSHDEMFSDIY KVRGDRGRGLCLEGGGRWVSRTEGTI D\DSLIGG\NAISAESPRGAKGTERHK*ST GV\DIVMNHHLPGNKFSQKEASKKVHQR ITMKS\KGP*KNRRPRKSKTFL*QGAA EQIKHILANFKKLQF/YFIGENMNPRWA WVLLLDY*RDGVPP\YMIFFKIDGLEME KMLTNVAIILDLSPCHP |
| 268 | 8319 | A | 1249 | 1 | 521 | MKNRSRNKGNVEWQAEGIRSKRSVGKQ RPSKAKIPSGDKNGVSLTHNEVINNDNP LESNDEKEGQEATCSRPIVP/EFQ**LF RPE*WRRASGNLQIPKRVSA*GTRGSP SKKGERVRRDAQQTATW*TRSPASGCF QICEGNKQDEACDVRGLQHCHERHSLAG PREYMP |
| 269 | 8320 | A | 125 | 50 | 230 | NLKGPLRRPVSGIIHVISLPLYQKCSKNE KKIPWRQMEM/C*NVPSANNPPLGLLKN IVF |
| 270 | 8321 | A | 1250 | 3 | 168 | |
| 271 | 8322 | A | 1251 | 3 | 249 | |
| 272 | 8323 | A | 1252 | 23 | 2669 | |
| 273 | 8324 | A | 1253 | 97 | 1609 | GGKMAGGGGDLSTRRLNECISPVANEM NHLPAHSHDLQRMFTEDQGVDDRLLYD IVFKHFQR/NKVEISNAIKKTFPFLEGLRD RDLITNKMFEQSQDSCRNLVPVQRVVY NVLSELEKTFNLPVLEALFSDVNMQEYP DFKFHIYKGFENVINHDKLPSPRKVEEEE KGRRLGLLPTKSLNKGTGENSFRKPDFG PPSGFPHPPCLGTTPE/NMGLSEHPCETE QINAKRKDTTSDKDDSLGSQQTNEQCAQ KAEPTECEQIA\VOVNMGDAGREMPCP \LPCDEVESPRGKSLHNHWNPKFNSLVLC ELVDIKKEKPFNSKVEICQAQARTHNN QASDIIVISSEDSGSTDVDEPLEVFISAPR SEPVINNDNPLAESNDEKEGQEATCSRPI IVPEPLIFRKLFT\FRESFRKRVIG/QKTHD FSESQ*GGGAPQEASSGGTEARHGEKA PIDF*EVHLTWEEYPSRKETFPVSDFS PE*MGERAFQETCSSSLRRGLG |
| 274 | 8325 | A | 1254 | 3 | 274 | FFASLLESPVSPRLAMDPCSCAAGVSC TCAGSCKCKECKCTCKKSECEAISMVW GCG*GCCSCCP/AAASKCAQGCVCCKGAS EKCSCCD |
| 275 | 8326 | A | 1255 | 788 | 1173 | |

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| 276 | 8327 | A | 1256 | 80 | 231 | IRPLPPRFKTESRSLPGPCLQPGTFLWSRN RRVLGFPSMNGEDMGLFLCSEWERSSE GWLCTEKGEVDTQLNPTAVPSCISLTAH CVFLFLVGGSCCTCAGSCKCKECKCTSC KKSECG/CH/PPGIWGCG*GAWFSQHEW RGHGASLPLL |
| 277 | 8328 | C | 1257 | 81 | 476 | |
| 278 | 8329 | A | 1258 | 3 | 452 | |
| 279 | 8330 | A | 1259 | 9 | 486 | NSARATDSERTHHGACLLPDKTNVKAIA WGKVGAGHAGEYGAEALERMFLSFPTTK/ TYFPHFDLSHGSAQG*RAHGK/KVADA LTKRRGATWDDM/PQTALSALSDLHAH KL/RVGPSTFKLL/SQLPCLGEPWAAHL PAEFQPLAVARLPWNKVSWGFC |
| 280 | 8331 | A | 126 | 814 | 1292 | GISPFYIFGQDMGLEKNPTSFPKMCFC PLESLPSYVGCWKTGNMSCVVCTVNW LRSVIYFIFWITNLSHFEVLALKRLLAPG GGGNMPPRVL*ACCRRTTGHRVWPSRP PEQTDQATARPPSWRPTL/CSPLPLPPPR SGREKGNRARFLKGPRIG |
| 281 | 8332 | A | 1260 | 3 | 497 | PTLLVPTDSERTHPWLLSPADK/TNVKA/ AWGKVGAGHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQV*GPRARKVADA L/TNAVAQRGT/DIAQRACPLSDLHAHK L/RVGPSTFKLLKATC/HCLGEPWAAHL PAEFQPLAVARLPWGQSLGFLKQRC |
| 282 | 8333 | A | 1261 | 1 | 1077 | MLSGVGGFVLGLLFLGAGLFIYFRNQKA EESFVSALSIDLSGGGMALLSMVCLKF PGGSCMAALT/VTLMVLSSPLALAGDTR VPPVRLRKTEDEPLGCVLSGLRVGPDSVF PGGRFCNRIVLVPPARFLEQVKHECHFF NGTERVRFDRYFYHQEEYVRFDSVVG EYRAVTELGRPDAEYWNSQKDLLEQKR AAVDTYCRHNYGVGESFTVQRRVYPEV TVYPAKTQPLQHHNLLVCSVNGFYPGSI EVRWFRNGQEEKTGVVSTGLIQNGDWT FQTLVMLETVPRSGEVYTCQVEHPSLTS PLTVEWRARSESAQSKMLSGVGGFVLGL LLFLGAGLFIYFRNQKGHSGLOPTGFLS |
| 283 | 8334 | A | 1262 | 3 | 825 | LFSSMVCLKLPGGSSLAALT/VTLMVLSS RLAFAGDTRPRFLELRKSECHFFNGTER VRYLDRYFHNQEEFLRFDSDVGEYRAV TELGRPVAESWNSQKDLLEQKRAAVDN YCRHNYGVGESFTVQRRVHPQVTVYPA KTQPLQHHNLLVCSVSGFYPGSIEVRWF RNGQEEKAGVVSGLIHNNGDWTFTL VMLETVPRISEEVYTCQVEAPRA*QAPL TVEWRARSESAQSKMLSGVGGFVLGLL FLGAGLFIYFRNQKGHSGLOPTGFLS |
| 284 | 8335 | A | 1263 | 11 | 885 | DLPASLAPGPVLFSSMVCLKLPGGSCMT ALT/VTLMVLSSPLALAGDTRPFLWQP KRECHFFNGTERVRFLDRYFYNQESVR FDSDVGEYRAVTELGRPDAEYWNSQKD FLEDRRAAVDTCRHNHNYGVGESFTVQR RVQPKVTVPYPSKTQPLQHHNLL/VFCV SGFYPGSIEVRWFLNGQEEKAGMVSTG/ LIQNEGDGPFQTLVMLETSFFGVERVNT/ SQVEHPKCARPLTVE*RARSESAQSKML SEVGGFVLGALLPLPGFLFIYFRNQKG HSGLOPTGFPELKR |
| 285 | 8336 | A | 1264 | 25 | 628 | EFHRLRENPPWCLSPADKTNVK/APAWG KVGAGHAGEYGSEALERMVLPPTPKP YFPHFDLSHGSAQV*GPRARKVADALA TNAVAQRGT/DIAQRAVPPLSDLHAHKLA RVGPSTFKLLKATC/HCLGEPWAAHLPA AEFQPLAVATSSLGTFKFGFLVEAPLLTF QITFKGWKLWLAIVFLPFGLPSPSSPFL HPYPRGL |

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| 286 | 8337 | A | 1265 | 1 | 625 | CKFIRVMAHTRLRLPLRRKKAHLMEIQ VNEGTVAEKLDWARERLEQQVPVNVQVF GQDEMIDVIGVTKGKGKGYKGVTSRWHTK KLPRKTHRGLRKVACKDGLIKNNAST DYDLSDKSINPLGGFVHYGEVTNDFVML KGCVVGTKKRVLTLRKSLLVQTKRRAL EKIDLKFIDTTSKFGHGRFQTMEEKKAF MGPLKKDRIAKEEGA |
| 287 | 8338 | A | 1266 | 1 | 1251 | |
| 288 | 8339 | A | 1267 | 1 | 903 | |
| 289 | 8340 | A | 1268 | 1 | 1131 | |
| 290 | 8341 | A | 1269 | 1 | 1345 | WALPAGFDGVMSHRKFSAPRHGSLGFL PRKRSSRHGKVKSFPKDDPSKPVHLTA FLGYKAGMTHIVREVDRPGSKVNKKEV VEAVTIVETPPMVFGVGVYVETPRGLRT FKTVFAEHMSDECKRRFYKNWHKSKKK AFTKYCKKWQDEDGKKQLEKDFSSMK KYCQVIRVIAHTQMRLLPLRQKKAHLM EIQVWAGGTCARESWDWGPREGKQOV PVKPSVLGRDEMIELHRG*PKGQKAYK GGHPVVWHTQESCPRKD/HHPRACAKV ACIGAFHPARVAFSVARAGQKGYHPR TEINKKIYKIGQG\YLIKGGKLIKNNAST DYDLSDKSINPLGGFVHYGEVTNDFVML LKGCVVGTKKRVLTLRKSLLVQTKAA GLWRRITLKFDITTSKFGHGRFQTMEEK KAFMGPLKKDRIAKEERSLMPGTDFAV GGVSIKVIFH |
| 291 | 8342 | A | 127 | 191 | 482 | DSSGQVQWLKPIIPVLGNLRQADHLRSG VQDQHVQHGETPSLLKIQKKLARHGGA CL*SQLLGRLR/QETH*NSGSRGCSEPL RHCTLA*ATEGDSI |
| 292 | 8343 | A | 1270 | 3 | 451 | |
| 293 | 8344 | A | 1271 | 9 | 487 | NSARATDSERTHHGARLLPDKTNVKA WGKVGAHAGEYGAEALERMFLSFPTNK TYFPFDLASHGFCPRLKGPQRWRPDA LTKIAVAHVVDGHAQTALSGPEATLHGA QSFQVDPVQLSSSLSHCLLG*PWAALP RPSSTPGGWNAPFGTKFPWVSC |
| 294 | 8345 | A | 1272 | 197 | 821 | RLFHSNQTVDSQKNVDITLKGWRPSNR VRAPKGTLRDRDFNPHQM*NSALLGKEQ QRGFRVDKWWGYQKGNWPTRSGLFGS HVQDMIKGWLPLGLPVTKMRSVYAHF PHPTLLSRENGVSLKSRNFLGEKYIPQ GFRMKTRVLLCQYLKAQKR*N*SLEGN DVGLVSNFSRLIPASPTRLKTKGIRKFL DGIFCLEKGLFRQA |
| 295 | 8346 | C | 1273 | 22 | 282 | MSEGPSVRSEEAICLYYEELGGGARQTH VRRPLSECSPGDWSHSGVAEGPXCIQFL HITSHGAKEALSTWLGLLTSGPATTAAV LP* |
| 296 | 8347 | A | 1274 | 60 | 1576 | GYLGAPVALGLWALCWSLAIAATPLPPT SAHGNVAEGETKPDVTERCDGWSF DATTLADDNGTMLFFKGEFVWKSXWG PGV*SSERWEGFSPSPCGMLAFFKVHN SVLS*SKGGDKVLGY*PSLKKKGRKGLP KVCISKIDFPGIPHSPALDAAVECHRGEC QAEIGVLLFFQGDREWFWDFAITGNHGR ERSWPAVWGTCSVALRWAGPLTYWLS RGNQFLRFRPCQGEVPPRIYPRDVREY FMPCPGKGHGTQEWGLGHGNSNHHGP *IYAACSPHLSLCLALTSDNHGANFCLS VGTHYWRLDTS\RDGWHS LAPLLIKWP QGSAVDAAFSWEEKLYLVQGHPGYY VFLTKGGYVLS*GGYPKRLGEREV\GDP SWGFI\DSVDAAFICPGVFLRLHYSWA GRRLVVGW/VP*KSGSPKPTWTELSTFGP HEKVDGALCMEKSPFGPKFMFPNPGP L\YLIHGPNTL\YSVVEKLNAAKALPQ |

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| | | | | | PQNVQTSPGACTH |
| 297 | 8348 | A | 1275 | 1 | 3431 |
| | | | | | MLPHERGLETTTPRGECIPVRIDTKLFEML VPQCHKEIALEHKFIYSFLVTLNTPPGY SHSHPEALLDPEVGDPTNGTNAQLKCFLL PLCPSFPLCPEECMHCSGENYDGKISK MSGLECOAWDSQSPHAHGYIPSKFPNKN LKKNYCRNPDRELRPWCFTDPNKRWE LCDIPRCTTPPPSSGPTYQCLKGTGENYR GNVAVTVSGHTCQHWSAQTPHTHNRTP ENFPCKNLDENYCRNPDGKRAPWCHTT NS |
| 298 | 8349 | A | 1276 | 111 | 2785 |
| | | | | | VNNVLGLGHTFWALLASPKMEHKEVV LLLLFLKSGQGEPLDDYVNTQGASLFSV TKKQLGAGSIEECAAKCEEGETCRAFA QYHSKEQQCVIMAEWNRKSSUIRMRDVV LFLKKKVYSLQSAKTGNGKNYRGTM KTKNGITCQKWASSTSPRRPRFSPATHPS EGLAENYCRNPDNDPQGPWCYTIDPE KRYDYCDILECEECMHCSGENYADGKI SKVTMSWDWECQGLGTFQEPHTVHG |
| 299 | 8350 | A | 1277 | 29 | 454 |
| 300 | 8351 | A | 1278 | 1 | 1368 |
| 301 | 8352 | A | 1279 | 1 | 1269 |
| | | | | | PPTRPPTRPAPGLVPKPSTTCTPACQGLS GAAMKSLVLLCLAQLWGCHSAPHGPG LIYRQPNCDDEPETEEAALVAIDYINQNL WGYKHTLNQIDAEVKVWPQQPSGRAVL RFEIRTPWGTTLPCCWDPTLVGQDASLE GSLKEHAVEGDCDFQLKLDGKFSVY AKCDSSQDSAEDVARKVCQHCPLLAPLA NDTRVVHAAKSCPGPPFNAQNGFQFFS LEEISRAQLVPLPPSVTYVAFTVSGTDL FA*KKATEAAKCNLSGQKSNMGFCVAT LSEKLGSGQRLQLTCTVFQTPVTSQP NPEGANEAVPTPVVDPAAPPSPPLGAP GLLPSWLTPKTTMVLAAAPPGHQLHRA HYDLCHTFMGVVSULGSPFRRKCSHPRK NT/RTVVEA*WLGAAAGATGFLPLFRGG IRHFKV |
| 302 | 8353 | A | 128 | 1445 | 1778 |
| | | | | | NLSRNKEVLLFGKNIPWVGWARWLVPG NPNTLGGQGRADHLKLGVDQPGQHGE IPSLKIQKLTRHGGVCL*SQNHLNPGG GGCSELRSHTCTPAWAME*DSIPKN K |
| 303 | 8354 | A | 1280 | 1 | 1254 |
| 304 | 8355 | A | 1281 | 1 | 921 |
| 305 | 8356 | B | 1282 | 70 | 572 |
| | | | | | MGKEKTHINIVVIGHVDSGKSTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFKYA WVLDKLKAERERGITIDISLWKFETSKY YVTIIDAPGHRDFIKNMILNHPGQISAGY APVLDCHTAHIACKFAELKEKIDRRSGK KLEDGPKFLKSGDAAIVDMVPGKPI* |
| 306 | 8357 | A | 1283 | 1 | 1410 |
| 307 | 8358 | A | 1284 | 1 | 1386 |

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| 308 | 8359 | A | 1285 | 70 | 1538 | KPKWERKRLIFNIVVIGHVDSGKSTTTG HLIYKCGGIDKRTIEKFEKEAAEMGKDSF K\FAWVLDKKAERERGITIDISLWKFET SKYYVTIIDAPGHRDFIKNMAITGDISRL DCAVLDLFA\SGVGEF*SLVSPKNGQ\TR EHALLAYTLGVEQLIVGVNKMMDSTEPP YSQKRYEEMWLREVSTFIKKIWLQPPTQ *HFVPISWFGIGDNMLEPSA\NMPWFKG WKVTRKDGNASGTTLEALDCILPPTRP TDKPLR\PLQG\HVKLGIGTVSSAPME TGFSNPGMVVTFAPSPR*QRKVKSCRKC THEALK*SSFLGTNVGLQLSGIVSCQGM FRPWQTVAG*PAKNDPTQWESSWASLV RGDYP*PIPGQNKAPGYAPCIGIGAHGLT FACK\FAELKEK\IDRR\SGKKLEDGPK\FL KSIGDAA\IVDIVPGRPMCYESFS DYPL GRFAVRDMRQTVAVGV\KAVDKKVCW SWARSPKFAQKG |
| 309 | 8360 | A | 1286 | 41 | 601 | APSPRRPWGHFTEEDQGLLSTSLWGK\W KCGKNAGRKKPLGKAPLVVL\HPWDPK RSFEQALGNPVLPSA\IMGNNPPKSRAG K\KVLT\SLGEMPIKHPG*SSKGTFAQA*S ELH\CDK\LVDPENFK\LLG\NVLT\VL\A AIPPSAKEFTPGGCRASWAERWVTWSW PVPCCSRIPLSSLAHDCRAFQG |
| 310 | 8361 | A | 129 | 3 | 369 | PGFPLFSFPEGNGPSKRQTGD*IRCLF*DG KVWECSPSSSSSPKRRKAVIF\CVPVQ TKCIVVEGGEETLVGDV*V*P*GSFKHV VAMFPEK\DC\CTLYEASFKTKESRRVD GFVCVRVGT |
| 311 | 8362 | A | 1290 | 2 | 217 | |
| 312 | 8363 | A | 1291 | 1 | 2283 | |
| 313 | 8364 | A | 1292 | 249 | 433 | KWRCGNWPRRTLMPWLH*NFVPTLGQT ELQLKEFLSICKEENMKFCWQKQHFEN KKVPAS |
| 314 | 8365 | A | 1293 | 778 | 1578 | PRQVDPSWGFHSRLSGPW/H\WTERDAT SLSKGKVPGAPGGHPLWKNDAGRGEIN ELKQVEGEASCSSRKGLIFFYEWNIK GWKGIVKESGVKHKGLIEIPNLSENEV DDT\EEFTTGMLPTKAMATQELTVKRR LSGNTLQVQASSPVALGVRIPTVALHMM ELFDP\T\S*SSLYSIFTVKEEERVCVLFSLT NKKIIMKWR\WGTWPEEHYAMVALNFV PTLGQTEQLKEFLSIYL*RKVP*NFCWQ KQHFEEIKGSLQLTPLNG |
| 315 | 8366 | B | 1294 | 46 | 386 | XIRHESGRSHSHCSTLSSIGDVAKKLGE MWNNTAADDKQPYEKKA\KLKEKYEK DIAAYRAKGPDA\AKKGVVKAESKKK KEEEDEEEDDEEEDDEEEDDEEED DDE* |
| 316 | 8367 | A | 1295 | 263 | 484 | |
| 317 | 8368 | A | 1296 | 157 | 886 | TWGKGDLLKPRANMSSYAFFVQTCRGG VHKKKHDPASVNFS\ESFSKKCSERWKT MSA*R\EKGFEDMAKADKARYER\EM KTYIPPQRGRQKRKF\KDSQLHPRGPPSG LLSSSCSEYR\PKIK\GEHP\GLSIGDVAKK LGRDVGINTAAD\DKQPYERRAAKLKE KYEKDIAAYRAKGPDA\AKKGVVKA KSKKKKEEEEGEEDDEEEDDEEEDDEE DEEEDDEEDDGLMNKLGSGAVFFFSCL |
| 318 | 8369 | A | 1297 | 1 | 450 | CKSRGSNLRVHFKNTRETAQAIKGMHIR TATKYLKDVTLQKQCVPFRRYNGGVGR CAQAKQWGW\TQGRWP\KSAEFLVIEHI QVNKAPKMRRRTYRAHGRINPYMSSPC HIEMILTEKEQIVPKPEEEVAQKKKISQK KLKKQKLMARE |
| 319 | 8370 | A | 1298 | 1 | 1725 | |

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| 320 | 8371 | A | 1299 | 278 | 879 | SVKMVRYSLDPGGTPRKSC/SQSGSNL RVPFKDHS*KLPQAHQGVCHIRKSPTKY LKDVHLTRNQCVPIPDYNGGICKVCR RPKQWGWWTQGRWPQKGVNLFLHML KNAE/SNAELKGLDVDFLVIEHIQVNKA PKMRRRTYRAHGRINPYMSSPCHIEMI LTEKEQIVPKPEEEVAQKKISQKKLKE TPTLWHGE |
| 321 | 8372 | B | 13 | 7 | 177 | MSVSARSAAAEERSVNSSTMVAQQKNL EGYVGFANLPNQVYRKSVKRGFEFTLM VVE* |
| 322 | 8373 | A | 130 | 412 | 616 | VFVCLFVCFETGSCSVTQAGGQWCNHG SLQPOPATSAS*IVGIVAGVYHHFQVFL LLLNRDEVLLY |
| 323 | 8374 | A | 1300 | 85 | 266 | |
| 324 | 8375 | A | 1301 | 1 | 1776 | |
| 325 | 8376 | A | 1302 | 207 | 1645 | LSQRALRLSPRARSFSLSPACPLPCLLALS LALSSRIEGLTTACGWGRETEAAAAQG KRGCSGSGSRKMSGEDQEQETIVD/DSL VVTKYKMGDIANRVLRLSVEASSGVS VLSLCEKGDAMIMEETGKIFKKEKEMK KGIAFPTSISIVNNWCM/CHFSPFERSDPG LYSSKEGDLVKUDLGVPCWMGFANVA SH/SFVVDVAQGTQVTGRKADVIKAAH LCAEAA/LRLVKPGNQNTQVTEAWNKV AHSFNCTPIEGMLSHSLKQHVIDGEKP*F QNPTDKQK/RAHEKADFEV/HEVYAVDV LVKPQERARPKDAGQRTTIYKRDPKQY GLKMKTSRAFFSEVERRFDAMPFTLRAF EDEKKARMGVVECAQT*TCWQPFNVL Y*EGRVILFAQFKFTVLAHGPNGPMT S/GPFPEDFYK/SEMEV/QDAELKALLQ/S SAKSEKPKKKKKKKASKTAENATGGIL CSLGNIRRK |
| 326 | 8377 | B | 1303 | 29 | 200 | MSRTRLVCPSLIPFCIYVVDVGFSPGPQS CTSHEPKDIHAKCELAFLHHQRFYKNEG X* |
| 327 | 8378 | A | 1304 | 138 | 1908 | ASRTAVARWECVLQNVREPPSPRAWP SQLRPIASTATKCRE/CGPGYSTPLEAMK GPREENVYLPCILPETQGTEGPRLSWAT VDVDPKSPQYCQVIHRLPMPNLKDELH HSGWNTC/GSCFG*LAPSRGTKLVLPSP HLLFGIYVGGTWGSEPRAPKLAQGSLS RDIHAKC/NWAFLLHTSHCLASGEVMISL GDVKGNKGKGFVLLDGETFEVKGWTER PGGAAPLGDFWYQPRHNMISTEWAA PNVLRDGFNPADVEAGLYGSHLYVWD WQRIEIVQTLSLKDGLIPLEIRFLHNPDR CPKAFVGCALQAPNIQRFQRTRGGTLF SGRR*FQVPPRKLKGWLLPKMPGLVTTI LASPWNDGFLYFSNWLAWGP*GKYDIS DPQRPALTGQLFLGGSIVKEGP/VQVLED EEL/TSPSPEPLVVKGKRVGEGPQMINQL SLDGKRLNNHHGRCTALGQSSFP*SQ SGERLLVNAGRVEW*DNSKKGGA*KLN PQLSWVDFGEGAPLPKPLPH*ARYPIGA DCSSDIWILNSPPSHPHSLFWALHFPGGP GLSFCISLGRTRLGKHVPTTAKLRLWQC VES |

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| 328 | 8379 | A | 1305 | 1 | 1000 | STRAPSPGPFSSKLAGAYKSWCRRDPR THSAGAAQAAAARSVPICAPTASATMS HHWGYGKHNGPEHWHKDFPIAKGERQS PVDIDHTAKYDPSLKPLSVSYDQATSL RILNN\GHAFNVEFDDSDQKAVLKGGP LDGTYRLISVFTFWGSGF*WDKVSEAY CGIKKKYAAELTLGHWNKYGDFGKA VQEPDGLAVLGIFLKVGSAKPGLOKVVD VLDSIKTKGKSADFTNFDPRGLLPESLD YWTYPGSLTTPPLLECVTWIVLNFPSV SS\EQVFEIP*TLTFNGGGVNPEELMVDN WRPA\QPLKNR\QIKASFQIRWSHLSYSK |
| 329 | 8380 | C | 1306 | 127 | 435 | MAASXNPEVLDITEETLHSRFLGVRNV ASVCLQIGYPTXASVPHSIINGYKRVLAL SVETDYTFPLAEKVKAFLADPSAFVAAA XLGCCHHSCSXCCCSPS* |
| 330 | 8381 | A | 1307 | 1 | 689 | KCFI/VGADNVASKQMQQIRMSFRGKAV C*WGKNTMMRKPIRGHLENNPALEKLL PHIRGNVGFVFTKEDLTEIRDMLLANKV PAAARAGAIAPCEVTPAQNTGLGPEKT SFFQALGITTISRGTIEILGVRNVASVCL QIGYPTVASVPHSIINGYKRVLALSVED YTFFPLAEKVKAFLADPSAF/VAAAP/VAA ATTAAPRAAAAPAKVEAKEESESEDED MGFGLFD |
| 331 | 8382 | A | 1308 | 68 | 1111 | RTAVMPREDRATWKSNYFLKIIQLDDY PKCFIVGADNVGSKQMQQIRVPWGEA CVLMGQKTMGMGQAHKGT*NNPSLW RKLLPHIRGNLGFCTQGGPSLEIKGHV CLANKGLPSWLPVVGANCPHGESHWWP APEHWSSGPEKTSFFPGL*AITTKUSQGA PIENPEVNVPAESRTGDQSGEPSEANAA* TCSNISPFSGAGSSQPGVSTNGSHLPL KGLDIHRNLCIFWLSWEGVRKCCPVSV CQIGYPTVASVPHSIINGYKRVLALSVA EPDYTFPLAEKVKAFLADPSAFVVAATC GLLPPQLLLVVVAAPAKVEAKEESESED EDMGFGLFD |
| 332 | 8383 | A | 1309 | 60 | 569 | STDLEELPTLGWF*KQELIILSCPFVSLTY RERLPANFFKFQFRNVEYSSGRNKTFCL YVVEAQGGGGQVQASRGYLEDEHAAA HAEEAFFNTILPAFDPALRYNVTWYVSS SPCAACADRIIKTLSKTKNLRLLILVGR FMWEEPEIQAAALKKLKEAGCKLRIMNLV |
| 333 | 8384 | A | 131 | 278 | 464 | YTHILRQLPTLRHEQKSRENCLEEMSLD RFQAAKPSPTPTHHTYKPTLAGH*KIHA MGLTRA |
| 334 | 8385 | A | 1310 | 62 | 858 | QLRWDSGARAWPRPACLSPLPQRLLSHS PSMAQKEEAATEAASQNGEDLENLD DPQKLKELIELPPFIVTGERLPANFFKFQ FRNVEYSS\GRTKTL\CYVV*STGARGG KVQASWGYLEDEHAACPLQKESFSFNT ILPAFRPKPLAVTNVT/WGYVSSSPCAA CADRNVKTLSTKNLRLLILVGRLFMWE EPEIQAAALKKLKEAGCKLRIMKPQDFRI LSWENFVEQ\EEGESKAFQPWEDIQENF LYYEEKLADILK |
| 335 | 8386 | A | 1311 | 1 | 727 | NTEDQRNEEKAQREANKKIEQLQKDK QVYRATHRLLLLGAGESGKSTIVKQMRI LHVNGFNGDEKATKVQDIKNNLKEAIET IVAAMSNLVPPVELANPENQFRVDHILS VMNVPDFDFPPEFYEHAKALWEDEGVR ACYERSNEYQLIDCAQYFLDKIDVIKQA DYVPSDQDLLR\CRVLT\SGIFETKFQVD KVNFIHIV*RGVGQORDERKWIQCFNDV TAIIFVVASSYNMVIREDN |

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| 336 | 8387 | A | 1312 | 2 | 1271 | PVRSSAPRRGHSVASAPRSGLRQVAGRR GAALPCSLAPGCGAAAGASPCPGAGRR RAAGGRCLACECTSLTCAGESGKSTIVK QMRILHVNGFNNEGGEEDPQAARSNSD GEKATKVQDIKNNLKEAETIVAAMSNL VPPVELANPENQFRVDYILSVMNVPDFD FPPEFYEHAKALWEDEGVRACYERSNE YQLIDCAQYFLDKIDVIKQADYVPSDQD LLRCRVLTSGIFETKFQVDKVNFMFDV GGQRDERRKWIQCFNDVTAIIFVASSS YNMVIREDNQTNRLQEALNLFKSIWNNR WLRITISVILFLNKQDLLAEKVLAKSKI EDYFPEFARVYTTPEDATPEPAGEDPR* TRAKYFIRDEFRLISTASGDGGHYCYPH FTCAVDTENIRRVFNDCRDIIQRMHLRQ YELL |
| 337 | 8388 | A | 1313 | 235 | 1571 | GRPRPPPPQGRAPPPPPRPMGCLGNSKT EDQRNEEKAQREANKKIEKQLQDKQV YRATHRLLLGAGESGKSTIVKQMRILH VNGFNNEGGEEDPQAARSNSDGEKAT KVQDIKNNLKEAETIVAAMSNLVPPVEL ANPENQFRVDYILSVMNVPDFDFPEFY EHAKVLWEDEGVRACYERSNEYQLID CAQYFLDKIDVIKQADYVPSDQDLLR/ CARVLTSGIFETKFQVDKVNFMFDV GGQRDERRKWIQCFNDVTAIIFVVGSS SYNMVIREDTGHNGLAGRL*TSKGIW DNRWAAAPSLVILFTKQ/EILLA*ESPLA GNSKIKDYFPEFARVYTTPEGYSRRPG EGPHGVYRGQVTPFEDEFRLSSNCPVED GRHYCYPHFTCAVDTENIRRVFNGLAV DIHFSGMHLSFSYGAGFKEGEPKFNLK A |
| 338 | 8389 | A | 1314 | 3 | 784 | |
| 339 | 8390 | A | 1315 | 3 | 2231 | PAMNGLSSELCCFLCPCPGRIAACKLA FLPPEATYSLVPEPEPGGAGAAPLGT RASSGAPGRWKLHLTERADFQYSQREVR STIEVFPTKSARGNRVSCMYVRCVPGAR YTVLFSHGNAVDLGQMSSFYIGLGSRL HCNIFTYDSSGYGASSGRPSERNLYADID ATWQALRTR*GRPLVGRVRARWRPRLT LLRRRQVRHQPGQHPSTGRSIGHGAPP WDWASRYECAAAILHSPLNLGHARRIPR HPRKTYCFDAFLHSRKVSKINVSPCSSS HGHEGRGDRLSRTGWALYEALPPRRVE PLWVEGAPGTTDIEPLQPVGAAGVAFIL PGAAQPARLAAAPNRPDLNKAAPGLHP APAPTQGLACGPPGRPRWRPGLGGARH EWAVDDVQATRTHSFPGSKKKIRENG QLKI |
| 340 | 8391 | A | 1316 | 1 | 1347 | |
| 341 | 8392 | A | 1317 | 53 | 1027 | NFRVEAGVRGVQKQKTCFAKVLESIGKL GLALSVAAGGAENSALYNVDAGHRAVIF DPIPGQK*QDIVVGEGETHFLIPWVQKPK LSNDCRSRPRNCCQSITGSKDLQNVNIT LRHPSSGPVRQPSFPRIFTSIGEDYDERV LAVPSQLENLKVSWARFDAGELITQRE LVSRQVSDDLITERAATFGLILDVSLT HLTFGKDF*AVIEAKQVAQQKQRRRA RFV/VLEKAEQOKKAAIISAEGDSKAAE LIANSIATAGDGLIELRLKGLQRTFAY QLSTLSGTSPYLPAGQSVLLQLPQLRAH PCLAPPAGLTWGHSPD |
| 342 | 8393 | A | 1318 | 424 | 598 | |
| 343 | 8394 | A | 1319 | 3 | 371 | |

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| 344 | 8395 | B | 132 | 639 | 1718 | MDPLGPAKPQWSWRCCLTTLFQLLMA VCFFSYLRVSQDDPTVYPNGSRFPDSTG TPAHSIPLILLWTWPFNKPIALPRCSEMV PGTADCNITADRKVYPQADAVIVHHREV MYNPSAQLPRSPRRQQRWIWFSMESPS HCWQLKAMDGYFNLTMSYRSDSDIFTP YGWLEPWSGQPAHPPLNLSAKTELVAW AVSNWGPNSARVRYQSLQAHLKVDV YGRSHKPLPQGTMMETLSRYKFYLAFE NSLHPDYITEKLWRNALEAWAVPVVLG PSRSNYERFLPPDAFIHVDDFQSPKDLAR YLQELDKDHARYLSYFRWRETLRPRSFS WALAFCKACWKLQESRYQTRGIAAWF T* |
| 345 | 8396 | A | 1320 | 1 | 1596 | |
| 346 | 8397 | A | 1321 | 2 | 556 | WDMMYVTRFASFLRNVLPSFISDWLYV QKMNTWFKHENYGLMPLNGYLKMEIFF IQKRGALI**IYLSIKPSVKEFTETSAVFED GTMFEAIDSVIFATGYDYSYPFLDETIMK SRNNEVTLFKGIFPPLMEKPTLAVIGLVQ SLGAAIPTADLQAWWAAKVFAWRWAIL SFIHFINEHLLNTCY |
| 347 | 8398 | A | 1322 | 955 | 1187 | IFFFFFFFKMESCFFAQAGVQWCDLGSLO ALPPGFTPFSCSLSSWDYRRPPPHLAN FLYF**TWVFTVLARMVSIS |
| 348 | 8399 | A | 1323 | 6345 | 9041 | |
| 349 | 8400 | C | 1324 | 182 | 433 | |
| 350 | 8401 | C | 1325 | 72 | 254 | MVSTQLRQASDPRTTIGRERFELLRRV DKLMSPRLPTGTLNPHHFWTLSIPQVGR CNAF* |
| 351 | 8402 | A | 1326 | 225 | 735 | GELRVNSLHVSTHFQIPEETDIGWLVSPO QGPAPFEDIQLWPPGSLMAAEPTDQSL EESH*DRWITFFTFARIQEGRKD*PQRS NEFKELVTOQLPHLALKDVGSLDRKN*G AWDVNQDFGGSRFNEYWRLLIGGAWPK EIRKEEKLKIQERSKAAWLEDGVGQGR T |
| 352 | 8403 | A | 1327 | 55 | 391 | |
| 353 | 8404 | A | 1328 | 996 | 1334 | WASVGLSGPRSPSSRPQ*ARPRPGAPAS LRQADLGRGWRDRLGAPRPPRTGGW RSCCRGRPGSRPRGARAGLPGAPGG WRRSRRSWTRARAATRPAAARGSRTP RG |
| 354 | 8405 | A | 1329 | 1 | 993 | |
| 355 | 8406 | B | 133 | 1154 | 2233 | MDPLGPAKPQWSWRCCLTTLFQLLMA VCFFSYLRVSQDDPTVYPNGSRFPDSTG TPAHSIPLILLWTWPFNKPIALPRCSEMV PGTADCNITADRKVYPQADAVIVHHREV MYNPSAQLPRSPRRQQRWIWFSMESPS HCWQLKAMDGYFNLTMSYRSDSDIFTP YGWLEPWSGQPAHPPLNLSAKTELVAW AVSNWGPNSARVRYQSLQAHLKVDV YGRSHKPLPQGTMMETLSRYKFYLAFE NSLHPDYITEKLWRNALEAWAVPVVLG PSRSNYERFLPPDAFIHVDDFQSPKDLAR YLQELDKDHARYLSYFRWRETLRPRSFS WALAFCKACWKLQESRYQTRGIAAWF T* |
| 356 | 8407 | A | 1330 | 72 | 496 | PPWARGSARRPPAWRTVRMPSCHPRMF GAPQKTFLRVSVWSRCRPWGIVMRMM* PMRGQVRRHNSCMAPKTEE*NPTVSATF CCCSFVSCSWPPVTRYSSILFTAAM |
| 357 | 8408 | C | 1331 | 202 | 378 | MTPYLTLFLSPLPPKGEIWGLLLFLTPLG FLLPSLPLLLPCAPAGVRRQWDGPTG A* |
| 358 | 8409 | A | 1332 | 1 | 1541 | |

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| 359 | 8410 | A | 1333 | 9 | 345 | YLSEVGVSVGIVIRPRQWIRREPGDPFHG GRLKMDPLRAQQLAAELEVEMMADMY NRMTSACHRKCVPFPFKEAELSKGESV CLDARCVS KYLADIHGA*WGKKFDRVLL QG |
| 360 | 8411 | A | 1334 | 170 | 842 | EHVYKLPKAKITRPLMLSSARGGAEES ERAEPPLRWAFLLLGLGTVVGVDESTAF SWPVCDMCGNGRLEQRPEDRGAFSCGD CSRVTSPVLKRHLQVSLDCRSRPQCRV KVKLLQRSISSLLRFAAGEDGLYSQWLIR SLLRIWKADRRWVPEGPG*RC*LRDTQ YGFCQFSGATK*RSVFGKEVGLLNCFVQ SVTAHPTSCIGLEEIELLSAGGASAEH |
| 361 | 8412 | A | 1335 | 2 | 2925 | FVLRRCQAALPEMPRGRSARGSKRK RSWNTECPSPFGERPLQRRAGLRTAG AAASLSEAWLRCGEFQNTSGNPISLTA EEKTVTEKHLELCPRPKQETTTSKSTSGL TDITWSSSGSDLSDEDKTLSQLQDELQF IDWEIDSDRAEASDCDEFEDDEGAVEISD CASCASNQSLTSDEKLSLKPSSIEILEY SSDSEKEDDENLVIDSESPHYHVQFA SDARQIMERLIDSRKSPETILHTP |
| 362 | 8413 | A | 1336 | 1 | 480 | NFALEAKNSARAISVVQTPMGHFTTED Q/ALTITSLWGKIVNVEDAGGETPGKGS LVVYPWTQRFFDSFGNLVLLPSCPSMG NPQKSKATWPRKVLTSLGDAITKHLADD LKGHLLPKPEVNLHLLTSLHVG*GTFKL PGEILLVTRFWAIPFSAKEFHP |
| 363 | 8414 | A | 1337 | 52 | 454 | SQTQREPTMVLSPADKTNVKA/WGMF LSFPTTKTYFPHFDLSHGSAQVKGHGKK VADALTNVAHVDDMPNALSALSDLHA HKL RVPVNFKLLSHCLLVTLAAHLPAE FTPAVHASLKD FLASVSTVLTSKYR |
| 364 | 8415 | A | 1338 | 3 | 616 | PTLLVPTDSERTHPWLLSPADKDQKQGP AWG*G*GSHPPSNVAKTLERIMVLFPPPT PKPYFPHFDLASHGSAQVKGHGKKVA DALTNVAHVDDMPNALSALSDLHAH KL RVPVNFKLLSHCLLG*PWAAHLPR PSFTPCGCKASLADKFPGLFVEAPLLEPSK LPLKLSRLAMLLCPFGFPQPLLPFA PVPPWSLK |
| 365 | 8416 | A | 1339 | 2 | 390 | GWDWNCVWEPHHWLCQSL/NSVTQAG VQLCNLSSLQPLPLGFKQFCLSLPSSWD YRNPSLKQQLFSYAILGFALSEAMGLFC LMVAFLNLSLPCGAVSTSHSPASGWPR VFLFLYLPRQPGERGWL RV |
| 366 | 8417 | B | 134 | 1029 | 2108 | MDPLGPAKPQWSWRCCLTTLFQLLMA VCFFSYLRVSQDDPTVYPNGSRFPDSTG TPAHSIPLILLWTWPFNKPIALPRCSEMV PGTADCNITADRKVYPQADAVIVHREV MYNPSAQLPRSPRRQQRWIWFSMESPS HCWQLKAMDGYFNLTMSYRSDSDIFTP YGWLEPWSGQPAHPPLNLSAKTELVAW AVSNWGPNSARVRYQSLQAHLKVDV YGRSHKPLPQGTMMETLSRYKFYLAFA NSLHPDYITEKLWRNALEAWVPVVLG PSRSNYERFLPPDAFIHVDDFQSPKDLAR YLQELDKDHARYLSYFRWRETLRPRSFS WALAFCKACWKLQESRYQTRGIAAWF T* |
| 367 | 8418 | A | 1340 | 13159 | 14007 | VLSPLRLKCSGTISAHCNLCPLGSDNSPA SASQVAGITGAHHHARLIFYFFILFYFIFL R/HESDSVTQAGVQLCNLSSLQPLPLGFK VHSLASASQVAGITGTHRYPQLIFVFFFL F/SFLRQSL/DSVAQAGVQWRGLGSLHP LPPGFTPFSCSLSSWDYKRLPTRLANF LYF**RQGVTVLARMVIS*PRDLPTSAS QSAGITDMSHCAQ/LIFVFLVETGFHQVG QAGLE/PPDLKQSTHLGLPKCWDYRREP |

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| | | | | | | PRLA\NFCIFSRDGVSPCWPGWSPTSFGK |
| 368 | 8419 | A | 1341 | 1 | 532 | DSGTRDTVLKLLREWYMIISREMFNPMY ALFRTSPGDRVTYINPSSHNCNPNHLSYF KFVGRIVAKAVYDNRLLECYFTRSFYK HILGKSVRYTDMESDYHFYQGLVYLL ENDVSTLAGYDLTFSTEVQEVGVCVRD LKPNNGGNILVTEENKKEYVHLVCQMR MTGAIRKQFG |
| 369 | 8420 | A | 1342 | 1 | 530 | AEADAIQMVRREGQRARRQQQAATSESS QSEASVRREESPMVDVQSPSAQDTQSI ASDGTPOGAEKEKEERPPPELPLLEQLAL DELWDMLECLKELEESHDQHAVLETH RTVLNQILRQSTTHLADGPFVAVLDYIR VLDFDVKRKYFRQELERLDEGLRKEDM AVHVRRDHVF |
| 370 | 8421 | A | 1343 | 262 | 587 | PVSKESEVAPLCDFCLPFQSESSQSEASV RREESPMVDVQSPSAQDTQSIASDGT QGEKEKEERPPPELPLLEQLSLDELWDM LGECLKELEESHDQHAVLVLQPA |
| 371 | 8422 | A | 1344 | 1 | 2502 | MTPPHLPRRASDDEFENLRIKGPNAVQ LVKTTPLKPSPLPVIPDTIKEVIYDMLNAL AAHYAPEEVGFTSPMLFDERKYPYHLM LQKFLCSGGHNALFETFNWALSMGGKV PVSEGLEHSDLPDGTGEFLDAWMLMLVEK MVNPTTVLESPLSLPAKLPGGVQNFQF SALRFLVVTQAAFTCIKNLWNRKPLKV YGGMAESMLAILCHILRGEPVIRERLSK EKEGSRGEEDTQEEGGSRREPQVNQQQ LQQLMDMGFTREHAMEALLNTSTMEQA TEYLLTHPPIMGGVVRDLMSSEEDQM MRAIAMS LGQDIPMDQRAESPEEVACRK EEEEERKAREKQEEEEAKCLEKFQDADPL EQDELHTFTDTMLPGCFHLLDELPTVY RVCDLIMTAIKRNGADYRDMILKQVVN QVWEAADVLKAAALPLTTSDTKTVSEWI SQMATLPQASNLAIRILLTLLFEIEVRS WSYPPFQDKDHCKKEKENFEAIAAALA AERESKPPVRDTRESQLAHSKDEPPPLSP APLTPATPSSLDPPFSREPSSMHISSSLPPD TQKFLRFAETHRTVLNQILRQSTTHLAD GPFVAVLDYIRVLDFDVKRKYFHFQELER LDEGLRKEDMAVHVRRDHVFEDSYHTA SQSLTHTNDWMYPGFSQAQLFSASAFLCR YIVFEGEEGQDAGGLLREWYMIISREMF NPMYALFRTSPGDRVTYINPSSHNCNPN HLSYFKFVGRIVAKAVYDNRLLECYFT RSFYKHILGKSVRYTDMESDYHFYQGL VYLLENDVSTLAGYDLTFSTEVQELITA HPSQSGRSNSQVHLRTSTA |

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| 372 | 8423 | A | 1345 | 1 | 2218 | MPQLPGISLPEGVDPSFLAALPDDIRREV LQNQLGIRPPTRTAPSTNSSAPAVVGNPG VTEVSPEFLAALPPAIQEEVLAQQTAEQQ RPELAQNASSDTLMDPVTLIQTLPSDLRR SVLEDMEDSVLAVMPPDIAAEAQALRRE QEARQRQLMHERLFHGSSTSALSAILRSP AFTSRLSGNRGVQYTRLAVQRGGTFQM GGSSSHNRPSGSNVDTLRLRGRLLLDH EALSCLLVLLFVDEPKLNTSRLHRVLRN LCYHAQTRHWVIRSLLSILQRSSESEL CIE TPKLTSEEKGKKSSKSCGSSSHENRPLD LLHKMESKSSNQLSWLSVSM DAALGCR TNIFIQRSGGRKHTEKHA SGGSTVHIHP QAAPVVCRHVLDTLIQLAKVFP SHFTQQ RTKETNCESDRERGNKACSPCSSQSSSSG ICTDFWDL LVKLDNMNVS RKGKNSVKS VPVSA GENKVSEA QANS GSGASSTTTAT STTSTTTTAASTTPPTAPTPTVTSAPAL VAATAISTIVVAASTTVTTPTTATTTVSIS PTTKGSKSPAKVSDGGSSSTDFKMVSSG LTENQLQLSVEVL TSHSCSEEGLEDAAN VLLQLSRGDSGRD TVLKLLNGARHLG YTLCKQIGTLLAELREYNLEQRR AQCE TLSPDGLPEEQPTTKLGKMQSRFSGL GSASSIQA AVRQLEAEADAIQMSSESSQS EASVRREESPM DVDQPSQAQDTQSI A |
| 373 | 8424 | A | 1346 | 59 | 6349 | KISQYYMHTPI SPHPRLLISPIAPRK VEW TGLKVKSQDRLFAQQLQVELVALPLVLC LAASALGRSTTSFVSLGQPHAAIQ TYSQ KWPTAVSASPFLPLRGSGTGNGSSRIPRE SAPEMATAESLVEELSEDAAGGASPGVE LPALGCSELPAAEVSP TASSKNLETICEY AYCMAMLPETGLDPYPKRGFLD LTQERI WTDIPSPGNIP TTHPLMVRHADHSSLTL GSGSSTTRLTQGIGRSQRTL RQLTAN |
| 374 | 8425 | A | 1347 | 1 | 746 | MAAAGAFRLRRAASALLRSPRLPARSC RPRPDSITRSPPDVRLPLEKQLKNAINQR GTKGPYIRYYPEVVDHYENPRNVGSLDK TSKNVGTGLVGAPACGDVMKLQIQVVG *KRGFRVGC*GFKTFSAVGSAIASSSLSH LNGVKGKTVEEALTIKNTDIAKELCLS FPWKLALAPMLGLKVAFKAALADYKIE TRTQKKGEAEKKWSPPLGEASSRPTPAV PQPAVPVTL DVSGSRLPSPTEGAL |
| 375 | 8426 | A | 1348 | 2 | 832 | SARGSTVAAIICSPRLTPPRTRDAKAACE RLRRVGVEPQLSRGLALFWSPRNPPEE MSGGLAPSKSTVYVSNLPFSLTNNDLYP DIFQSIGKSL*KVTNQ*KSKRY/HRKEVK GVAFILFLDKDSAQKICARA INNKQLFG RVIKASIAVDNGRAAEFIRRRNYFDKSK\I CYECGÆSGHLASYACPKNMLGEQ*/RLP KKKEKKKKKKKAPEPEEEIEVEESEDEG EDPALDSLSQAIAFQQA KIEEEQKKWET QFQGVPSNIRMIPRRTRIKKSTYFQ |
| 376 | 8427 | B | 1349 | 165 | 520 | XNLKLLDNWDSVTSTFSKLREQLGPVTQ EFWDNLEKETEG LRQEMSKDLEEVKAK VQPYLDDFQKKWQEEMEL YRQKVEPLR AELQEGARQKLLPVLESFKVSFLSALEE YTKKLTNQ* |
| 377 | 8428 | A | 135 | 885 | 1173 | LSQGP RRHSSAVQPPPHSHRGHHDDCA SPSQVRQNYAINRQINVELYASYIYLSM SYFFDHNDVALKNFAKYFLHQ SHEERE HAKKLMKLLHFDC |
| 378 | 8429 | A | 1350 | 3 | 558 | |
| 379 | 8430 | A | 1351 | 3 | 118 | |
| 380 | 8431 | B | 1352 | 28 | 384 | MKAAVLT L AVLFLTG SQARHFWQQDEP PQSPWDRVKDLATVYVDVLKDSGKDSV TSTFSKLREQLGPVTQEFWDNLEKETEG LRQEMSKDLEEVKAKVQPYLDDFQKKW |

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| | | | | | | QEEMELYRQK* |
| 381 | 8432 | A | 1353 | 2 | 1093 | GGASCCLPRSLWLPSSRFRPCRPGLWV PEVFSRSVPFSSPGCNEWGSTGLLHAEGT PLSQALLLLQVPHGPFRMKA AVLTLAVL FSDG*ARRRHFWQGG*SPPRAAWDRVK DLATRVPTVLKEQRTETVVSQFEGSA LGKVLNLKAPLTTGDSVDLPFFSKLRE QFGPC*PRDFLGINLGKRETEG*GKGR* GKDLWKEVKAKVAALTLDDEFQERSWQ EEIGAFTROKVEPLARKNFQEGARPESL HELARRSLSPLEEMRDRARA/HVDALR THLAPYSDELQRQLGARL/GALRENGGA RMGQYHA/QATEHLSTLSEKAKPAEDL RQGLLPVLESFKVSFLSALEEYTKKLNT Q |
| 382 | 8433 | A | 1354 | 119 | 301 | INDKRKKRPARPGAGGLHLQLCLSOPP QPRGHPAPIPTGQAGPRDSGPGASP*/GR DPPSD*WTPADLGSDPWAGPLPTQEP* GSRWPSSATVSLSASTATGTPCTYSHGT GWTQRLWTRGLPLSRDPPSD |
| 383 | 8434 | A | 1355 | 1451 | 2495 | RGLAGNFEDRKS AHYVFQTFRGGERRSL ELEAHLEGWSLGLRFLGLPKGPAAQ HFHPSLPISWRGAGVPHSR/SPFPTLGIP G*IFPPKPGRRPRGPPRKEDLGPGMVGR PSGPLQLPSAVLSADPAGPRPHVPFCEP/ SPSHGVRASPGSKWVEEIGGEEGRQ/PK CRQAFQEA WLMQG/GARGQGLPGS/GC WRINKPSKPSKRGKGLTCQTFSTNIC*S PPLMPRSLP/GPSFILHLISSQQP*SGLLFID PIPPEKGRGGLSERWGRAFGDSVACSFQ KPTPGWEVFEQDAWPNPWP/QGPPPEN FPKGNPSHSRNIHKGDEQSPVRTKTEPTP WGGKHSQFASR |
| 384 | 8435 | A | 1356 | 2024 | 2160 | KCLCPPR/RCPQPLTPYPC*GVKCPPSEIK YKP*MCPIGCPKPSIQC |
| 385 | 8436 | A | 1357 | 15717 | 16041 | |
| 386 | 8437 | A | 1358 | 41 | 544 | TKLVMMQKLLKCSRLVLALALILVLESS VQGYPTRKPRHQWVRCPNDSSSAHCLE EKGHMFELLPGESNKIPRLRTDLFPKTRI QDLNRIFPLSEDYSGSGFGSGSGSGSGS IGSWFLTGNGNRNYQLAVDEISDAFQ*QP LGSLDRNLP/SDSQDLGQHGLEEDSMV |
| 387 | 8438 | A | 1359 | 60 | 401 | |
| 388 | 8439 | A | 136 | 961 | 1051 | |
| 389 | 8440 | A | 1360 | 59 | 420 | QQHGRDLWGCRLIGTDKCVERINEMV NRAKRKAGVDPLVPLR/MLGGVVLISGT GSNCRLINPDGSESGCGGWGHMMGDEG SAYWIAHQAVKIVFDSIDNLEAAPHDIG YVKQAMFHYFQV |
| 390 | 8441 | A | 1361 | 80 | 384 | KEHNFVTSVFARGTMGSLTHLLGNSLT EKCKLPSWLPITAEGNSLKGFL/LALTQG KEIQANFFSSFILMKLRHSSALGGASLL PMDYSANAIAFYSTFS |
| 391 | 8442 | A | 1362 | 3 | 124 | |
| 392 | 8443 | A | 1363 | 189 | 242 | |
| 393 | 8444 | A | 1364 | 420 | 557 | |
| 394 | 8445 | A | 1365 | 284 | 362 | |
| 395 | 8446 | A | 1366 | 2087 | 2226 | |

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| 396 | 8447 | A | 1367 | 1 | 2956 | MNTSQLLEIANQVFNRAAVSLEENRKE NGHQARRNTDLVVSCSNQRGOESLEKL LGRYFYISHLSALAKTMRQRFVTCRHHN ARQGPVPPGIQAYAAAPIEDLQAIRNNI TAGVYTPCDIGGNIILCPLAYYQRYQTG VYYTPCDIGSIILSTSGCPSHTEPRNLTG VSEFLLGLSEDPQLQPVLPGLSLSMYLL TVLRNLLIILAVSSDSLHTPMYFFLSNPS WADIAFTSATVPMIVDMQSGVVVSV |
| 397 | 8448 | A | 1368 | 149 | 1323 | PRNEPNSPERRPLAMDAGVTEGLNVT LTIRLLMHGKEVGSIIKKGESVKRIREE SGARINISEGNCPERIITLTGPTNAIFKAFA MIIDKLEER/DINSSMTNSTAASRPPVTLR LVVPATQCGSLIGKGGCKIKEIRESTGAQ VQGWRGICLPNSTERAITIAGVPKSVTE CVQADFAWVMLETL/SPSFPQGRSSWTI PYQPMFASFPSSSCAGGQDRCSDVGG YPHGHP*PGKGPLLDGLFDFKGQHTISPL DLGQA*TRIGKPTSLNVHMMHGGTGF AGIDSASPEVKGYWAKFECIYPKTPHEL TIPNNIAGCIHQADSDLMRSAQMSG QDQKLA\NPVEIGSSGRQVTINTGLCCPVI SLAQYLINA\RLSSEKGMGCS |
| 398 | 8449 | A | 1369 | 2 | 125 | |
| 399 | 8450 | A | 137 | 2 | 804 | SSGFPASTVLGRNPALVPHGRPPIASPPS PLHRTLGLPQGPRRRSSAAQPPPPAAASP LVAAMKTAVPPRKVRQNYHQGLKRAA HQPARIINPGSSTASYVLPCMSYLLLRD DGGL*RTFAKYFL\HQFSMKEEGNHAEK T**KLAEPNEGGRNLSFKDIQEPDCSDW GERGLNAMECALHLEKNVQNQSLLELH KTGPLTKMTPHLCDFIETHYVLNEQGES HQKNLGDHVTNLRKMGAPESGICAEY LFDKAHPWGDSDNES |
| 400 | 8451 | A | 1370 | 18 | 1374 | LAEQIVPRGVGIRPPDKADQAPCRSPIRT PAPESWHCDSRQFRQDSSRMKMRVLG LVVCLVLWTLHSESGGKLTAVDPETN MNVSEHSYWGFPSEEYLVEDGDYILCL NRIPHGRKNHSDKGPKPVVFLQHGLLA DSSNWVTN\GNSRLGFILADAAIDVWM GNTRGNTWSPKHKTLSVSQDEFWAFSY DEMAKYDLPASINFL\NKTGQEQVYYV GHSQGTIGFIAFSQMLELAKGLKMFFA WGPVASVAFCTSPMAKLGRLPDHLIKDL FGDEEFLPQSAFWKVAGVPHLATHVIL KELCGNLCFLLCGFNERNLNMSRVDVY TTHSPAGTFVQNM*HWSQAVKFQKFQA FDWGSSAKNYFHYNQSYPTYNVKDML VPTAV*TGGHDWLEDVYGVNI*LTQIT NLVFHESIPEWEHLDFIWGLDAPWRLYN KIINLMRKYQ |
| 401 | 8452 | B | 1371 | 77 | 471 | ANREKMTQIMFETFNVPAMRACSTPPE DHRHRAGLRRRVTHNVPIYEGYALPHAI MRLDLAGRDLTDYLMKILTERGYSFVTT AEREIVRDIKEKLCYVALDFENEMATAP PPPPWKRATSCQTGX* |
| 402 | 8453 | B | 1372 | 101 | 391 | MCDEDETTALVCDNGSLVKAGFAGDD APRAVVPSIVGRPRHQGVVMGMGQKDS YVGDEAQSQRGILTLKYLIEHGIITNWD MEKNGPHLLHEL RV* |

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| 403 | 8454 | A | 1373 | 92 | 1323 | LPAQKLDTMCEDETTALVCDNGSGLV KAGFAGDDAPRAVFPISVGRPRHQGVM VGMGQKDSYVVGDEAQSQRGILTLKYPN EHGIITNWDDMEKIWHHTF/YTNELRV GFPKEDP/TLA*PKAPLKFPKANREE/M NEPQIMFETFNVPAMVVAIQAV/LCSLY ASGRYTGIVLDSDGDGVTHNVPIYEGYA/ LPHAIHAPWTMAGRD/LTDYLMKILTE RGYSFVTTAERIEIVRDUKEKLCYVALD FENEMATAAIHPSSLEKSYELPDGQVITI GNEARFRCPETLQFQPSF/LSGMEVGGAFH ETTYNSIMKCYIRHPGRIFYANNVLSG GTITVPLGFADVRMQERDSPAAPQHP* GSRIHSPPERKIYSVWIGGFHPWRLST SQQKW/VSPKQEYDEAGPSIVHRKCF |
| 404 | 8455 | B | 1374 | 53 | 302 | MTSALTQGLERIPDQLGYLVLSEGAGLA SSGDLENDEHAASAMSELVSTACGLRLH RGMNVHFKRLSVVFGHEHTLLETRVLTEX * |
| 405 | 8456 | B | 1375 | 277 | 573 | TSALTQGLERIPDQLGYLVSSGDLENDEQ AASAISELVSTACGFRHLRGMNVFPKRL SVVFGHEHTLLVTVSGQRFV* |
| 406 | 8457 | A | 1376 | 209 | 413 | EAGRREAELPLGSSPPLPVPPPRAGAGA HQTGA*RAHSMPRCSRKPQAVLTSSEM ALAACSSFSRSPDDASTAPSLSTR*PSTTT KGRGRGSPDRRLKGTFNAAVQPETAGC ADQLRDGTGCLLIJLQVPR |
| 407 | 8458 | A | 1377 | 116 | 1253 | NPGPVQVGVEGGQEEGPSSKKQAKTRQ WSPASITEAPGPKIRFSEPLRPPAGCRHQ LASRPRVLP/PSQTPFCPG/PPSPSSVCSP KDHWRDTPDRRLKGTFMPCRSRKTAG CAEQLOQRWHWLPAAHSPGPQMTPALHL HSVPGSRAGLGFAPAPGSAQKSSG*RCK S*EAC*RDGRPDTLHLQTQVSGLTWPQ VFSFSPQVSRPPPPYMLNLDLPEPPSA PTLAPRLPWPSTSHLCYKGPVLPPLWPLP SDP/SSPPFVSARPA/ALPAAPEHPPTDPSP AFSSPSLPFPSPPLPRADRR*GWSAGPPG G/EPHRLGSRDAEPPAGPLAHASSLTIAV FGAGGAPYQIGSFRLQAPVTCLQPLRSSF CLRHWPPLAPPLA |
| 408 | 8459 | A | 1378 | 24 | 364 | PTEY/ENL/FPCIKEAF/VVEWVKETLAV L/WPAKQYPFVTPIERILMEEGKAFFPSR STAKQKLDGNPVSPTPVIGLSPTPNKEE KHLNLCPFEPHTGHLDGARDTAGPSWLH HRF |
| 409 | 8460 | A | 1379 | 24 | 2858 | VAGNKRGFPLDRRTMPLRLDIKRKLT RSDRVKSVDLHPTPEWMLASLYNGSVC VWNHETQTLVKTFEVCPLPVRAAKFVA RKNWVVTGADDMQIRVFNYNTLERVH MFEAHSYIRCIHVHTQPFILTSSDDMLI KLWDWDKKWSCSQVFEGHTHYVMQIVI NPKDNNQFASASLDRTIKVWQLGSSSPN FTLEGHEKGVNCIDYYSGGDKPYLISGA DDRLVKIWDYQNKTCVQTLEGHAQNV CASFHPE |
| 410 | 8461 | A | 138 | 3 | 402 | HGKIFYFILFYFFIFLRRSLALSPQVRT ADCS/GAISAHCKL/RLPGFTFSLSLPS SWDYRRP/HPRPANFFLYFLVETGVSPC* PGMGLDLLNS/SIPRLGLPKCWDYRREP PRPVETFFLKAENVRVNYI |
| 411 | 8462 | C | 1380 | 110 | 508 | |
| 412 | 8463 | A | 1381 | 93 | 180 | |
| 413 | 8464 | C | 1382 | 128 | 382 | MYLGISRRLSMMLTFLAYLHPRERPPHR APXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXQQAQGTGISIPRTCTST GL* |
| 414 | 8465 | A | 1383 | 3 | 140 | |

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| 415 | 8466 | A | 1384 | 1 | 609 | |
| 416 | 8467 | B | 1385 | 1 | 690 | MASWDEKDLTVQPDTRKGSVLRCLGS SRALRWAGRGHVAAGWRPLAPESAGG WGMAAAAMVPGRSESWERGEPRPALY FCGSIRGGREDRTLYERIVSRLRRFGTVL TEHVAAAELGARGEAAAGDRLIHEQD LEWLQQADVVAEVTQPSLGVGYELGR AVAFNKRLCLFRPQSGRVLSAMIRGAA DGSRFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT* |
| 417 | 8468 | B | 1386 | 1 | 975 | MSPPGREQGLLLNLLRPSGLDNAGKTTI LKKFNGEDIDTISPTLGFNIKLEHRGFKL NIWDVGGQKSLRSYWRNYFESTDGLIW VVDSADRQRMQDCQRELQSLVVEEVGS SYPLCTWRFFSYLRIEQMYNLVLYRDIQ FPDFCFNSNTDWSKGLKTHARFGNTSLH VAHTDSTNTTNFVDVWRGRTKSLACLL QLSSLTCIYTAGKMRLQDRIATFFFPKG MMLTTAALMLFFLHLGIFIRDVHNF CITY HYDHMSFHYTVVLMFSQVISICWAAMG SLYAEMTENKYVCFSALTILMLNGAMFF NRLSLEFLAIEYREEHH* |
| 418 | 8469 | A | 1387 | 25 | 353 | EVCYYSSEAFFSELIKVILRHLCVAGK GLCSIPQLNTRGSQLRRISKRGSPLAVEI EEGHCLCLPLGTECLGIKPIVHLLNSEIG EKPPFSPLSPCSSAAFLLR |
| 419 | 8470 | A | 1388 | 79 | 467 | RPESQRANGVDSPNLKTVQPDTRKGS VLKWISKRGKPLAVEIEESHCLCLPLRTE CLGIKPIVHLFSCTRPVIVPSLELHYDIDS IAHMFVADLLLITLLSYIIPFYLGFQNA ITGNHRAWFY |
| 420 | 8471 | A | 1389 | 368 | 611 | LCPSHFAPTTLTQSGSSLKTCVVLNSRFK ACRAVPGPCLVNQMFASSILGKSHHSL VPINQGHNAWKAAGVPLPKAGY |
| 421 | 8472 | A | 139 | 210 | 1640 | DPARAGTGVGASFRGATWQQGQGRGS ACSTQCPPATCLLTGADAPTSRPWSLL SRLLGHCFSVLTVPAAAPPPGSLPEPPR AGPQCP*TRPPLR*PGCSHLAGPHSGSPR PCSLLGASATLYGFRHFLAGPAAQGGGQ AVGSQGDHPTRAQPP*WSSPQTPLNLSA AQEFEPRGTCPTRW*SRPDALPWPRPW EPWSG*AEGWEQE*WRLQPQGTAAAPRA TSSGYSGSSRGQRARPGPARCGDGGGA GRC/GHVRGRWRQLGHRP/RGSSAPAVC CGTLSAAPPGPQHSLSL*SSAPGPQWCP HWHPPQSGRQG*/SPLPPPGPGWRPPCAPC SGSPSA*GGCTPGCPTAP*GRRQGRWR*P RTGRLSPLGHLPGCRSQAASVSHRCWPL LPPPRPSGPPPLRSGSSPGG/PLPKGC*C QGGERPQQHKEAGQGAQQTWLHPQ APGGRRPSHTGWGGGAPGG*QRRNLA* RPLLP |
| 422 | 8473 | A | 1390 | 441 | 1178 | FVALPQPLCPSHFDPTTLIQGAHKNMC CIKSRFKRDLGLCRTCLVNKMFTSSILGK SHCHSLVSINQGHNAWKAAGVLPFRA GYC/QGFSPCDSLKYGSWDEKDLTVQPD DTRKGSVLRWISQRGKPLAVEMEEGHC LCLPLGTECLGIK/PIVHLFNSEIGENRP VMVGGRRHVLO*CCLG*FL*LPLRCLGAGE KHKSGL/HVHIPVIVLSLELNYDIDSFH MFF/SVDLLLITLLSYIIPFC |

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| 423 | 8474 | A | 1391 | 3 | 1078 | TRAAGLRAGVRVPRSPGPSRRMPARSGA QFCRRMGQKKQPARAGQPHSSSDAAQ VPAEQPHSSSNPAQAPCPRECLGPPTT PGPYRASIYFSSPKGHLTRLGVAEFFDQPA VPLARAFLGQVLVRRLPNGTELRGPHR WETEA/YTLGPEDAEAPLQGGWPGKTP R\NRGMFH*KPGD/LWVVYIIYGYFCM NISSQGDGA\CVFLRALEAPGKSWRPMR QLRS\TLRK\GTRQARVLKGPPLCSGPIS KL\COA\LPINKSF*PEGTLAQDEAVWLE RGPLEPSEPAVVGS/APRVGVGHAGEWA RK\PLRFYVRGSPWASVVDRAEQDTQ ACAKGLPRQDFLHCLKTRINVLFLEKKK KK |
| 424 | 8475 | A | 1392 | 3 | 452 | |
| 425 | 8476 | A | 1393 | 26 | 493 | NSTDSETHPWLLSPARQRTSRPAWGK VGAHAVRSMCAEALERMFLSFPTNTKY FPHFDLASHGFCPG*RATGKKVDDSDQ TPWPTWDDMPKRRCPP*SDLHAHKLS/R LDPV\NFKAPKATCLAG*PLAAHLP\AEF QPLAVARLPWGQISWGFC |
| 426 | 8477 | A | 1394 | 1 | 409 | |
| 427 | 8478 | A | 1395 | 9 | 817 | HGSSSEQEEDKNNQSATPIHSGPATM NSIG*YPTQPTYPVQSPGNPVYPQTLNL PQAPPYTADAPPAYSELYRPSFVHPGAAT VPTMSAAFPGLASLYLPMAQ\SVAVGPL GSTIP\MAYYPVGPIYPTLAPQVLGGKG GYDAG\ARFGAG\ANGGN\PSPPPG\CPP WAAQLAVMQGANVLVTQ\RKGNFFMG GSDGGYTHLVRNQGHLCAREKTSHTLQ HFSQCNCFSHINLKLOFRHMLLGCLSGA QTRHFSNLIRNHVMVAVPP |
| 428 | 8479 | A | 1396 | 1 | 367 | |
| 429 | 8480 | A | 1397 | 625 | 2919 | |
| 430 | 8481 | A | 1398 | 2 | 76 | HHYAKLGTRAVRRARRCAGWQSYVDN LMCDGCCQEAAGYCDAYVWAATA GGV\FQSITPIEIDMIVGKDRKGFFTSGL TLGA\KKCSVIRDSLYVDGDCTMDIRDK QS/QGGEPTYNVA\VGRSGRALVIVMG KGV\FHRRHTLTRKAYETPLYT*RQAW HEGSAKGSKMCRLAELRG |
| 431 | 8482 | A | 1399 | 149 | 421 | |
| 432 | 8483 | A | 14 | 79 | 533 | SSIMTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPE/RS*VFINSAGQKSADT GWSSSKPQN*HLSSFHQAVVGMIQPSHS QFLMKRKAASPRKLEWEH/LQPLHPMTL LYR*DGKPFPR*VLLSTYTYCSSRDRPKSS GKNARRFPAHGSS |
| 433 | 8484 | A | 140 | 885 | 1173 | LSQGPRRHSSAVQPPPHSHRGHHDDCA SPSQVRQNYAINRQINVELYASYIYLSM SYYFDHNDVALKNFAKYFLHQSHEERE HAKKLMKLLHFDG |
| 434 | 8485 | A | 1400 | 1 | 1107 | |
| 435 | 8486 | A | 1401 | 25 | 1486 | GPQPHSRSTHASGRPQSLSPVLSLSPDS MSFTTRSTFTSNYRSLGSVQAPSYGARP VSSAASVYAGAGGSGSRISASRSTSFRRG MGSGGLATGVAGGLAGMGGIQNEKET MQLNDRLASYLDRVRSLETENRRLAES KIREHLEKKGPQVRDWSHYFKMEDLAR AQIFVANTCGTMPRIRARIDNARLAVAD DFRVKYEDRSWPMCPVLWRTDIHGLPK VH/IDDTNYHTDLQLETENEALKVEELLFQ *RRNHEEGS*KALRRQISSSGMNAWRL DAPKSQDLAKIMADIRAQYDELGSKK NPRGSLDKYWSQQNEESTTGGSPQKSA EVGA\VETHAHRSLKRTVPVLGRSTLDS MRNLKGQLWRTSLREG*RPAYALTRLE PAPTGSLHLESELVAQTRARGTAARPRE |

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| | | | | | | YEALLNLIKVKLEAEIATYRRLLEDGED FNLGDALDSSNSMQTIQKTTTRRIVDGK VVSETNDTKVLRH |
| 436 | 8487 | A | 1402 | 36 | 389 | |
| 437 | 8488 | A | 1403 | 204 | 433 | |
| 438 | 8489 | A | 1404 | 3 | 392 | |
| 439 | 8490 | A | 1405 | 1 | 1314 | |
| 440 | 8491 | A | 1406 | 2 | 279 | |
| 441 | 8492 | A | 1407 | 3 | 1462 | TSCSSAAPFAAALARDPNPASPLPEHRPR LHRGPGPPARLAAAMADPKYADLTGIA RNDPDVYETSDLPEDDHAEFDAFAQELE ELTSTSVAEHNVNPNAAVDKFKDKRVG DKGI*FSQIVLGKTKRTGYESGEYEMLGE GLGVKETPQQKYQRLLEHVQELTTEVEK IKTTVKE\SAAEKLT\PVLLAKQ\LAALK QQ/VWVASHL/EGKLLGPDAAINL\TDPD GRPGLRRLLLQ\LEATKNSLGGSRGKTPG TPPD\SSLVTYELHSRPEQDKFSSSLPKS QKLEKRL\TEL\ETA\VTLLIQDAQNPLSAG LQGACLMETVELLQAKVSALDLAVL\DQ V\EARL\QSVLGK\VNEIAKH*SLC*EGAG YTKARLHQLIETITALGAPLPSTLPGAGC RRLVTHQSSLHEASPCQFGQLLDT/HLDT TQPMIANFLGRNTNPL*PQVADKPLRE NLAHQKGNFAQQ*RNG*KKLGKSEAH LGKLEEPGG |
| 442 | 8493 | A | 1408 | 1 | 4629 | |
| 443 | 8494 | A | 1409 | 96 | 721 | PGQLSSLTPPRASLLPWRAAYLFLALFLP AGLLAQGQYDLPLPPFDHGQYTHYM DQIDNPYYDYQEGTPRPSEGQFQ\FQS QQEVQQGVIPSPNPRAQGNAL\EPTEPG PLDCREEQYPC\TRL\YSIHRPCK\QCLNE VCFYSLRRVYVINKEICVARTVCAHE\EL LRANDLCSGTSFSKCGR*WASSGL\QSV\A AASCAIRSCGSF |
| 444 | 8495 | A | 141 | 170 | 737 | IVTATCLWGSVLVTHSVFFQSYFDRD DVALKDFAKYFLHQSHEERGTCRLNLM KLQNPGR\GLIFLQDIKVNKRS*GCHTSSS GSRVSEIT*TSNCPYKVMHWAFAFCA FLGLPSKLN*ANSNVFPAKTWWLEMMG LLTSRLVGRDALTYSHSKPDCDDWESG LNAMECALHLGKNVNQSLLELH |
| 445 | 8496 | A | 1410 | 118 | 256 | MFCFFLKPIAEAPFKFDMELDDLPEKVL KELIFEETARFQPGYRS |
| 446 | 8497 | A | 1411 | 457 | 839 | AVGGFWGCPVELHMLVHITPLSHFKC GCFSNHVPLRI*QRGTLRL*MRKYTILF PSTACQHLKFIFQPTV*QFVIKPPGAHDV KHCSVLKYNSISDTAESDCQKKLSTNSC LELYPYFTDLFKYL |

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| 447 | 8498 | A | 1412 | 310 | 1784 | RRRPRQPTMAAAVVGGRGPEVWSAGTL FDVGPRYTNLSYIRRGRLTTCVC SAYDN VNKVRVVAIKKISPFHQTYCQRTLREIK\N ILLRFRHENNINGINDIIRAPTNEQMGCCI* *YRDLMETDLYKLLKTQHL\SNDDHIWYF LYQILRGLKYIHSANVLHR\DLKPSNLL LNTVTCDLKICDFGLARVADPDHDTGF LTEYVATR WYRAPEIMLNSKGYTKSND IWSVGCILAEMLS*QGPFQKGHYL\DQ L\NHIFGVFLGSPSQEDLNCIIF*KLGN Y LLSSHTSKIMVPLEHACPNADSKSSGTL LGQNCLTFNPHKRIEVEQALA/HTPYLE QYYDPSDAEPIAEAPIQVRPWKLLDLPKE KLKGTNFKRLARFIQPGVQILNFVQTK GSEGLDVLRRHRCSSSOFLTPGPVFQPCLG LSTLTPLPFGRGRFLGSCGFYGFSKISFS PGGFLGQPCCVHPLVTLRAVCTSVHL TAYCCFSH |
| 448 | 8499 | A | 1413 | 2 | 294 | GNKMAAPKGS LWVRTQLGLPPLLLLT ALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPKVGPRVRSGLRPFPCSPFL GSPHVCRLWQPGC |
| 449 | 8500 | A | 1414 | 366 | 1412 | QRGTRWRRERGS LWVRTQLGLPPLLLLT MALAGGSGTASAEAFDSVLGDTASCHR ACQLTYPLHTYPKEEEL YACQRGCRFLS ICQFVDD\GIDLTRTKLECESACTEAYSQ SDEQYALPFLGCQNSACHFAELRQEQL YVPRWPKMAPTFFL*LLGEGSFWELT*W DSAQSFITSSWTFYLQADDGKIVIFPV*S QKSQYAPHFGAREPTNFEENHLLSKMSS DLQMGKFHQAHQGIFLKNEERDGLFKK PSILNSGWILTTTLVLSVMVLLWICCAT VATAVEQYVPSGEAGVTMGDLEFMNEQ KLNRYPASFSCLVRSKTE\DH EAGPS YLPKVNLAFFLEI |
| 450 | 8501 | B | 1415 | 76 | 384 | MSGWGVLSGRLNPAAREKDVERFFKGY GRIRDIDLKRGFGFVEFEDPRDADDAVY ELDGKELCSERV TIEHARARSRGGRGRG RYSDFSSRRPRNDRRNAPP* |
| 451 | 8502 | A | 1416 | 3 | 229 | |
| 452 | 8503 | A | 1417 | 152 | 536 | PDIMSGCRVFIGRLNPAAREKDVERFFK GYGRIRDIDLKRGFGFVEFEDPKDADDA VYELDGKEL\CSERV TIEHARARSRGGR GRGRYSDRFSSRRPRNDRRNAPPVRTEN RLIVENLSSRVSWQVC |
| 453 | 8504 | A | 1418 | 771 | 1383 | ILIEYKCGKCHVCTLSNIFSSSLVFFISCD CLCVFPPLLCLTQLSCVKDLKDFMRPAG EVTFA DAHRPKLNEGVEFASYGDLK NAIEKLSEKEINGRKIKLIEGSKRHRSR RSRSRSTRSSRSRSRSRSRSKSYRSRS RSRSRSRSDVPVLLSRSPRA*EEPRNRGS SSRSKSPASVDRQSRSRSRSRSDSGN |
| 454 | 8505 | A | 1419 | 236 | 1377 | PDIMSGCRVFIGRLNPAAREKDVERFFK GYGRIRDIDLKRGFGFVEFEDPRDADDA VYELDGKELCSERV TIEHARARSRGGRG RGRYSDRFSSRRPRNDR/RVCEGWMAA LNNYW*G*PFKIQESLAVMILGPAV*SVL LFPR*PIVLDESI*VIEHKSIDGSH*NGL*Y LMA*TCPQLNTSAVIAFLPL*IRIFFLRNA PPVRTENRLIVENLSSRVSWQDLKDFMR QAGEVTFADAHRPKLNEGVEFASYGD LKNAIEKLSGKEINGRKIKLIEGSKRHRS RSRSRSTRSSRSRSRSRSRSKSYRSR SRSRSRSRKSRSVSRSSPCPEKS\QKRG S\SRASKSPSHLWNRPEVPGPRSRSQQLD QWPIKPVK |

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| 455 | 8506 | A | 142 | 1 | 809 | VVGVSFCNSAWTEPGARSPRPAHNSQP SVTSSPHPRTPAPPPPLQRREATAAGRR LSLVAAMTTASHLAGCAKNYHQGLKRP PINRQDQPWKLYGLLRFTLSHVLTNFDP RMMLAFERTFAKYFLHQFSMKEEGNHA EET**KLQNQRGWPEFFLAQDIKETQTC DWEERGLNAME\CALHL\KKNVESSHL LELHKTGQLDKNDPPFCVTFIETHYVNE QVKGHQRIWGDHVTNLARKMGSAPNLA WAKYLFHDHSTSLGDSNES |
| 456 | 8507 | A | 1420 | 568 | 770 | PDIMSGCRVFIGRLNPAAREKDVERFFK GYGRIRDIDLKRGFGFVEFEDPRDADDA VYELDGKELCSERVITIEHARARFTRLGR GRGRYSDRFNNSAELRNDRRNAPPVRP ENRLIVENLSSRVSWQDLKDFMRQAGE VTLPDITRLNLNEGVEFASMGDLRNLAI EKLSGRELNGRKIKLIERPAKRPQ*VQQS RSSDPGTQKSPGPRSRSPSPVANLNSR SKK/RRGSREPGSPEPSRSC*VGSSPVP* ERFFKGYGRIRDIDLKRGFGFVEFEDPRD ADDAVYELDGKELCS |
| 457 | 8508 | A | 1421 | 1 | 1317 | |
| 458 | 8509 | A | 1422 | 1 | 816 | |
| 459 | 8510 | A | 1423 | 19 | 2867 | PPDPLPGLPCPPGGPPLPAFGGGWGGAR GSWHWSSRACSRRRRLVHAPRAPLLPR AAAEKAKRPAGARQMGLKARRAAGAA GGGGDGGGGGGGAANPAGGDAAGD EERKVG LAPGDVEQVTLALGAGADKDG TLLEGGRDEGQRRTPQGIGLLAKTPLS RPVKRNNAKYRRIQTLIYDALERPRGWA LLYHALVFLIVLGLILAVLITTFKEYET VSGDWLLLETTAIFIFGAEFALRIWAAG CCCR |
| 460 | 8511 | A | 1424 | 2 | 508 | PDSSGPHRLRENPPMVAVSCPTKTNVKG PPGGKVGAGHAGYGVSEALERMFSLFPT VTKTYFPHFDL\SHGLCPRLKGHGKVA DALTNVAHVVDMPNGVVRP*SDLH AHKLVRVDPVNFKLLSHCLLVTLAAHL PAEFVTPAVPRPPWDKFPWLSVKHRCLT FKYR |
| 461 | 8512 | C | 1425 | 257 | 358 | MILLVFLPXHQVFLERXQSEILHHLNTL ADVL* |
| 462 | 8513 | A | 1426 | 64 | 467 | PAAWLPILVAARQLTVQMMQNPQILAA LQERLDGLVETPTGYIESLPRVVKRRVN ALKNLQVKCAQIEAKFYEEVHDLQRKY AVLYQPLFDKRFEINAIYEPTEECEWK PDEEDEISEELKEKAKIEDEKDD |
| 463 | 8514 | A | 1427 | 1 | 795 | |
| 464 | 8515 | A | 1428 | 1 | 836 | |
| 465 | 8516 | A | 1429 | 1 | 410 | ARAKTYRMRSEPDDSDPFPDGPIMGC TGCQIDWKKGKNVTLKTIK\KKQKHM RGTVRTVTKTVSNDFFNFFAPPEVPES GDL\DDDAEAILAADFEIGHFLRERIIPRS VLYFTGEAIEDDDDDYDEEGEKS |
| 466 | 8517 | A | 143 | 776 | 1115 | APGVDPKPRQNE/PPVSTKNM*LGVD CLRGLRQEDHLNQEVPGCSEP*CHDQAT ALPAWATQQDPVSKKKKKKWWREARK GKPQ*GDGEKDSTTHSWL*RWRSLKSRI TVSL |
| 467 | 8518 | A | 1430 | 502 | 765 | LQKQKQANKQQIT*K*ACQMV/SNSSFP GKQKVDPTTKRCLVNGGLNLKIQ/LIQ ANF*KSRFIHLTVVPVTLISQVTLQLTMS PKTQ |

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| 468 | 8519 | A | 1431 | 58 | 1335 | VTACAAPAAWLPILVADIWSSYNMADID NKEQSELDQDLDDVEVEEEETGEETKL KARVQLTVQMMQNPQILAAALQERLDGL VETPTGYIESLPVRVVKRRVNALKNLQV KCAQKETQFYEEVHDLERKYAVIYQPL FDKRFEIINAIYEPTEECEWKPDDEDEIS EELKEKAKIEDEKKDEEKDPKGIP*IWAL TVFKNVDDLSDMVQEHDEPILKHLKDIK VKFSDAGQPMFVLEFHFEPNEYFTNE VLTKTLRMSSIPDSDPFFF*MEPEH*G CTGCQIDWKKGKNVTLKTIRKRPKPQG TWGQFRTVN*NQFPNDSFSNFFCPLKFL ESEDNRNDAAEAILAADFEIGHFLRERIIP RSVLYFTGEAIEDDDDDYDEEGEEADEE GEEEGDEENDPDYDPKKDQNPACCKQ Q |
| 469 | 8520 | A | 1432 | 1 | 645 | PLKRSDGCGNDGRPTRPPTRPDTTVFTSNL KQTLVHLTPVEKSAVTALWGKVNVD VGGKALGRLLVLPWDPKRSFQSPGE SVPTP*MAKEKVLGCLVVGGLASPGTTL KGHLCPHWSELALLTSLPRGIPEELQGS WGKRAGSCVAWAQSTFGQKNFNPKNL QGLPNQENWLAWCWLNALGPTSNHLSL AFLAGPISN |
| 470 | 8521 | A | 1433 | 240 | 461 | |
| 471 | 8522 | A | 1434 | 2 | 206 | |
| 472 | 8523 | A | 1435 | 2940 | 3296 | |
| 473 | 8524 | A | 1436 | 189 | 736 | ENKISSVFKADFLPPAPCSLPGLEVSVP KGKNTSGRESGFGWAIWMEGLVFSRLSP EYYELARPHLRDEEKS\CPCLAQEGPQ GDLLTKTPELGP*ITRTCLTIVQKT*RK MVDKPTQRSVSNAAATRVCRTRGRSRWR DVCNFMRRYQSRVTQGLVAG\ELAAQ NLVSTSRLCIPSTGPL |
| 474 | 8525 | A | 1437 | 3 | 452 | |
| 475 | 8526 | A | 1438 | 3 | 485 | PTLLVPTDSERTHPWLLSPADK\TNVKG PGGKVGAAHVSRMCAEALERMFLSFPT TKTYFPHFDLSHGSAQV*GPRARKVAD ALVNAVAHVGRTPNALVPPLSDLHAH KLARVGPSTFKLLKATCLAGLTLAAHL PARVQPLAVASLPWDKVSWSAC |
| 476 | 8527 | A | 1439 | 217 | 474 | RTCASLSLHRPHGSHGHGQRGGFL*VF SSSFDSSDGWVQVCSPPGGQIPPTCPHHCC DPESPSSSGPPVPWHLPCAVQGPSPGGL |
| 477 | 8528 | A | 144 | 1 | 419 | |
| 478 | 8529 | A | 1440 | 569 | 737 | REHPVAGLQEHLLQGGSGQQDLRG*WA YFS/HR*SRKVPTSW*RRWKMVAPWAA RRV |
| 479 | 8530 | A | 1441 | 520 | 1319 | SWPQVPKTNKIEPRSYSIINTSCGIRRLGP ALNTLIFS\K*NASGPAGHSASIEGAPRG KGRGRAVARLAADRPPAPKIQLPSFV/LR STL*YPLLELELPRLLATHLPSNGS\SLK\ DLKWT\HSNYRASKEP\CIVIFVTTSPGR EWWICAPAAFLG\CGSRFSGSPLPE\SNP* FPV\TRGHHGRHGDYHRKLIGQTFEWVV VRRHGGVRAIGPRLSRVTKAAGARPPAG AGEG/LDRVGFDLINAPSPPAKGVSARR HVLALELPQLSK |
| 480 | 8531 | A | 1442 | 2 | 239 | RKTQTTRRGPLWAGPGG*RGGWWSR RLLLAAGFLGTHPGSTHPGLQQPRFKWD HTRSSQGAFIFTFFPRGGQEHSTST |
| 481 | 8532 | A | 1443 | 234 | 491 | |

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| 482 | 8533 | A | 1444 | 126 | 890 | PRSIGEGGLPSLLCGSGRARFSSGGMSGP RLVVLGSPSGA/GKSTLLKRLQEHSGNF GFSVSRESRALVEG/TTRNPRPGEGRQK ITYFVTREVMQRDIAAGDFIEHAEF/SGN LYGTSKVAVQAVQAL*PHRVCLDVADL QGVVRNIRPTDLRPNLHLLFSPPTATCW KQPGFRQPQQLTEGRAWLKAGLLLAQ ADMEEPAKEAPALFDVVHPLNDQPGT QA/YAELKEALSEEIKKAQRTGALRLAV CSR |
| 483 | 8534 | A | 1445 | 978 | 1440 | AGVGVGRGTTGRLVVRKFLTIFGNPLFL VAPPKPHSEWSQRLTYRRRPSPYNTAIS NKTURLSPNPDGNRICLPFIPKKVGKAPQS LHVVCAPGRLRGVRAVRPKV/LL*RLSK TKKHVSRAYGWFHCVLKCGDRIRKACF SLIGGSRKIRCGKSV |
| 484 | 8535 | B | 1446 | 43 | 674 | MDWTWSILFLVAATTGVHSQVHLVQSG AEVKKPGASVKVSCASFNSFDTYGFN WVRQAPGQGLEWMGWVSAFNGDTNYI RKLQGRVTMTTDSSTSTAYLELRSLKSD DSAIYYCAATNSDKYFWGQGLTVTVSA ASPTSPKVFPLSLCSTQPDGNVVIACLVQ GFFPQEPLSVTWSESGQGVARNFPPSQ DAFGDLYTTSSQLTLPATH* |
| 485 | 8536 | A | 1447 | 3 | 1637 | SPGIFRGFSQVIRTEQRELTMESGLNWLL LVAVLKGVQCEVQILESGGGQVQPGGSR TLSCAASGFIFSNYVMTWVRQAPGKGLE WVSSTAASGANTFYAESVKGRFTVSREN SENMMYLQMSLRDEDTGIYYCAKDG VPLNGVAWIVAGPGNVRPRKWFDAWG QGTTVTVSSASPTSPKVFPLSLCSTQPDG NVVIAISCLVQGGFFPQEPLSVTWSESGQ VTARNFPPSQMASGDLYTTSSQLTLPAT QCLAPKSVTCHVKHYTNPHPDVDGPCP VPSTPPTP/CSLNSTYPISLMLPPTVTAPT GPSKDLFLGSEANLTCLTGLEWASGCH FQSEGLQVGKSAVQGPPEA*PSVAAYSV VQLSCRGWREAMEPLVRPFTCTAALPRS PRTRANRPPSSKSGKHISGPEGPPCCRPPS EELALNELVTLTCLAR/AFSPQGPCWVR WLQGSPKLPRKST*LG/PPAGA QARAP TTFAVTSILGR/VQPEDWKKGDTFSCMA GHEALALAFQTQIDRLAGKPTHVNV VVM AEVDGTCY |
| 486 | 8537 | B | 1448 | 113 | 249 | XAAMTTASTSQVRQNYHQDSEAAINRQI NLGALRLRLRPVHVL |
| 487 | 8538 | A | 1449 | 846 | 1193 | VMGPKPLPGIVPEFLKNWPRPSGLLIEFC PHWDTTDMTSN/CLV*EENYSEQCLELL NPVGMDLILRGDCESYHGKPNRKLGS QHLSDQAALTGRLSSPCLMKRRRSASFR FTQAG |
| 488 | 8539 | A | 145 | 3 | 1363 | HASGITMAAGTLYTFSVNWRAFKALIA AQYSGAQVRVLSAPPHFHFQQTNRTP VLRKFPAGKGPAGFEGDDGFCVFESNAIA YYVVSNEELRGSTPEAAAQVVQWVSFAI DSDIVPPASTWVFPTLGMHMHNKQAT*E CKGRK*GRILGLVDAYLKTEDFCWGAN VERLSGITVACTLLWLYKQVLEPSFRQ AFPNTNRWFLTCINQPPAVLGGSETC VRRAPFGA*KVLQRPQPKIDTPRKEE GFTGKKKQKQPAERKEEKAAAPGPEI EEMDECEQALAAEPKAKDPFAHLPKSTF VLDEFKRKYSNEDTSLVALPYFWEHFDK DGWSLWYSEYRFPELTQTFMSCNLITG MFQRLDKLRKNAFASVILLGTNNSSIS GVWVFRGQELAFPLSPDWQVDYESYTW RKLDPGSEETQTLVREYFSWEGAFQHV KAFNQGKIFK |

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| 489 | 8540 | A | 1450 | 2 | 1087 | AIEHCQSGDNPESRRGFLLQQLGRNPA LVPHPGRTGHSQPPVTFHRHPSDCQRSP AGRFKGGPSHRGQPPPFHKSPMTTARP TSQVRQNYHQDSEAAINR/QINLELYA SYVYLSMSYFDRDVAALKNFAYFL HQSHEERAEHC*ENLMKACRTNEGWPNL SFQDIKETKTCDWESGAECQWKALH LEKNVESSHYNLHLKLAATDKN*PPICV DFI*DTFTLNEQ/V*KAIKRIWGDH/V*PK LWRKMGSAPNLGFGEYLF*QSTPWETV IMKAKPRANFPNSRGVTFVLTKAVHAC WGFLYLFYKLYQNIHLSSICTIPSNKEI WYPGVVFEVLDESEIYPGYLPDSL SAVV QF |
| 490 | 8541 | A | 1451 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFGNLSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGT AQLSELHCDKLHVDPENFKLLGNVLT LAJHFGKEFTPEVQASWQKMTGVASA LSSRYH |
| 491 | 8542 | A | 1452 | 41 | 542 | APSRRPWGHFTEEDKATITSLWGKVN VEDAGGRKPLGKAPWLSTPWTQRFFDS FGNLSASAIHQTPKVKAHGKKVLT LGDAITKHLDDLKGTFAQA*SELHCDK LHVDPENFKLLGNVLT/VLAIPFSAKE FTPEGCRASWAERWVTWSWPVPCSSRY H |
| 492 | 8543 | A | 1453 | 1 | 1233 | |
| 493 | 8544 | A | 1454 | 233 | 884 | ESPGVGCSARRGPRPSGPPPAAPGTPR PHGIPLYTRAGHQ**GEIRRRPCTFISKFL RPQGSASERQLPDLQARAWQELLGRP NKHHWFPR*SPCKGIGVTRCIRNP*KW IPLIGPGQHSAILGLSSQELFRLLPSEL TLWG*PIEVSYRIGEDGSHLCACMKPSPA GGSTQNTQNVQMVDWSRISCKEELLG RTEFPFKTTNMMTVSG |
| 494 | 8545 | A | 146 | 3 | 452 | AVPGPGFGLSPTMVTALVLLAALLA TVSGYFVSIDAHAECEFFERTVSGTKMG LIFEADGGFLDIDVVITLPR/RKIKPRL KKKGGQ*TYRSFMDVTFKLCYNLRMSW MNPNIHNHNLWLLTSIKFLITQFRSSLS YLSSCIQSE |
| 495 | 8546 | A | 1460 | 255 | 2154 | LAEPEVATDSGQADLPAEGGDPRAEAS CSQLHSPHAMADSRDAASDQMOMHWK EQRAAQKYLGVDLGHKKADVLTGGA GNPVGDKLVITVPRGPLLVQDVVFTD EMAHFDRERIPERVVHAKGAGAFGYFE VTHDITKYSKAKVFEHIGKKTPIAVRST VAGESGSADTVRDPGRFAVKFYTEDGN WDLVGNNTPIFFIRDPILVSFLFSDRGIPD GHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYG IRDLFNAIATGKYPSWTFYIQVMTFNQA ETFPFNPFDLTKVWPHKDYPLIPVGKLV LNRNPVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQGRFAYPDTHRLGPNYLHIP VNCYPYRARVANYQRDGPMMQDNQGG APNYYPNSFGAPEQQPSALEHSIQYSGEV RRFNTANDDNVTQTSLYLTFRFMENIEK VRAFVYNVLNEEQRKRLCENIAGHLKD AQIFIQKAVKNFTEVHPDYGSHIQALLD KYNAEKPKRSLAFIRVTRSSLEDSPVLD VQMNASGFKIENPTFYSRLCENNFAISPG ENEALTIEQMGSTEANCLLRNSVQLVAF VIEITSRKSDIVERHKCAWT |
| 496 | 8547 | B | 1461 | 129 | 321 | XYWMLCSKAEGCCSGAPKAVGVVWST TLIVLHAHRAVTLVVGHSSSTRDSSQVY EDNWVPGWR* |

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| 497 | 8548 | A | 1462 | 70 | 2954 | RMLITGSPALGSAIPGTPGRRGEALQLLG QSGTLPFRLLGISGLQASFGEPCEPIGL PILACLAPSSQSEGSPPGAGRGGGADW LSLKSPRTRGNRQICLLRVETHEPRPPAV FCTANRTLWLTAGIPPATRCSTGRSSGPR RIEMRACTTSIQGNVQDKWKSNCCEVP DVECACTFLESCLKPGWLQSKQGAQRS GGDECLQSSHLWEFVRDLLSPEENCIL EWEDREQGIFRVVKSEALAKMWGQRKK |
| 498 | 8549 | A | 1463 | 3 | 452 | |
| 499 | 8550 | A | 1464 | 2 | 521 | PDSSGPHRLRENPPWCLSPADKTNVKA AWGKVGAAVRSMCAEALERMFLSFPT TKTYPPHFDLSHGFAQV*GPRARKVAD ALD/TNAVANVGRTLPNALVRPLASDLHA HKLSSGTRFNFKAPKGHLPLGEPWAA HLPRPSFNPWRLQRLPWGQSFLGFLKH RCLNLPNYR |
| 500 | 8551 | A | 1465 | 154 | 678 | PPLHLRDCFSPPGRALSPVGLYPYRVS PTWLKLTSDDVKEIYKLAACKGLTPS IQIGVILRDSHGWAQVRLGTGHDFTKI LKSKGLDPDLPEDLYHLIKKAVAVRKH LERNRKDKDAKFRLLIE'SRIHPFWLRY YKTKRVLPPNWEI*NHLTASALGRINL VWCTPSK |
| 501 | 8552 | A | 1466 | 23 | 636 | FSYLPPGPGSHGTWGLWELQFKMRFGVC RHLMEDSMDMDVSLR/PQNYLFSCELK ADKDDHFKVDNDENEHQLSLRTPTVSL GVFEITPPVLLWLKCGSGPVHISGQHLV AVEEDAESDEEEEDVKLLRISGKTKTF MATNGKEYKHYSSEKSLDNKYKTRTP GFQAFGFEDLHPWPLGSQAFYLSLRVTP PVFLVRLLED |
| 502 | 8553 | A | 1467 | 3 | 618 | AKD/ELHIVEQGHDIRGRSIKIT/LATLKM S/VQPTFS/LGGFEIQTVV*GLKCVSGPC HISGQHLVA/VEEDAESDEEEENVKLLS ISERRSAPGVVSMVPQKKVKLAADDD DDDDEEDDDDDDDDDFDDEEAEEKAP VKKSIRDTPAKNAQKSNQNGKDSKPSST PRSKGQESFKKQEKTPKTPKGSSVEDIK AKMQASIEKAH |
| 503 | 8554 | A | 1468 | 1 | 1689 | |
| 504 | 8555 | A | 1469 | 3 | 535 | DSVLRGCSLEQRSFISVRLLSYLSACRHP MEDSMDMDMSPLRPQNYLFGCELKAD KDYHFKVDNDENEHQLSLRTVSLGAGA KDELHIVEAEAMNYEGSPIKVTATLKM SVQPTVSLGGFEITPPVVLRLKCGSGPVH ISGQHLVVYRRKHQELQAMQMDCRAL STS*ASSAPRPS |
| 505 | 8556 | A | 147 | 90 | 512 | VQGLGVERVPLGSHRGWMGPPRLLSP QERASCLLLLLPLVHVSATTPEPRELD DEDFRCVLQLSPEPQPDWPEALHRASAV QA*ISAGGSHLQSSFLIGRLRLKTVTVLL WPLFVLICVYLSVYLPFRLCLDTLSCVV |
| 506 | 8557 | A | 1470 | 1 | 1025 | SVLRGCSLEQRSFIYGRLLSYLSACRHPM EDSMDMDMSPLRPQNYLFGCELKADKD YHFKVDNDENEHQLSLRTVSLGAGAKD ELHIVEAEAMNYEGKSN*T*HLATLKMS VQPTVSL/GGAFEITPPVVLRLKCGSGPV HIKWTSTYVAVEGKMQKSRLKKEGRI. VKLLKVYLGKRSAPWKVGSKVSTKK VKTLA*WKDDDRMNDEEDDDDEDD DDDFDDEEAEEKAPVKKSIRDTPAQKC SESQNGKRLQKPSFTPKNQKQESFQ ETRKKLLKTPKGPSVEDIKAKMQASIE KGGSLPKVEAKFINYVKNC SRMTDQEA IQDLWQWRKSL |

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| 507 | 8558 | A | 1471 | 3 | 490 | SSGPTRLRENPPMVAVSCPTKTNVKAIA WGKVGHAHVSRMCAEALERMFLSFPT TKTYFFPHFDLEPRFLPRFKGHGKKVADA LTNAVAHVDDMPKRAVPPLSDLHAHKF RVGPGSTFKLLKPLALLG*TLGRPTSPSE FQPLAVARLPWQGSFLGFLKQPC |
| 508 | 8559 | A | 1472 | 35 | 1288 | |
| 509 | 8560 | A | 1473 | 1 | 1641 | |
| 510 | 8561 | A | 1474 | 212 | 369 | HPVTVYLLGYLLFQLPCGSEFSTSETHG HSADRLGAAFAVSRLEQDEYAPG |
| 511 | 8562 | A | 1475 | 63 | 255 | VLMFSSSHG*GYQSSRLQCKLQIVQLIQ DILLFFSF*IFE*LLS*LTPLKIFPLHQNGPS DFVS |
| 512 | 8563 | A | 1476 | 169 | 391 | |
| 513 | 8564 | A | 1477 | 85 | 1534 | KSSHCIKMGPQIFHKTSSELVLPATSCPSC PDQNEEDVSQTQYKECCGGWCSSHSIF AVWHFI*RPDAT*FGLEQRLTGLLASGP VSLREVV*LYSSLGTVISGK*KTSNVG*R GLALGSWAFSDKYSWFTMTWACISGP TKALTTGVGLIAFGQCDVIVAGGVEL MSDVPIRHSRKMIMLMDLNKAKSMGQ RLSLISKFRFNFLAPELPAVSEFSTSETMG HSADRLAAAFVSFLDQDEYALRSHSL SKKAQDEGLLSDVVPFKVPGKDTVTKD NGIRPSSLEQMAKLKPAFIKPYGTVTAA NSSF/LLTDGASAMLIMAEKALAMGYK PKAYL/RRDFMYVSQDPKDQLLGPTYA TPKVLEKAGLTMNDIDAFEFHEAFSGQI LANFKPMDSDFAEWNYMG*KKPRFGL PPLWRRFNNWGGLSLGHPFGTGTGCR LVMTAANRLRKKGGQYGLVAACAPG GQGSATDYVEAYPK |
| 514 | 8565 | A | 1478 | 2 | 359 | |
| 515 | 8566 | A | 1479 | 1 | 585 | PRGVIGHGPLGTSFIGKYCGDYWVKAF LDRPSQPNQGPKNFEVVDLVDVNTPI DLMAIPVSARKKERKVS CMFIPDGRVSVS ARIDRKGFCEGDEISIHADFENTCSRIVVP KAAIVARHTYLANGQTKVLTQKLSSVR GNHHSITCASWRGKSLRVQKIRPSILGC NILRVEYSLLIYVSVPGSKQVFIKAL |
| 516 | 8567 | A | 148 | 98 | 440 | KDDTNTKCW*AWNCSSTRAHWKRTLT LLGRLTMNIPHDSAIPLLAGHPT*MWA YVHQNP GTVMLTETLFMIATNWLHKC PQ**KE*CNGAVTEWSAALKQNKQLQH VTPRV |
| 517 | 8568 | A | 1480 | 218 | 1677 | SEIIFCKGVSSIWSFFFLPPSFLT LKTNVSP SWVMFKKIKSFVVFNDPGKGVTAVG EKVAIGRVNSGRCEVTRVKAVRIPAC RSGLKCLWMPGIPSRCKQTS EYPRYEDT VFLAEDQPTGENEMVIMRPGNQYEYKFG FELPQGP LEHSFKGKYGCVDYWVKAF LDRPSQPTQETKKNFEVVDLVDVNTPD LMAVPS/ALKKEKKVSCMFI PDGRVSVS ARIDRKGFCEGDEISIHADFENTCSRIVVP KAAIVARHTYLANGQTKVLTQKLSSVR GNHHSITCASWRGKSLRVQKIRPSILGC NILRVEYSLLIYVSVPGSKKVILDPLV* LGSRLSSRTSISMGRSRTS/LRMSWVD LNIPDTPEVPS/CILGCSFPEGSTVWESPT TPALLDDMDGSQNSPUMFYAPEFKFMP RTYTEVDPACIFNHQCAVSMWKKRSFT LLVSFWPSLPWTVHFFQRLNSLCNGSVG PTLSPLTS |
| 518 | 8569 | B | 1481 | 21 | 410 | MPSKVRCSXVQVFDAMKTATAVAHCK RGNGLIKLEPVLLGKERFAGVDTRVR VKGGGHVAQIYAIRQSISKALVAYYQKY VDEASKKEIKDILIQYDR TLLVADPRCE SKKFGGPGARARYQKSYR* |

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| 519 | 8570 | A | 1482 | 1 | 456 | MPS/KGPLQSVQVFGRRKKTATAVAH/CK RGNGLIKVNRPLEM/IEPRTLQYKVLGS GTGVSGWRTLGD RDVV ALESWGAGISN GMFRSCVGCQW AAGASSASRQERFAG VDIRVRVKG GGPWPRFMSKKFGGPGAR ARYQKSTD KPIVTQNSLV |
| 520 | 8571 | A | 1483 | 172 | 661 | LLEPVLLLGKERFAGVDIRVRVKG GGHV AQIYGESQELGAWRRWLWEGGLHSAPV PFNCVSFSQLSVSPISKALVAYYQK WSE HGSFP*GRWVCGDQVKDSV*LSKSSLL FLPDVDEASKKEIKDILNQYDRTL VADP RRCESKKFGGPGARARYQKSYR |
| 521 | 8572 | A | 1484 | 1 | 556 | GAARVRLSSPRSDAMPSK/GVPLQSVQV FGRRKDSGQLLAHCKRAWGLIQG*TG GPLEMIEARARLQYK LLEPVLLLGKNER FAGVDIPCPV*KGGWSTWPQIYAIRQSI SQKPLVAYYPEM*VSMGPSHE/YVDEAF QRREIKDILHPSYDRNPAGLAGPFVRCE SKKF GGPGA RARYQKSYR |
| 522 | 8573 | C | 1485 | 127 | 435 | MAASXNPEVLDITEETLHSRFLEGVRNV ASVCLQIGYPTXASVPHSIINGYKRV LAL SVETDYTFPLAEKVKAFLADPSAFVAAA XLGCCHHSCSXCCCSPS* |
| 523 | 8574 | A | 1486 | 1 | 689 | KCFI/VGADNVASKQMQQIRMSFRGKAV C*WGKNTMMRKPIRGHLENNPALEKLL PHIRGNVGFVFTKEDLTEIRDMLLANKV PAAARAGAIAPCEVTVPAQNTGLGPEKT SFFQALGITT KISRG TIEILGVRNVASVCL QIGYPTVASVPHSIINGYKRV LALSVETD YTFPLAEKVKAFLADPSAF/VAAAP/VAA ATTAAPRAAAAPAKVEAKEESESEDED MGFGLFD |
| 524 | 8575 | A | 1487 | 66 | 1104 | RTAVMPREDRATWKSNYFLKIIQLDDY PKCFIVGADNVGSKQMQQIRIVPWGEAC VLMGQKTMNGPGPSEGHLENNPASEEL LPH*VRGHLGFCFTREDLTEIRDMLLAQ *GCQAAARCWCQLPPCEVTVPAQNTGL GPEKTSFFPGL*VSPTKNLPGGTH*KS*S YVQLIKTGDKMGSQTKAKAAEKM LKN LPPSPFGAGQPKQGVVRKNGKHPTNPESA *ISTRGKLCHSRFLGGCPANVAKCLSCKI GYPATVASSTPIINNGYKRVPGPCLWTP DYTFPLAEKVKAFLADPSCLCVLLPPV GAAATTACFALLQPPAKVEAKEESESED EDMGFGLFD |
| 525 | 8576 | B | 1488 | 98 | 264 | XQVVCKKYRGFTIPEAFRGVHRYLSNAY AREEFASCPDDEEIELAYEQVAKALK* |
| 526 | 8577 | A | 1489 | 155 | 1217 | DPPSPVPAPPSSPRDGHFLVPDATMAEEQ PQVLELVKAGSDGAKIGNCPFSQRLFM VLWLKGVTFNVTVDTKRRTETVQKLC PGGQLPFLLYGTEVHPD TT KIEEFLEAVL CPPRVYPKLAALNPEVQHSWGWDIFAK FFLPNIQEFQTPALN*QSGRRGFLESP*KV LDNYLTSPSPSEEVDETSC*KIEGVSQR KFLDGQRRPHPWLDLQTCCKVTH*VQ VVCKRK*PGNSPHPPKAFPGKCHRVPS KMPYAPGKNSPSHPVPDDEEIELRPM SK VAKALQISPSLGLPSTPSIFSTKAPGGFHI ATPMGHTPKLASGQILGDIEPAKGVVE EGMRERNNGPGSDF |
| 527 | 8578 | A | 149 | 535 | 917 | LVSPGKPPPEQQQLP*PRCQII*LVSPGK PE/PTGTAPRSQPRLSVCPSTQDICRICH EGDEESPLITPCRCTGTLRFVHQSLHQ WIKSSDTRCCELCKYDFIMETKLKPLRK WEKLQMTPRERRKIFCSVTFRNRGSPV WFGLCMY |
| 528 | 8579 | A | 1490 | 2 | 746 | |

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| 529 | 8580 | A | 1491 | 217 | 1007 | LNHNRLAVIMANLGCWMLVLFVATWS DLGLCKKRPKPGGWNTGGSRYPGQGS GGNRYPPQGGGGWGQPHGGGWGQPHG GGWGQPHGGGWGQPHGGGWGQGGGT HSQWNKPSKPKTNMKHMAGAATAGAV *GGLCSYSLGSAMSRPIHFGSDYEDRY YRENMHRYPNQVYRPMDEYSNQNNF VHDCVNITIKQHTVTTTTKGENFTETDV KMMERVVEQMCITQYERESQAYYQRGS SMGLFSSPPVILLISFLIFLIVG |
| 530 | 8581 | A | 1492 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGRLLV VYPWTQRFDFSFGNLSSASAIMGNPKVK AHGKKVLTSLGDAIKHLDLKGTFQALS ELHCDKLHVDPENFKLLGNVLTVLAIH FGKEFTPEVQASW/QEDGDWSGQCPVLQ IPLSSLPMMQSFQG |
| 531 | 8582 | A | 1493 | 41 | 597 | APSPRRPWVISQRRTKATITSLWGKVN VEDAGGETLGRLLVYPWTQRFDFS FGNLSSASAIHGQPPKVQGTWSKKVLT LGEMP*KHLDDLKGHLKPEVNLHC KPAMWDPENFKAPGEMLLVTRFWAIPF SAKEFHPWRLAGLPQKDG*LGVGQCP CSFQIPLKPLGP*IQSFQG |
| 532 | 8583 | A | 1494 | 1 | 478 | DTRFLERLRSLSSLPDAMGHFTEEDAK ATITSLWGKVNVEDAGGETLGRLLV VYPMDPRGFFDFSFGNLSSASAIHGQTPK VKATRAKKVLTSLGKMPIKHLGLIFGT FCPSLS*TCTC*QACMWD*GTFKLPG MLLVTRFWAIPFSAKEFHP |
| 533 | 8584 | A | 1495 | 3 | 370 | SVCVRAHESVVKSEDFSLPAYMDRRDH PLPEVAHVHLSASQKALKEKEKASWSS LSMDEKVELYRIKFESFAEMNRGSNE WKTVVGGAMFFIGFTALVIMWQKHGYL ASKWDYEKNEWKK |
| 534 | 8585 | A | 1496 | 24 | 305 | |
| 535 | 8586 | A | 1497 | 197 | 745 | LASEQFSTSVVCTSSMKVFVKSEDFSLPT YMESAVTHPLAGRPHVVKAPCSAQPRR PLKEKEKALLGAAFSMG*GKFELLFALK FKEEALLED*TRGLRTELKGTGLFGPVPL FPSIGFSRLVIHVQKHYVLTAPFPQSF *TKSWVGPSRTKRMLGQ*R*TPIQGLAS KWDYEKNEWKK |
| 536 | 8587 | C | 1498 | 78 | 281 | MELSNNHQLSMLVELSMLVWDANLL GWGKSCELTGPSWLVSTSRHSRKKGS SWHLPAKLCSTC* |
| 537 | 8588 | A | 1499 | 302 | 687 | |
| 538 | 8589 | C | 15 | 354 | 416 | MKESPGGELPQTGKKPVFL* |
| 539 | 8590 | A | 150 | 116 | 830 | EGFPGRSLSGGLCCRLRRRFPIDGYRPW RRRRWSCCPGVRPVRMRSHKSWIESTL TKRECVYIIPSSKDPYRCLPGCQICQVL RCFCGRVLVKQHAWFTASPAMKYLDVKL GDHFNQAIIEWSVEKHTEQSPTDAYGVI NFQGGSHSYRAKYVRLSYDNQPLVILQ LTVKEWQMEPLKLVISVHGGMQKFELH PRIKQLL*KGLIKA AVTTGALILTGGRN TGVGKHGGDAPQRTC |

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| 540 | 8591 | A | 1500 | 1 | 1622 | MSKPKCLVILVGIQSSQMPQFPFPAGSE RRRGIRQWEMGVVGGEMGVWVPPGVQ GSPPQAHRRRLGSREQLFAPPLKEKSHIPP WGYSRENYPIPEPGPNRGPVTEVWGSPG PTVQGWGWEGLHEALSPALINQAQKDPE VRLGAMVRVSVDTHTPPPLTPRQSGPLSA LEELGVSFPTLSYLTPEPQLLGEHQIKGSF PGRSTALLLKEVLLRMHSGVICGSDVH YWEYLS/RFGNFIVKKPMVLGHEASGT RKSGIIGKSTLKPGRVIAIEPGCSPEEN* WNSCQDGR/RRYNLSPSIFFCATPPDDGNL CRFYKHNAAFICYKLPDNTFEEGALIEP LSVGIHACRRGGVTLGNKVLVCGSWAN RGWVTLLVAKAMGAAQVVVTDLSATR LSKAKEIGADLVLIQSKESPQEIARKVEG LLGCKPEVTIECTGAEASIQAGIYATRS GTLVLVGLGSEMTTVPLLAHAIREVDIK GVFRYCNTWPVAISMLASKSV/DMSKPL VTHRVSWSRKVLEAFETFKKGLGLKIML KCDPSDQNL |
| 541 | 8592 | A | 1501 | 1 | 804 | |
| 542 | 8593 | A | 1502 | 178 | 1093 | TFLLPACLLAALLPLRHHVRGRAVWVQ SILNEGVG*ALKDLINEACWGY*APAG VNLQSMGHRPTVSLVQLTLRV*GASTP YRC\DRNLGHGR*NLTSMKILKMAAG NED/ISLTLRAEDNAGYLGR*YFEGTKPG RKFSDEYEMKMDLDVEQLGIPEQEYSC VVKMPSGEYA/RICRESQPILGDAVVISC A/KDGSSENFASGELGNETVILKSQTSNVD KEEEA\PIKMNEPVQPNFCH*GYLNFFT KATPLSSTVDTPVCSADGTPLVGRSIIA GYGDHLKYLLGLPKDPRIEESLGHS |
| 543 | 8594 | A | 1503 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGRLLV VYPWTQRFFDSFGNLSASAIMGNPKVK AHGKKVLTSLGDAIKHLDLKGTFQALS ELHCDKLHVDPENFKLLGNVLVTVAIH FGKEFTPEVQASW/QEDGDWSGQCPVLQ IPLSSLPMMQSFQG |
| 544 | 8595 | A | 1504 | 1 | 591 | NFALEAKNSARAISLVPDAHGVISQRT KATITSLWGK\VNVEDAGGETLGRLLV VYPWTQRFFDQLLANLSSASAHGQPPK VQGHMAKKVLTFLGEMPIKHLDDLKGH LLPKPEVNCTVDKPMWDPENFKAPGE MLLVTLFWAIPFSGKEFTP*RLQASWAE RWVTWS\GQCPCSFQIPLKPLGP*IQSFQ G |
| 545 | 8596 | A | 1505 | 49 | 273 | |
| 546 | 8597 | A | 1506 | 81 | 720 | LFKAPEPHVEED\DDDELDSKLNYPKPPQ KSLKELQEMDKDDESLIKYKKTLLGDG PVVTDPKAFNVVVTRLTLVCEAPGPI TMDLTWKIWKALKKGNHLVLKGRFVNI RSSKFHFPKLNRG*LLFRA*NYVQHTYR TG\VKVDKATFMVIGSYGPRPEEYEF/LS LPVEEASQRAWLARRHVTTKSPFFTDDD KQDHLSW\EWNLISIKKEWTE |
| 547 | 8598 | A | 1507 | 5 | 290 | FNLTHIESRPSRLKK/DEYE/FFTHLDKRS LPALTNIIKILRHDIGATVHELSDKKKD TVPWFPRTIQELDRFANQILSYGAELDAD HPVSPWPVG |
| 548 | 8599 | A | 1508 | 68 | 312 | |
| 549 | 8600 | A | 1509 | 317 | 916 | TSSPPSSLCFLSFSDICHELLGHVPLFSDR SFAQFSQEIGLASLGAPDEYIEKLATYIW FTVEFGLCKQGDSIKAYGAGLLSSFGEL QYCLSEKPKLLPLELEKTGIQNYTVTEFQ PLYVVAESINDAKEKVGNSAATIPRPFV RYDPYTQRIEGLDNTQQAHDLG*FHLTV EIGILCSALQKNKVKAMDRMVVCQAVE |
| 550 | 8601 | A | 151 | 770 | 950 | CHSEHRNYKNNHHSIIKVRPRWRIHFHS NVIS*SLVHISKVFVAYKCNQYFHIRKFR |

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| | | | | | | SVT |
| 551 | 8602 | A | 1510 | 389 | 1881 | NLQPHVLFANLPVPEALKSQRPHSRGAS MSTAVLENPGLGRKLSDFGQETSYNED NCNQKWVPISLDPHLLKERKLGALGPKY CALFEENDVNLTWHIESVRPSRLKXDEYG FFPPFGIKRSLPALTNIIKILRHDIGATVH ELSRDKKKDTPVWFPRTIQELDRFANQI LSYSGSNWDAADHPGFKDPVYRARRKQ FADIAYNRYRHGQPIPRVEYMEEKKTWG TVFKTLKSLYKTHACYEYNHIFALLEKY CASHEDNIPQLAEDVSQFLAQTCTGFRLRP VAGLLSSRDFLGDLAFRVFHCTQYIRHG SKPMYTPPEPDICHELLGHVPLFSDRSFAQ FSQEIGLASLGAPDESIEKLAPIYWFTVEF GLCKQGDSIKAYGAGLLSSFGEFYCLS EKP KLLPL/ESLEKTAIQNYTVTEFQPLY YLAESFNDAQGEI*GTFAATIPRPFVSR HDPHTPQRIGGSWDNTQQLKILA/DSI*Q *IGIPFAVALQNIK |
| 552 | 8603 | A | 1511 | 1 | 191 | MQK*ITAWAPAPMKIKIIASPERKYSVWI GGSIWQQLST/FQQMWISKQEYDESGPSI VHRKCF |
| 553 | 8604 | A | 1512 | 1 | 360 | SGACPAFLVDRNLRHHETTFLNIMKCDV DIRKDLANTVLSGGVTMYPGIADRMQ KEITAL/APPSTLRFRIAPP/ERRKYSVWI GGASILASLSTFQQMCLGKQEYDESGPSI VQRKCF |
| 554 | 8605 | A | 1513 | 13 | 1277 | INPPPLSRRCQLSHSVLPPLRRRVSLPVA MEEIEAALVIDNGSGMCKAGFAGDDAP RAVFPSIVGRPRHQGV MVGHGPRDTSY VGDEA/QRSKRGILTLKYPIEHGIVTNWD DMEKIWHHTFYNELRVAPEKHPVLALT EAPLNPKANREKMTQ/ILCFETFNTPGHV PWPIQAVLSL*SLWAQPIGIVMDSGDGV THTVPILRGATLLHAILRLGPGIARDL TDYLMKILTNERGYSFTTHGPSGKTFRNI KGEACATSPLDFEQVEMGTAASSSSLEK SYELPDGQVITIGNERFRCPEALFQPSFLG MESCGIHETTFSIMKCDVDIRKDLAN TALSOGTTMDPGIADKIAEGRSTALAAP AP*KIRUIAPP/ERKYSVWIGGSILASLST FPARFWISKQEYDESGPSIVHRKCF |
| 555 | 8606 | B | 1514 | 93 | 366 | XTSVVRPFACLVRPPVQVYGIEGRYATA LYSVLNPHYVKRSIKVKSNDITAKERFSP LTTNINLLAENGRLSNTQGVVSAFSTM MSVHRGE* |
| 556 | 8607 | A | 1515 | 1 | 785 | FRRQARAPLRVFLFPLGFDLQPPGRRW AAPAVISGLSRKVRCFSTSVVRHFAKL GPSIVQVYGIEGRYATAYLSAASKQNK EQLEKELLRVAQNPEGNPKVAASVLPN YVVKRSIKSEKALNDITSKKRRFSPPSTT QPWIKFALPE/NGSD*SKYPQGSPPALFP THDEVSHPRIGGYPCTVDLWHLLEGSSQ TPPGI*KLSLKSPL*VKGQVLKLEAKTDP SILGGMIVRIGEKYVDMSVKTKIQKLG RAMREIV |
| 557 | 8608 | A | 1516 | 1 | 2199 | |

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| 558 | 8609 | A | 1517 | 9 | 1618 | PALCPTLSSGTSARFRGKNQFSGGLPQIT LSPLAQPCGRLAAMYSNVIGTVTSGKRK VYLLSLLDSFGDCVTCHGSPVDICTAK PRDIPMNPNCIYRSPEKKATEDEGSIEQK IPEATNNRVRVWELSKANSRFLPLSYS APGQNSKD*H*LTFFCSPLSIFQGFLLWT KVIGACNDTLQQLMEVFKFADTISEKTF* SRSHFFFAKLNCRLYRKANKSSKLVSA NRLFQDKSLTFNETYQDISELVYGAKLR PLADFKIENAEQSRVAAINKWVSNKTEG RIHRCSPFSGRPFNELTVLGGFNNTIYFQ GACWKISKFPENTRKELFYKADGESCA SASMDVTREGKFRYSGAWLEGT/QVLV VCPFKGDDITMVILPKP*EGAWAKVEK VELTPEVLAKSGWD*FWREMLLVHMP RFRINEDGLQV*REQLQRHGLSDLFSP* KSPKL/LPGIVAEGRDDLYVSDAFHKAF LEVNEEGSEAAASTAVVIAGRSLNPNRV TFQGGQLFPGFLLREVPLNTIYLHGAEL ANPCV |
| 559 | 8610 | A | 1518 | 2 | 363 | ELDTLCDLYEP*PSPSIIFINTRRK/VDWLT EKM HARDFTVSAMHGDMQKERVIM REFRSGSSRVLITDLRIGRGGFRGRKG VAINMVTEEDKRTLRIETFYNTSIEEMP LNADLI |
| 560 | 8611 | A | 1519 | 201 | 648 | GPCGHGRVFPLPSLAAHMDA*GLLLRDR VSSVHMLKRLSFLT*ARGIDVQQVSLVIN YDLPTNRENYIHR*A*IWNTPLPLHTWPS LGLKLLIFLIPFLVFQNGRGRFRGRKGVA INMVTEEDKRTLRIETFYNTSIEEMPLN VADLI |
| 561 | 8612 | A | 152 | 1 | 253 | SKLAAEMTANRLAESLLALSQQEELADF PKDYLLSQSQDIEGDNDGERKHHKLEA ISSLDGKNRRKLAEMSDVILMM*EFVVA |
| 562 | 8613 | A | 1520 | 49 | 1720 | GSTISSASQDSRSRDNGLDGIEPEGVIESN WNEIVDSFDDMNLSSELLRGIYAYGFEK PSAIQQRAILPCIKGETSQSOKTLWTVPD LGRVASGW*CPSHISQGSNLLVHPSLA FDPCCPLVHALDT*VSFKEVVL*PAYICI YSHVSSPAWCAILDELITGPCF*SGSHCV TVLIGKVCEP*NAWFIGCLTSLT*DLNI PKGMLFTTFNS*FICLGYDVIAQAQSGTG KTATFAISILQQIQKVVMAIGDYMGAS VCHACIRGAPTCVAEVQKLAQMEAPHIHR GVPPGRVF*YALPEDTLPKYNKMFVLD EADDEMLSRGFKGQIYGHQKAQAAPPR VVLLSATMPFDIVLEVTKKFMRGPPFRIL VQKGELTLEGIRQFYNNVEPEEFNLDT LCDLYENLDHHRPVIHFQPPGGKVDWP HPRRMHAADF/TLYSAMHWRFTQKER RT*L*REFRSWLLARIFDTQLDLLGQRA LMCQQVSLVIQTYDPFPPTRGKLLIHRV GSRVDRFGRKGVPINMLTE/EKTKRNLE DIETFYNTSIEEMPLNVA |
| 563 | 8614 | A | 1521 | 3 | 607 | FCPRGQEFEGGNKLLSPRRPWVISQRRRT KATITSLWGKVKCGKNAGKEETPGKGS LVVL/HPWTPRGSEQLWQTCPSALCPS MGNPQSQGTMAKKVLTSLGRCP*STLDA DLKGHLLPKPEVNLHLLTSLHVGS*RTF KLPGEMLLVT/LFWAIPFAKEFHPLKVA GFPQKDG*LGVGQCPCSFQIPLKPLGP* IQSFQG |
| 564 | 8615 | A | 1522 | 23 | 437 | KTPGKGS LVVL/HPWTQRFDSFGNLS/ SASAHHGQPPKSKAHGKVLTS LGDAI KHLLDLKGTFQAQSELHCDKLHVDPEN FKLLGNVLTVLAIHFGKEFTPEVQASW QKMVTCSGQCPVLQIPLSLLPMIQSFQG |

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| 565 | 8616 | A | 1523 | 23 | 249 | APSPDAMGHFTEEDKATITSLWGKVNVE DAGGETLGRLLVVPWTQRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKH LDDLKGTFAQLE*TCPLPLPSWATPKSR HMARRC |
| 566 | 8617 | A | 1524 | 46 | 379 | SQTPMGHFTEEDKATITSLWGKGEMW KKCWKEKTPGKGSLLVVL/HPWTPRGSA DSFGKPVPLPSAHPWATPKVKAPWPRRC LTSLGEMPIKHLGLIFKGTFCPSLK*TCT C |
| 567 | 8618 | A | 1525 | 21 | 457 | NPRVRGALTMELSESVOQGFQMLADPR SFDSNAFTLLRAAFQSLDDAQADEAVL DNKNSLEILLGSGRSLPHITDVSWRLEY QIKTNQLHRMYRPAYLVTLSVQNTDPS YPEISSSCSMEQLQDLGGKLDASKSLG KSTQL |
| 568 | 8619 | A | 1526 | 1 | 455 | |
| 569 | 8620 | A | 1527 | 3 | 468 | |
| 570 | 8621 | A | 1528 | 50 | 895 | THASDGAITMELSESVOQGFQMLADPR SFDSNAFTLLRAAFQSLDDAQADEAVL DHPDLKHIDPVLKHC\HAAA\ATYLE AGKHRA\DKSTL\STYL\EDCKILTEKRIEL FFAREYQ\NNKNSLEILLGKY*GRSLPS YNRVFSWALWIIQVKDQSTFHRM\YRP AYLGD\KVVQNTGIPPS\YPRELVFSCQP WNQL\QDL\VG\ETLKDASKKPWKRA\TSV VTLGK\VNRSP\SSRRKTQKPLPF\SWNH RLCRAGCPFSVEKNFSLNLYPFIHFGHF KNV |
| 571 | 8622 | A | 1529 | 1404 | 1586 | ENESRFSDRNQASAGLYLSDSL*QWIV GNGHATDLWQNCSTSSSGNVHHCFS SSP NGSG |
| 572 | 8623 | A | 153 | 1 | 759 | |
| 573 | 8624 | A | 1530 | 187 | 701 | AELAARMLLLLLSIIVLHVAALVLLFVST IVSQWIVGNGHATDLWQNCSTSSSGNV HHCFS SSPNEWLQSCSRGTM\DPVDSSFS ILSLFLFFCQLFTLTGGGRFYITGIFILA GLCVMSAAAIYTVRHPEWNLNSGYAS* RFA*ILAWVAFPL\ALLSGVIYVILRKRE |
| 574 | 8625 | A | 1531 | 1 | 485 | |
| 575 | 8626 | A | 1532 | 2 | 459 | |
| 576 | 8627 | B | 1533 | 1 | 2784 | MAAMAVGGAGGSRVSSGRDLNCVPEIA DTLGAVAKQGDFLCMPVFHPRFKREFI QEPAKNRPGPQTRSDLLSGRALEIGAD LPSNHVIDRWLGEPIKAAILPTSIFLTNKK GFPVLSKMHQRLIFRLKLEVQFIITGTN HHSEKEFCSYLQYLEYLSQNRPPNAYE LFAKGYEDYLQSP\QPLMDNLESQTYEV FEKDIKYSQYQQA\YKCLLD\RVPEEEK DTNVQVLMVLGAGRGPLVNASLRAAKQ AD |
| 577 | 8628 | A | 1534 | 2 | 607 | |
| 578 | 8629 | A | 1535 | 1 | 207 | |
| 579 | 8630 | A | 1536 | 232 | 755 | LSCCADDGVSIPGEYTSFLAP\MFSPKLYN KVRACRKKARDLKAQFEMPIV\RLHNS NQLSAPQPCSTFSHPNRDPMIDNNRYCT LEFPVEVNTVLQCFAGYFETVLYQDITL SIRPETHSPGMFSWFPI\FPIKQPIVREG QTICVRFWRCSNSKKGSSHQSMKTSGQG VRN |

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| 580 | 8631 | A | 1537 | 35 | 2271 | LCDWLLVSRNPGVDSARRKMAAMAVG GAGGSRVSSGRDLNCVPEIADTLGAVAK QGFDFLCMPVFHPRFKREFIQEPAKNRP GPQTRSDLLSGRDWNTLIVGKLSPWD FVPDASKVÆKIRRNSEGGPCLQELNFGVA YLGPAFLPLNQEDNTNLARVLTMQIH TGHDFYMFWRRIHLKKPEDLRDDIEN APTTHTEEYSGEEKTWMWWHNFRTLCD YSKRIAVALEIGADLPNSHVIDRWLGEPI KAAILPTSIFLTNKKGFPVLSKMHQRLIF RLKLEVQFIITGTHHSEKEFCSYLQYL EYLSQNRPPPNAYELFAKGYEDYLQSP QLMDNLESQTYEVFEKDPKYSQYQQA IYKCLDRVPEEEKDTNVQVLMVLGAG RGPLVNASLRAAKQADRGIKLYAVEKN PNAVVTLENWQFEEWGSQVTVVSSDM REWWAPEKADIIVSELLGLIC*PIELSP*V PWIGAQHFP*KMIGVKHPPGSYTSFLAPI SSSKLYNEVRACREKDRDPEAQFEMPVY VRLHNFRQLSAPQPCFTFSVHRNRDPMI DNNRYACTLGFVPEVNTVLHGFAGYFET VLYQDITLSIRPETHSPGMFSWFIPLPY* GSPLTVRERAKPFCVRFWRCRQFPRKV WVWSGGC*QAPVCCLIQKPPKGPPQYT HWPLLSPCRAPSVEALGKPAFRFLPPCS NSKVPVTSYGAVIPPWPIQRREHFQSCFP CPYIQGGPRDYN |
| 581 | 8632 | A | 1538 | 137 | 303 | |
| 582 | 8633 | A | 1539 | 122 | 385 | YPALEHILKAQAIQSRGCDSCLPSPAPW DHPGPTTPSPGRRAAADPWHLSPIDGRE HLR*VPVLPVTPSPSTLGHVWVTDPSPGV GG |
| 583 | 8634 | A | 154 | 1 | 921 | |
| 584 | 8635 | B | 1540 | 277 | 480 | GTGHFYGRTPSDTNCQEYTHRKLCQIK SKADLVLMKNSKSLTRVIRNILAPQDQN HQQNPLNSQFLQ* |
| 585 | 8636 | A | 1541 | 32 | 1386 | VLLGPKAERTNSRRNYQRRDYFSAPRSI TSNQSAKSSSRGVYSAYQAPDIHECCH FRSASFFLDKMATPAVPSAPPATPTPVP AAVPASAPASVPAPTPAPAAAAPVAAAAP ASSSDPAAASATTAAPGQTPASQAQAPA QTPAPALPGPALPGPFPGGRVVRHLHPVI LASIVDSYERRNEGACPS*SGTLFGKLV DKHSVEVTNACFSVPHNESEDEVAVDM EFAKNMYETGIKKVSPNKLILGWYAT GHDITEHSLVLIHEYYSREAPNPIHLTVAD TSLPGTGRMSIKAIYVSTLMGIPLGRT/L WGVMTPLTVKYAYYDTERIRRLTLIM KITCF*PPTRVIWTSQVDLQEGGGIQLR NPGMPLSTSVANMPEGCTCLGKVSADN TIRKVGHFLMSLVNQVPENRKPMTFET MLNSNINDLFMVITYLANLTQSRNALNE ELVNL |
| 586 | 8637 | A | 1542 | 1 | 3399 | |
| 587 | 8638 | A | 1543 | 1 | 3126 | |
| 588 | 8639 | A | 1544 | 115 | 348 | |
| 589 | 8640 | A | 1545 | 1 | 513 | FHFTPLFRDGETYVV/MLDSTLPRSQYAY ILPQVSFTAVGYHKKHITLIFNPARKLPEQ DIAQGSYIALPLTLLVLLAGYNHDKLIPL LLQLTSRLQGVALGQAASDNSGPEDA KRQAKKQKTRRTLRLQEEFQLMWCLVP WRGTLGIHLFSSLPFASEILLETTATCIHY |
| 590 | 8641 | A | 1546 | 1 | 888 | |
| 591 | 8642 | A | 1547 | 1 | 4710 | |

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| 592 | 8643 | A | 1548 | 37 | 3683 | LGLGLSMLVGQAGPLGPAVVTAAVVL LLSGVGPAHGSSEDIIVGCGGFVKSDVEI NYSLEIKLYTKHGTLYQTDCAPNNGY FMIPLYDKGDFILKIEPLGWSFEPTTVEL HVDGVSDICTKGGDINFVFTGFSVNGKV LSKGQPLGPAGVQVSLRNTGTAKIQAT ATQPPGGKFAFFKVLPDYEILATHPTW ALKEASTTVSVTNSNANAASPLIVAGYN VSGSVRSDGEPMKGVKFLFSSSLVTKED A |
| 593 | 8644 | A | 1549 | 1 | 474 | |
| 594 | 8645 | A | 155 | 1 | 424 | |
| 595 | 8646 | A | 1550 | 1 | 1554 | |
| 596 | 8647 | A | 1551 | 87 | 736 | FIMDNLSSEEIQRAHQITDESLESTRRI GLAIESQDAGIKTITMLDEQKEQLNRJE EAWAQIHKDMRAETEKLTTELNKCCGLC VPCNRTKELLSLGQGFIKTTWGRWWE KTSPWQC*YSKQGP/VWTNGQLQQPTT GAASGGYIKRITNDAREDEMEENLTQVG SILGNLKDMLNIGNEIDAQNPQIKRITD KADTNRRFVLDYCPMPEQK |
| 597 | 8648 | A | 1552 | 99 | 362 | |
| 598 | 8649 | A | 1553 | 184 | 360 | |
| 599 | 8650 | A | 1554 | 3 | 403 | |
| 600 | 8651 | A | 1555 | 1 | 872 | EFGTRWDFSMVAFADLDLRAGSDLKAL RGLVETAAHLGYSVVAINHIVDFKEKK QEIEKPVAVSELFITLPIVQGKSRPIKILT RLQIMLSDHSPAKVLKNTLKRGA*DA VGAGFPKAEKAFFILLCTHLDVDLVCIT VTEKLPFYFKRPPINVAIDRGLAFDLALIP LLSKDSTMRRYTISPVLQF*CKSCKGKN VIISACKKRPF*KIRGPILTWANLGLPV WGFSESERQGGCPNPCRAALLHGETR KTAFGIISTVKKPRPSEGDEDCLPASKKA KCEG |
| 601 | 8652 | A | 1556 | 46 | 584 | SRPWVISQRRRLSTSLWCKVNVEID AGGETLGRLLVVYPWTQRFDSFNL SASAIHGQTPKVKAHGKKVLTFLGEMPL KHLDDLQGAFFQA*SELALVDKPFAM WDP*GTSKLPGELLVTRFGQSLFRQKNF TPGGARVSWGRKMGDLELASALVPSRL PLSSLAHECRAFQ |
| 602 | 8653 | A | 1557 | 1476 | 1747 | GNFNSRLSKTQLCAHCLYPHTFGRQR WVDHLRLGVRD*PGQHGETPSLLKNNN NNTKISWAWWHEPVIPAMGEAEAGES LEP/GRRRLQ |
| 603 | 8654 | A | 1558 | 1 | 507 | |
| 604 | 8655 | B | 1559 | 15 | 400 | MSMLRLQKRLASSVLRCGKKKVWLDPN ETNEIANANSRQQIRKLIKDGILIRKPTV HSRARCRKNTLARRKVRHMGIGKRKGT ANARMPEKVTWMRRMEILRHLLTRYRE CETINRAMHLLNLKVMs* |
| 605 | 8656 | A | 156 | 3 | 1371 | INIVVIGHVDSGKSTTTGHLIYKCGGIDK RTIEKFEKEAAEMGKGSFKYAWVLDKL KAERERGITIDISLWKFETSKYYVTIIDAP GHRDFIKNMITGTSQADCAVLIVAGVG EFEAGVSKNGQTRAEHALLAYTLGVKQLI VGVTKMDSTEPYPYSQKRYEIVKEVSTY IKKIGYNPDVAFVPISGWNGDNMLEPS ANMPWFKGWKVTBKDGNASGTTLEA LDCILPPTRPDKPLGLPLQDVYKIGIGT VPVGRVETGVLKPGMVVTFGPVNVTE VKSVMHHEALGEALPGDNVGFNVKNV SVKDVRRGNVAGDSKNDPPMEAAGFPA QVILNHPGQISAGYAPVLDCHTAHIACK FAELKEKIDRRSGKKLEDGPKFLKSGDA AIVDMVPGKPMCVESFSDYPLGCFVR DMRQTVAVGVKAVDKKAAGAKVTK |

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| | | | | | | SAQKAQKAK |
| 606 | 8657 | A | 1560 | 15 | 710 | INPPPPAFLSLLRPQCSMLRLQKRLASVS VLRICGKKKVWLDNETNEIANANSRQQ NRKLIKDGILIRKPV*RVHSRARCCKNTL VARRKGTAH/CGIGKREGYSPMPRMP/TR KVTWMKENEGFWRLASERYR*NLKKI RFATLLSQALYPEG*RGNVVSKTRRVFH GNTFHKLEGRQRPKKAPWLDQA*G/RR RS*DQKGKHKRAREERLPGQRKEEINQRL YSKEEETKK |
| 607 | 8658 | A | 1562 | 2 | 419 | MASGRARCTSNLRNWVVEQVESGQFPG VCWDDTAKTMFRIPWKHAGWAIFKGGK YKEGDTGGPAVWKTRLCALNKSSEFK EVPERGRMDVAEPYKVYQLLPPGIVSGQ PGTQKVPSKRQHSSVFSEKKEEDAJAN CTL |
| 608 | 8659 | A | 1563 | 20 | 431 | |
| 609 | 8660 | A | 1564 | 107 | 400 | |
| 610 | 8661 | A | 1565 | 191 | 353 | PHSSTTCPPAPMLVF*KRDPPSLGPHDAL VPPCPVPVEILRSSAKTRCGKKASS |
| 611 | 8662 | A | 1566 | 553 | 690 | SRRRFPMGSGTKLV*G*GEMESLEEQAQ GKGTECALHPVDLFSSPGPLFNSLCLSK PMAPPTL |
| 612 | 8663 | A | 1567 | 2406 | 4031 | GGRAGDGPLSATCTYAPSLWLDEGSPCL PGLVTEADRRGTLGTEYPPQAEVAEGK GPDEGPMACSLRNSSSTNKEASYHPGFL VVLLPEFDWYLKSPNMYQVGTVGECRC TGVHSSPEVPGLTPGNWPPWGSHTGVTQ RMASGRARCTRKLNRNWVVEQVESGQF PGVCWDDTAKTMFRIPWKHAGKQDFRE DQDAAFFKAWAIFKGYKEGDTGGPAV WKTSLCCALNKSFDKEVPERGRMDVA EPYKVYQLLPPGILASGHVPGTQKVPSKRQ HSSVSSEVRKEEKDAMQNCTLSPSVLQD SLNNEEEGGSGGAVHSDIGSSSSSSSPE TTRKITDTTEAPFQGDQVRSLEFLALPEP D*SLLLTFTYNGRVVGEAQVQSLDCRLV AEPGSESSMEQVLFPPKPGPLEPTQRLLS QLRRGILVASTPQGLFRCSAFCPPIFWGI APQAPPVPGPHLLPSNECVELFRTAYFC RDLVRYFQGLGPPPKFQVTLNFWEEESH GSSHTPQNLITVKMEQAFARYLLEQTPE QQAAILSLV |
| 613 | 8664 | C | 1568 | 77 | 325 | MSLIQEALHLVLTDPDAPAGDDPKYRE WHHFLVVMKGNDISNGTVLSDYXCAA PPKAPSHVPQFSVACIIDFSSSCPPWHG* |
| 614 | 8665 | A | 1569 | 60 | 287 | |
| 615 | 8666 | A | 157 | 1 | 92 | TSHQSHCSTFLTVSKW**LKTAYCLYHY HS |

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| 616 | 8667 | A | 1570 | 3 | 703 | VEFFSSQRAELYATPLTPAPGPNNGGIPGW TLWLALPRPGNLRKGPGLSLQEVDEQP QHPLHVITYAGAAV/DDELGKVLTPQTQVK NRPTSISWDGLD/SKGKLYTLVLTDPDA PKQKDPKYRE\WHHFLGWSTLKGQMT SATGTVLS\DYVGLGGLPKGTGLHRYV WL\VEQ\DRPLK\CDEPHPSATRS\GDHR GKIQRWASLPVKK**SSRAPGGWAPCYP QPEVGMNQCAPKL |
| 617 | 8668 | A | 1571 | 1749 | 2411 | APSCLVSEHSAPGPQRELPOPLLTFOAYE QILGITC\GSCPAQGWGAWSSDAVPOLL ARRPPLPHGLPACGEWGRGELGVKPSGL PSHAGPAWGHQVRTVCATAHPQDCISPE GAVEEEIVGG*GC\TEGQSQRVLQIWP'S QGVSSLSALVPLNMFTELLIEYYEKIFST P\EAPGEHGLAPWEQGSRAAPLQEA VPR TQATGLTKPTLPPSPLMAARRRL |
| 618 | 8669 | A | 1575 | 1 | 254 | |
| 619 | 8670 | A | 1576 | 3 | 308 | |
| 620 | 8671 | A | 1577 | 1 | 380 | IPTPLIGNFGPRGPRIRHERPQKRDDRREP SSFGRRRQ*DGTL\LC\RRCGS\KA\YHLQ KSTCGKCGYPAKRKRKYNSAKAKRR NTTGTGRMRHLKIVYRRFRAWDFREGT TPKPK*GSLLOHSSSS |
| 621 | 8672 | A | 1578 | 41 | 544 | APSPRRPWGHFTEED\KAT\TSLWGK\VN VEDAGGETPGKGS\LVVY\WTQRFFDS FGNLSSAF\AHHGQTPKVKAHGK\KVL\T SLGDAIKVH\DDLKG\TFAQA*VNLHL*QS CNVDP\ENFQAPGEMLLVTR/VLAIHF\G K\LEFTPGGCKASWAEDG*LAVGQWPCSS RYH |
| 622 | 8673 | A | 1579 | 1207 | 1369 | |
| 623 | 8674 | A | 158 | 232 | 552 | SLH*PRMATQRKHLVKDFNPYITCYICK GYLIKPTTVTECLHTFCKTCIVQHFEDSN DCPRCGNQVHETNP\LEMLRLDNTLEEIIF KLVPGLREQE\ERESEFWKENKPQNGGQ DDTFKSLTNRK |
| 624 | 8675 | A | 1580 | 1 | 1716 | TCIAAVKMEG\PLSVFGDRSTGETIRSQN VMAAASIANIVKSSLGPVGLDKMLVDDI GDVTITNDGATILK\LEVEHPAAKVLC LADLQDKEVGDGTTSVVIAAELLKNAD ELVKQKI\HPTSVISGYRLACKEAVRYINE NLIVNTDELGRDCLINA\AKTSMSSKIIGIN GDFFANMVVD\AVLAIKYTDIRGQPRYPV NSVNILKAHGRSQMESMLISGYALNCVV GSQGM\PKRIVNAK\IACLD\FSLQTKMKL GVQVVITDPEKLDQIRQRES\ITKERIQKI LATGANVILT\TGIDDMCLKYFVEAGA MAVRRVLKRDLKRIAKASGATILSTLAN VEG*ERFEGAMWDQAEV\VQERICDDE LILIKSTKARTSASHISRV\IDSMCDEMERE SL\HDA\LCVV\KRVLES\KSVVPRIGGAV EAALSIY\LENYANTSMGSREQLAIAEFA RSLSGYSPI\AVNAAQDSTDLVGKN*R/ RLFHNEAPGLTPE\RKNLKWIGLDLSNG KPARDNKQAGVFEP/TPIVKV\SLKFATE AAITL\RIDDLIKLHPRK*R*\KHGSYEDA VHSGALND |
| 625 | 8676 | A | 1581 | 1 | 513 | PRVRNLSREWLC\DRHLREKMFSSVAHL ARANPFDTPH\QLVHDGLGDLRSSSPGP TGQPRRPRNLAAA\VEEQYSCDYGSGR FFILCGLGGHSCGTTHT\ALVPLDLVKCR MKVADPQKYKGIFNGF\SVTLKEDGVRG LAKGWAPTFL\GYSMQGLLQVLAIFYEVF KVLVY |

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| 626 | 8677 | A | 1582 | 2 | 1296 | ALCEPQPFQSGSCVIALGRKMFSSVAHL ARANPFNTPHLQLVHDGLDLRSSSPGP TGKPRRPSQ/HMAAAPVEEQYSCDYGSG RFFILCGLGGIISCGTTHTALVPLDLVK/C RMQVDPQKYKGMFNGFSVTLKEDGVAR GLAKGWAPTFLGYSMQGLCKFGFYEVF KSLAYSNMLGEENTYL*RTSLYLAASAS AEFFADIALAPMEAACKVRIQTQPGYANT *EGISFPKCIKEEGLTSILQGGLLPLWMR QIPYTMN*SSPCLERTVEALYKFVVPK PRRE*FKRQSRLVVTIW*QVTIARVFCAN CFSPLPEFLG*PVLG*GKKVSQCFLWVLQ RDLGFKGVWKGLFARIIMIGTLTALQ WFIYYSVKGYFR/LPRPPPPPEMQESLKK KLGVNSVVRIKANCGLNLLVDPVFEESA KGTFIYLTV |
| 627 | 8678 | A | 1583 | 127 | 433 | RPLESWIGLVRNICRSPIAEAVFRKLVT DQNI SKNWRVDSAATSGYEIGNPPDYRG QSCMKRHGIPMSHVARQDLNRKSNRV KTCKAKIELLSYDPQKQL |
| 628 | 8679 | A | 1584 | 2 | 535 | |
| 629 | 8680 | A | 1585 | 551 | 1299 | PADPPRPSYYRHRTPPQAHWSRLRRSRL RRRGSHTRCPVGAGLRRRAGARLAV RLRASACGTPRCLGASARGKMAEQATK SVLFVCLGNICRSPIAEAVFRKLVTQNI SKN/WEGRQRGNFRWVIDSGAVSDWNV GRSPDPRAV\SLRNHGIHTAHKARQIT KEVFPTFDYILCMDESNLRDLNRKSNR VKTCKS*KFELPWEL*SPQQLIIED\PIY GE*LWTLETVYQQ\CVRICCRAFLAEKAH |
| 630 | 8681 | A | 1586 | 1 | 1239 | |
| 631 | 8682 | A | 1587 | 298 | 408 | |
| 632 | 8683 | C | 1588 | 92 | 244 | MRCEIILVLIPIVYFYFYNKLLCSRLXXXX XGGAVLKNPWGGQSLPGLAR** |
| 633 | 8684 | A | 1589 | 33 | 191 | RDDPRVRPPNSHT*PQQEPGL*LIKCTSP PQAPAPRTVHGPFYFYMRLIKMF |
| 634 | 8685 | A | 159 | 445 | 673 | RECLH*PRMATQRKHLVIDFNAYITCYIC KGYLIKPTTVTECLHT/FCRCMEAFPSLL LA |
| 635 | 8686 | A | 1590 | 3 | 1285 | |
| 636 | 8687 | A | 1591 | 3 | 3469 | QPGHTIYLLPTVVICNLLPCELDIFYVKGM PINGTLKPGKEAALHTADTSQNIELGVSL ENFPLCKELLIPPGTQNYMVRMRLYDVN RRQLNLTIRIVCRAEGSLKIFISAPYWLIN KTGLPLIFRQDNAKTDAAGQFEEHELAR SLSPLLFCYADKEQPNLCTMRIGRGIHPE GMPGWCQGFSLDGGSGVRALKVIQQGN RPGLIYNIGIDVKKGRGRYIDTCMVIFAP RYLLDNKSSHKLAFQAQREFARGQGT |
| 637 | 8688 | C | 1592 | 398 | 655 | MMFPLAFSLPLKNAFHISVCRVCPGYTG FAKRALTALNLDTSLSANCCNTPPAEXP NVHNPCYMGLSKPARXSKLGSMCKGSS XH* |
| 638 | 8689 | A | 1593 | 1 | 930 | |
| 639 | 8690 | A | 1594 | 1 | 134 | |

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| 640 | 8691 | A | 1595 | 3 | 2455 | HASVCPAVGVQRLCLFPCVSLQALFMGS PLRFDGRFFLVTGAGAGLGRAYALAF ERGA LVVNDLGGDFKGVGKGS LAADK VVEI RRRGGKAVANYDSVEEGDKVVK TALDAFGRIDVVVNNAGILR/DINSFARIS DEDWDIHRVHLRGSFQVTPAAWEHMK KQKYGRSIMITSSASGIYGNFGQANYSA KLGLLGLANSLAIEGRKSNHWN TIAPNA GSRMTQTVMPEDLVEALKPKYVAPLVL WLCHQSCEENGGLFEVGAGRIGKLWE RTLGAIVRQKNHPMTPEAVKANWKKIC DFENASKPQSIQUESTGSHIEVLSKTDSEGG VSANYTSRATSTATSGFAGAIGQKLPPFS YAYTELEAIMYALGVGASIKDPKDLKFI YEGSSDFSCLPFGVHIGQKSMGGGLA EIPGLSINFVKVLHGEQYLELYKPLPRAG KLKCEAVVADVLDKSGSVVIMDVYSY SEKELICHNQFSLFLVSGSGFGGKRTSDK VKVAVAI PNRPDAVLTDTTSLNQALY RLSGDWNPLHIDPNFASLAGFDKPIHGA LCTFGIFCQGVLLQQFCR*MDVVQGFKG N*RARFAKPVYPGANFYQT*ECWKEIG NRNSFFKPKVQGNLETLVISKWHMWDL GTQHSGYFSLRTPSEGPSFRVPLVFEEM GRRLLKDIGPEVVVKVNAVFEWHITKG GNINGAKWTIDLKSGSWEKLYQGPS/KK GAADTTIH/ILSDEDF/LWEVVLGQA*PSR KAFFSGPG*RPQGGTSM*AQKLSDGFL KDYAKLLKGTPTLLIKMESIKIPPHQIC LDYSAKS |
| 641 | 8692 | A | 1596 | 2 | 289 | |
| 642 | 8693 | A | 1597 | 1 | 397 | |
| 643 | 8694 | A | 1598 | 1 | 410 | STMISPVLLFSSFLCHVAIAGRTCPKPDD LPFSTVVPLKTFYEPGEEITYSCKPGYVS RGGMRKFICPLTGLWPINTLKCTPRVCP FAGNLRKMGAVRLITDFLNYSPTRFSFL LTWGFILEWALDSAKCIEGG |
| 644 | 8695 | A | 1599 | 19 | 1215 | CQCDSSMIFSRCSLSSFLCHVAIAGRT CPKPDPLPFSTVVPLKTFYEPGEEITYSC KPGYVSRGGIEESLSCPLATGTVPFNTSG NVTPRVCPFAGIFRKMGGRTLITTF*NYP NTDPVFSLLTLGF*FWNGALDFWPSCTG GKGKWSPELPGLVAPIICPPSP/TGFA TLHVLLRPFRLGNNSPPIGDTAVFECLAH NMAMFGWNTITCTTHGKLDLNYPECR GSKMPFPFHQDPDNGIW*TYPCQNPNTL FTRVKAPHLGLPHDGIFSGMGPRKENE *PQTWKGKPGSWPLAPSW*KPSLVKGTPV KKRPTVVYPQGERVKDSREKFKEWECL HG**KFLSFCKNKEKKCSYTEDAQCIDG TIEVPKCFK\EHSSLAFWKT\DAS\DVKPC |
| 645 | 8696 | A | 16 | 3 | 145 | SSSSSDFAGQTL*STQTVQN*FKKVLKPG RLYPVPIATMGIKEPLIS |
| 646 | 8697 | A | 160 | 22 | 849 | WIERDLLNCIKRLK/PTTNMMLNDEIVNIS PKIIKIRQGYLLSMILFGIVQKOLTRKLM QGRETGIEIRKEVKL*KRKRI*ISICRCH E*IW*VPCIKVMQKAFYDIPAKNMENEIL KKQCHFKDPSSA*REKMR LICFEELYPEN KITKEERDRI/RTTISKLLLPKPHLQP*NP RQVSLMLN*QANF*EFICIFQKSKIVKAI L*NGQRLKFLNIKT CYKAIEIMKVL IWH KDKKLD*WNSIQVSKVDPRVYHHSFE KGDIEV*WGKGCSFQ |
| 647 | 8698 | A | 1600 | 1 | 282 | |

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| 648 | 8699 | A | 1601 | 1 | 453 | EFGSQQLGRREEWQRQGSVSRRLSARR GPQAPGTRLPRRHPARAFPAATMPKRKV SSAEGAA*LEPNRSARLSAKPPAKGEA KPKKAAAKDKSSDKKIVQTKGRGAKG KQVAEVANQETKEDLPAENGETKTEESP ASDEAGEKEAKSD |
| 649 | 8700 | A | 1602 | 146 | 824 | TWKGKDPKKPRGKMSSYAFFVQTCREE HKKKHPDASVNFSEFSKKCSERWKT SA*R/EKGKFEDMAKA\DKARYEREMK TYIPPQRGRQKRKFDSQLHPRGPPSGLL SSSCSEYRPIK\GEHP\GL\SIGDVAKKLG RDVGINTAAD\DKQPYEKK\AAKLKEY EKDIAAYRAKGKPDAAKKGVVKAES KKKKEEEEDEEEG\DEEEDEEEDEE DEEEDER |
| 650 | 8701 | A | 1603 | 1 | 223 | |
| 651 | 8702 | A | 1604 | 1 | 400 | FADD\PSDK\FFTSNNGMQFSTGHNDND KFEGNCAEQDGSWWMNKHAGHLNG VYYQGGTYSKASTPNGYDNGHIWATWK TRWYSMKKTTMKIIPFNRLTIGEGQQHH LGGAKQVRPEHPAETEDSLYPEDDL |
| 652 | 8703 | A | 1605 | 18 | 365 | NILIKVYFNSKNDFKIFHELFFKQNYMKN MYKSVINVIDIFMKNKFQ/SEKYPII/DKGS LNK*MLTILALKSNTTVRLJRDATFYVVR EHIINVSSKRARYWVCVGF*ASC*QPPL F |
| 653 | 8704 | A | 1606 | 212 | 1645 | HYKARSSGHSIMSWSLHARNLILYFY ALLFLSSTCVAYVATRDNCCILYERFGC YCPITTCGIADFLSTYQTRVD*DLQSLAED ILHQVENKTSVEVKQLIKAIQLTYNPDES SKPNMIDAATLKSRLMLEIMKYEASVIL THDSSIRYLQEI*FQIIQKIVNLAKKVAQ LEAQCQEPCKDTVQIHDITGKDCQDVAN KGAKQSGLYFIKPLKANQQFLVYCEIDG SGNGWTVFQKRLDGSVDFKKNWPYK EGFGHLSPTGTTEFLAGEMRKIHFD*GTQ SAIPYGI*GVGTGKTWEWARNQYCRSM PLFKVVHEVDK\YRFTYAYFAGGDAEDA FDGYDFG\DDPSDKFFHIPIMAMQFTYLG TMDNDKV*KANCA*/QQGWDPGWWDG NKCCHAGHSSMGVLFQTQGWALYFQKAS YLPNGLWIMGIIWATWK\TRWVFR*RK TMKIIPFNRLTIGEGQQHHLGGSQTGLE TF |
| 654 | 8705 | A | 1607 | 2 | 529 | GTVAACGACYWLLGLMAVRASFENNCE IGCFAKLNTYCLVAIGGSENFYSVFEGE LSDTIPVVHASIAGCRIIGRMVCVGTTEEIL ADV LKVEVFRQTVADQVLVGSYCVFSN QGGLVHPKTSIEDQDELSSLLQVPLVAG TVNRGSEVIAAGMVVNDWCAFCGLDTT STELSVVE |
| 655 | 8706 | A | 1608 | 18 | 889 | GVQGTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLNTYCLVAIGGSENFYS VFEGELSDTIPVVHASIAGCRNIGRMVCV GNRHGLLVPNNTTDQELQHISATGLP RHSGRFRAGWKERFLSLWGNFFNHLAID YVGLGSNQD\LDKGRQEEISGQMLFKGW EVFRQTVADQVLVES\YCVFSNPGRAW VPSRPFQ*RPNELSSISFKVPLVAGTC* TKGSEVICLLGMGEMNWCAFCGPOTP NPAQSCQVVEECLQS*NEAPALAPIANR ACGNSLIDSLT |
| 656 | 8707 | A | 1609 | 1 | 248 | GPLIWEPASPEPPPLPWGKPRMQ/SG*Y G*TP*IPKIRFPKPPPPPPQALEPQQKGP N*AHP*EPTPAKKYSPQRVQKVPK |

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| 657 | 8708 | A | 161 | 796 | 1381 | SLTSDKRQWALGSMDFKFKHWICH/PIK MLHLGVGPKGLSVTQQFSSQN*FPVCAF QSSQYIPLPAQKLMYSQ*PVQNRCSNQ TIPVAHPMSGHQVSHHRPANNPGKEEV PGQEGKN*NKDVNNF*TGQPWTKGNLEI STWPERNLILALKVPIKAELKRSWASSN CKQT*LRHPQCDDVFISMKEQSMKCRN F |
| 658 | 8709 | A | 1610 | 290 | 1414 | NKRHPSRVYMSLPQAEKVQAMYIWDG TGEGLRCKTRTLDSEPKVEELPEWNFD GSSTLQSEGFTQVNMVLPAAAMFRDPFR KIDPNKLVLCIEVFRYNNRRPAETNLRHT CKRIMDMVSNQHPWFGMEQVEYTLMG TDGHPFGWPSKGFPQPGQYLLGVGAG DRSLGRDIRAEHYRACFYAGTRIPGTK AGVSPLQWEFQIGPEGIKQGG/HIFWV ARFILHRVCEDLGVIATFDP*/RPLGN WNGAIGCHTNFSTKAMRKENGLKYIEK AI*KL TNRHKSHIRAYDPKRGDNRRL TGFHETSNINDFSVGVANRSASIRPRTV GQEKKG YFEDRRPSANCDPFSVTEALI RTCLLNETGDEFFQYKN |
| 659 | 8710 | A | 1612 | 129 | 1182 | |
| 660 | 8711 | A | 1613 | 1 | 353 | FGTRSFDSRSEAEAAKNALNGIRFDPEIP QTLRLEFAKANTKMAKNKLVGTPNPSTP LPNTVPQFIAREPYELTVPALYPSSPEVW APYPLYPALAPALPPAFTYPAASLHAQ ETL |
| 661 | 8712 | A | 1614 | 129 | 1238 | APPSPPSSGCSPPQQLSALTPGTRVLAPSF ASFLPSFFLPPLAPALPLQVALPGPDCLG SPLPARALPRLSLALPESPAAAVADSPRE PQPNPSPTATAPAPAPAPQPAAPARGSPG ARGRLQWASAPSPSPAPQPCPARRGRTG KMNNGGKAEKENTPSEANLQEEEVRTL FVSGPLDIPREL YLLFRPFKG YEGSLIK LTSKQPVGFVSFDSRSEAEAAKNALNGI RFDPEIPQTLRLEFAKANTKMAKNKLVG TPNPSTPLPNTVPQFIAREPYELTVPALY PSISPEVWAPYPLLPRRELGACFYLPFG/S FTYPASLAWPRCAGSLPRLLLRAGSPVS SAEYITLQQWLLEGRTIALWLYG |
| 662 | 8713 | A | 1615 | 129 | 1143 | APPSPPSSGCSPPQQLSALTPGTRVLAPSF ASFLPSFFLPPLAPALPLQVALPGPDCLG SPLPARALPRLSLALPESPAAAVADSPRE PQPNPSPTATAPAPAPAPQPAAPARGSPG ARGRLQWASAPSPSPAPQPCPARRGRTG KMNNGGKAEKENTPSEANLQEEEVRTL FVSGPLDIPREL YLLFRPFKG YEGSL* KLTSKQL*GFVSFDSRSEAEAAKNALNGI RFDPEIPQTLRLEFAKANTKMAKNKLV GTPNPSTPLPNTVPQFIAREPYELTVPAL YPSISPEVWAPYPLYPALGPALPPAPAF TYPASLRCGPNPVEKEIQDSV |
| 663 | 8714 | A | 1616 | 1 | 669 | |
| 664 | 8715 | A | 1617 | 267 | 1057 | GRTMMFGAKRRQEEWEKVRKPEDPEEC PEEVYDPRSLYERLQEQKDRKQELRGT VSNCKNMVVRGLDEDETTFLDEVSRQQ ELIEKQPKRAEELERT*RNTEITSRLEFSQ ENKKEVEKKLTCE/VL*KPRTKFSQANVL GQEL*SMKSSSESGHQCEKT*NRTPED*Q ESRALILAKSLGNNLPLSGFFHPLAPSAA SMYRHPPRPGWPTLGAATPSPASDSEGTI QCHRKDCSPPCFRNTNFTLRGPLSFRRSLH REAPPQG |

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| 665 | 8716 | A | 1618 | 1 | 641 | DTRFLERLRLSISSYVQTPMGHFTFEEDKA TITSLWCKVNVEDAGGETLGRLLVVYP WTQRFDSFGNLSSASAIMGNPKVKAH GKKVLTSGRLP*KHLDDLKGVTFAQA* SELH/CDKAALLDPENFKLPGEILLVTR FGQHFRAKNFTPEGCQAISWQERWVT WSWPVPCSSRLPLKLNCP*MQSFSRIRLL FLQAITNNKSISAKRSP |
| 666 | 8717 | A | 1619 | 1 | 194 | |
| 667 | 8718 | A | 162 | 3 | 1116 | LNQWQEQTGNPERTHRPSEGSGLLLQDP GDFSNTLSAPTAEEVEKGDPLPKIPPLEEL KETHLTHKDSHKLKIKGWKKAFLANGH QKQTGEAILIPDKTKFKATAVKRDEGD YIMVKGLVPQENITILNTYASNTEAPKFI KQLLIDLRNEIDSNIVVGNFNTPTAIDR SSKPKVNKETMDLNYTLEQMDLTDIYRT FHPTTAEYTFYSTVHETISKIDHMIGHKM SINTFKKIEIMSSLTLDHSGIKLKINSERNL QNHANTWKLNNLLNEHWVKNEIKMEI IQLFELNNNNDDTTYQNLWDTAKVVLRG KFIALNAYIKKTERAKKTIYSHTSGI*KQE QTKPKPSRRKEIIRAELEIETKKT |
| 668 | 8719 | A | 1620 | 98 | 1136 | ASDAFHLSAPGLRLGSRSAARPATMTE QAISFAKDFLAGGIAAAISKTAVAPIERV KLLLQVQHASKQIAADKQVYKGVDCIV RIPKGAGGVLSFLEGQPLPTVIRYFPVTA FNFRPFKD/KSYKQIFPGGAWDKHTQFVW R*FGGANWASGVAAGADHPSCFVYPLD FARTGLGKGRWKSQAQASFRGLGDCL VKIHQVQTASRGYQGLPVSPFTATIIYP AAAYYGVYDTAKGHASPTPSNTHILLS RMNRARTVTARGAVGCPNPKTVRRIR MIDAIRGAKGADIMYTG/TLVDC*RKNLS EDEGGQRPFKGCVVQTLRGHGGRPSV LVPVRTSSRRVI |
| 669 | 8720 | A | 1621 | 4 | 101 | VQWNDFGSLQNPFGVSPFFWLSLNNL GFKGSSSRPGFPLKF**KP/EVFRVNDGF PPAP*FGPPGPPKSWGFP*PPPGVSPFF WLSLNNLGFKG |
| 670 | 8721 | A | 1622 | 3 | 1728 | GDRTDGVWWLGLSRRYAIPFNSLEPSS LGSCPLSIGTHKVALHALELTITDIQCGK AFNSSSSFRYHERHTHTGEKPYECKQCGK AFRSASLLQTHGRHTHTGEKPYACEKCGK PFSNFSFFQIHERMHREEKPYECKGYGK TFSLPSLFHRHERHTHTGGKTYECKQCGR SFNCSSSFRYHGRHTHTGEKPYECKQCGK AFRSASQLQIHGRHTHTGEKPYECKQCGK AFGSASHLQMHGRHTHTGEKPYECKQCG KSGFWASRLQMHGRHTHTGEKPYCKQC GKAFGWPSNLRHGRHTHTGEKPYCKNQ CGKKWKDQNIIEYQNPFRNFRSLIEGN VNEIKEDSHCGETFTQVPDDRNLNFQKK ASPEAKSCDNFVCGEVGIGNSSFNMINR GDIGHKAYEYQDYAPKPYCKQPPKAF RYHPSFRTQERNHTGEKPYACEKCGKTF ISHSGIRRRMVMHSGDGPYKSSFLRSH KVPGHGRRFAMNPTLLNKEDERGKKNV VTREHLDRMKNSCIVCNMGHSNTEIDV NVVMGNRYERLERDARMTIRKRRKRYSD IRFRIMGRYTVRVEVLTAVNSE |
| 671 | 8722 | A | 1623 | 1637 | 5763 | KPGNGACAGREWCDGGGAAWNWRDP GLPVGDSGVWDRVLELLGPRSPRPLDV GGPAAAGTPGVLSRPCSTAALAPKPFCA APRPQPDAPACAGATGGSCADFDGSDVDF VRRRSSGLWGPQPLSPVKNYTEMFQDP VAFKDVAVNFTQEEWALLDISQKNLYR EVMLDTFWNLTSIGKKWKDQNIIEYQ NPRRNFRSVTEEVNEIKEDSHCGETFT VPDDRNLNFQKKKASLK*NHVTALCVQK |

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| | | | | | LA*VTHL |
| 672 | 8723 | A | 1624 | 2 | 656 APTPTGQRVVRATPAQSAPVRLRRRSYD VNNPIPSNLKSEAKKAAKILREFTEITSR NGPDKINPGSTVIAKAK\GLANSCLLNQS PGSLVTFQRGGPGVLVARLPDGKWSSP FS/ALGIAGFG\GGFEIGI*GIQTLVILEF/D DPCC*EAFKGGNLTGGNLTVAVGPLG RNLEGNVALRSSAAVFTYCKSRGLFAGV SLEGSLIERKETNRKFYC |
| 673 | 8724 | A | 1625 | 141 | 1307 FHVNNPIPSNLKSEAKKAAKILREFTEITS RNGPDKIIPAHVIAKAKGLAILSVIKAGFL VTARGGSGIVVARLPDGKWSAPSAGIA GLGGGFEIGI/EDTFTATYSL*ALPWLPSS VECHSSFLRLPSA*HIFLHPFTVNLMSD LVIIILNYDRAVEAFKGGNLTGGNLTVA AVGPLGRNLEGNVALRSSAAVFTYCKSR GLFAGVSLEGSLIERKETNRKFYQCDIR AYDILFGDTPRPAQEDLYENLDSFTEK YENEGQRINARKAAREQRKSSAKELPPK PLSRPQQSSAPVQLNSGSQSNRNEYKLY PGLSSYHERVGNFYQPIDLTALYSFEGQ QPGDLNFQAGDRITVISKTDSHFDWWEG KLRGQTGIFPANYVTMN |
| 674 | 8725 | A | 1626 | 167 | 401 |
| 675 | 8726 | A | 1627 | 133 | 312 VRVGEKLKPCFWPPEANPD*CYLHLWI LDSQTKSKPVLTS*PAPPNGILGTSVCFT FY |
| 676 | 8727 | A | 1628 | 1759 | 1967 SGCKPLTFPPP*SDSPVKEDPCR/SPPSHP RLPPHSLPALPFTPNPPPKIYTAVSRIW EMKDRCNPI |
| 677 | 8728 | A | 1629 | 167 | 1378 GNTLVTNMTEFWLISAPGEKTCQQTWE KLHAATSKNNNLAVTSKFNIPDFKGWA RWDVLVGLSDELAALGKIL*EGSWLKE SRLQLHGLDVLEDSKDKVQENLLANGS GLGLPYITKVPSGDMAKYPIKQSLKNISE IIAKGVTQIDNDLKSASAYNNLKGNLQ NLERKNAGSLTRSLAEIVKKDDFVLD EYLVTLVVVPKLNHNDWIKQYETLAE MVPVPRSSNVLSEDDQSYLCNVTLFR/RR AVDDFQDTKPGENKFIVRDFQYNEEEM KADKK\EMDRASTDKKKQFGPLVRWL KVNFEAFIAWIVKALRVFVESVLRYG LPVNLQHMIFHRNNNPFKPLRQVLHESY IHLDSAA\AIIDAPMDIPGLNLSQEQYY PYVYYKIDCNLLKFK |
| 678 | 8729 | A | 163 | 41 | 1133 HRTYKTKIHLKKQKQSTQATKSRMNAV VPHISILTLNVNGLNVPLKRYRVA*WIRI YQQTICCLQETHLTPNTKDSHLKLVKG WKK\AFHANGHQKQAGVAILTSDKTNF KATAVKKDKKEGHYIMVKGLDQQENITIL NIYAPNTGAPKFMKQLLIDVRNEIDSNTII AGDFNTPLTALDRSSIQKVNKETMDLNY TLEQMDLKDHYRTLHPTTAEYTIYSTVH GTFKIDYMTGHKTSLNKFKKSEISSL DHSGIKLEIDSKRNHQNANTWKLNNLL LNEHWVKNKIKMEIKTF/FELNDNNGTA YQNLWDTAKAVLRGKFTALNAYIKKYE RAQTDNLRSHLKELEKQQTTPKSSRRKK K |

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| 679 | 8730 | A | 1630 | 569 | 1050 | PLESRRLARSSGGWAGITGTPMNIPTGPD PGPSERSAQPRVWDSTCCLKSNCWFRK VKATTPMSSMMRQIPRMYMNA/WEKV QVVTEGRQHTNEGDHEHDDAQEDDDG WSQEGTFKGFIFLPLNLCIDAHQRDQGP NQTCNPSTLGGRGGQITRPGDRDH |
| 680 | 8731 | A | 1631 | 1 | 595 | |
| 681 | 8732 | A | 1632 | 2 | 1121 | ARGCGRSSRSRSHRCLPFPPPPSRRPA SLGPERRPGSSRAAPAASRSLSGLSRASG TASCGRPPACPPARSPLPAGPWAARAMG TDSRAAKALLARARTLHLQTGNLLNWG RLRKKCPSTHSEELHDCIQKTLNEWSSQI NPDLVREFPDDLLECTVSHAVEKINPDER EEMKVSAKLFIVESNSISSSTRKVQLTW ACSVLGS/VAQLGFLWIHWLSPPI*KDGG LIFPWEHLQPYWEGI*KNLVQRQKGLLP* GTSDDLKTQLEQLYQWAQVKPNSNQVN LASCCVMPPDLTAFKQFDIQLLTNDP KELAFWKASFQGRLFQGKAFDIDSSGTE WGAAGVLLRYSVIVKSRGIKSKGYILQA KRRGS |
| 682 | 8733 | B | 1633 | 63 | 458 | SLENTVSTAISKAQNGAPSWGGSYPSIHA AYQLPGTVKPLPAAVQSVQVQPSYAGG VKSLSSAEHNALLHSPGSLTPPHKSNVS AMEELVEKVTGKVNKKEERPPEKEKSS LAKAASPIAKENKDFPKTEE* |
| 683 | 8734 | A | 1634 | 3 | 2303 | EMEGKEDAQKVLKCMYCGHSFESLODL SVHMIKTKHYQKVPLKEPVPAITKLVP TKKRALQDLAPPCSEPAAGMAAEVALSE SAKDQKAANPYVTPNNRYGYQNGASYT WQFEARKAQLKCMCEGSSHDTLQELTA HMMVTGHFLKVTTASAKGKQLVLDPV VEEKIQSIPLPPTTHTRLPASSIKKQPDSP AGSTTSEEKKEPEKEKPPVAGDAEKIKE DSEDSLEKFEPSTLYPYLREEDLDDSPKG GLDILKSLENTVSTVINKAQNGAPSWGGS YPSIHAAYQLPGTVKPLPAAVQSVQVQVQ SYAGGVKSLSSAEHNALLHSPGSLTPPH KSNVSAMEELVEKVTGKVNKKEERPPE KEKSSLAKAASPIAKENKDFPKTEEVS KPQKKGPEAETWEAKKEGPLDVHTPNG TEPLKAKVTNGCNNLGIIMDHSEPSFIN PLSALQSIMNTHLGKVSKEPVSPLDPLA MLYKISNSMLDKPVYPATPVKQADAID RYYYENSQPIDLTKSKNKPLVSSVADS VASPLRESALMDISDMVKNLTGRLTPKS STPSTVSEKSDADGSSFEALDELSPVHK RKGRQSNWNPQHLLILQAQFASSISETT EGKYIMSDLGPERVHNSKFTGLSMTTI SHWLANVEVTSRRTGGVTKFLKEPGTQ GHPVFFACNDCASQFRTASTYISHLETHL GFSKDLKSLPLNQIRQQNV*KVLTN KTLGPLGATEEDLGSTFQCKLCNRTFAK QARSQTAP |
| 684 | 8735 | A | 1635 | 133 | 500 | YNTVNYKSHPEGQSMCWSMPVITATFG NPRRVDQPLRSGVQDQPGQHGKIPSLK IQKLAGHGAGCL*SQLLGRLRKENCLN/ SPGGGGCSEPSRHCIPAWAIA*DTI*KIK K*KPPKMRN |
| 685 | 8736 | B | 1636 | 1568 | 1588 | MGDQQLYKTNHVAHGSNLFYQQPPLG VHSGLNHNHYGNAVTTGGMDAPQASPI PHFPQDTRDGLPLVGSKNLGMDSR QGGWGSAGPGNHVQLRGNLANSNMM WGAPAAEPTDGYQYYSQASEIRTQKL TSGVLHKLDSFTQVFANQNLRIQVNNM AQVLHTQSAVMDGAPDSALRQLLSQKP MEPPAPAIPSRYQQVPQQPHPGFTGGLS KPAQVGVGHPTQGHLYYDYQQPLAQVP VQGGQPLQAPQ |

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| 686 | 8737 | A | 1637 | 2 | 251 | FFFFLINKTKRLFTP*ALQWGYPSGSCG SVSQSCKCILRGRSRATISIEAEMVDL |
| 687 | 8738 | A | 1638 | 36 | 530 | NKVLPPAAASEHSDCQISKHQVQLCP/PNII TLADIVKDPVSRTPALVFEHVNTDFKQ LYQTLTDYDIRFMYEILKALDYCHSMG IMHRDVKPHNVMIDHEHRKRLRIDWGL AEFYHPGQEYNVRVASRYFKGPELLVD YQMYDYSLDTWRMGCMCLASMIHQKEP |
| 688 | 8739 | A | 1639 | 1 | 1833 | |
| 689 | 8740 | A | 164 | 265 | 446 | |
| 690 | 8741 | A | 1640 | 3 | 430 | |
| 691 | 8742 | A | 1641 | 137 | 1368 | FHISLFEENRVLKQGSPLPPAAFLNTVTA QISQTSKSQALSRQPCSDHVGDPVPKAG HRVYTDVNTHRPREYWEYESHVVEWG NQDDYQLVRKLGRGKYSEVFEAINITN NEKVVKILKPVKKKKIKREUKILGGIW RGGPNITLADIVKDPVSRTPALVFEHV NNTDFKQLYQTLTDYDIRFMYEILKAL DYCHSRGIMHRDVKPHNVMIDHEHRKL *LIDWGLAEFYHPGQEYNVRVASRYFKG PELLVDYQMYDYSLDMWSLGCMLASMI FRKEPFFHGHNDYDQF/VCRMALVLTGTE DLYDYDKYNIELDPRFNGYLGHRHSRKP MGTALSENENQH/LSSPEALDFLDKLLR YDPPSHGLLAREAMEHPYFLHCCEGPRP RNGFHLAMPGCSTPVQQRPI |
| 692 | 8743 | A | 1642 | 874 | 1183 | TPMLEQLGNRYLQNIACYFFRNMCTYQ LGCSGSR*SQHFGRPRQVDHLRSGVRD QPGQQGETPSLLKVQKFSWAWWRTPI SATWEAEAGEVLEPGRRRLK |
| 693 | 8744 | A | 1643 | 2 | 498 | |
| 694 | 8745 | A | 1644 | 49 | 538 | SQTPMGHFTEDQGLLSKSLWGK/VLNV EKMLGRKKTPLGKGSPLVPTPWDPKR FL*TSFGKTLSPALLPHQWANPPKVKG HHGKEGCLTFPWEDAHKAPLDDPQAP FAPA*SELHCDKLHVDPENFKLLGNVL VTVLAIHFAGKEFTPGGCRASWAEDG |
| 695 | 8746 | A | 1645 | 53 | 393 | |
| 696 | 8747 | C | 1646 | 116 | 379 | |
| 697 | 8748 | A | 1647 | 3 | 200 | |
| 698 | 8749 | A | 1648 | 1 | 637 | MRSAARGPRQSCSAFNRFRANSSSPGF GAPCGRQCWIWESLGKERAKEGKDGLL QSPRTSLKERPKTRITGALPMDHTEGLPA EPPAHAPSPGKFGERPFPKRLTREMR NYLKERGDQTVLILHAKVAQKSYGNEK RFFCPCPCVYLMGSGWKKKKEQMERDG CSEQESQPGAFIGIGNSDQEMQQLNLE GKNYCTAKTLYISDSDKR |
| 699 | 8750 | A | 1649 | 111 | 748 | GKREGAGERDQGRRRGESREGWSFGES LWKMAPVVTGKFGERPFPKRLTREMR NYLKERGDQTVLILHAKVAQKSYGNEK RFFCPCPCVYLMGSGWKKKKEQMERD GCSEQESQPCAFIGIGNSDQEMQQLNLE GKNYCTAKTLYISDSDKRKHFMLSVKM FYGPTSDDIGVFLASKRIKVISKPSKKKQS LKNADLCIASGTKVALFNR |
| 700 | 8751 | A | 165 | 283 | 398 | NWQEKCTFQIIGGRKRMSFRILINFFHN* DRTVCYVP |
| 701 | 8752 | A | 1650 | 1 | 519 | IISTD/KAETY/FYEGMGPVFTPTVPV ESLQNLNAGGDVAMLELTGQNFPTNLRV/ WFGDVEAETMYRCEQSMCLCVVPDISGF REGWRWVRQPVQVPTLVRNDGNIYS TSLTFTYTPP/GPRPHCSAAGAILRANS SQVPPNESNTNSEGSYTNASTNSTSVTSS TATVVS |

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| 702 | 8753 | A | 1651 | 238 | 1713 | STMAWIKRKFGERPPPKRLTREAMRNYL KERGDQTVLILHAKVAQKSYGNEKRFFC PPPCVYLMGSGWKKIKLQMKCDGCSEQ GSQPCAFIGIGNSDQEMQQLNLEGKNYC TAKTLYISDLKQKHFMLSVKVFGNSD DIGVFLSKSSKPSKKKQSLKNADLCIASG KERWALFNRLLSQTVASTRYLHV/EKEGN FHASSQQWGAFIHLDDDDGSEGEFTV *DGYIHYGQTVKLVCSVTGMALPRLIRK VDKQTTLLDADDPVSQLHKCAFLEDTE RKYLCLSQERIIQFQATPCPKENKEKIN DGASWAIISTHKAKHTFYRESGPLSLAP/ VSCPPALSVESLKLNNGGDEPSLKLNR EFQLPKFYKVWFGDVEAEAMYRCGES MLRVVPDVSAF*EGWRVYSQQPIQVSVT LVRNDGHIYSTSLTFTYTPEAGPRPHCSV AGAILKASSSHVPPNELNTNSDGSYTNA STNSTSVTSSTPTTVS |
| 703 | 8754 | A | 1652 | 1 | 309 | FF*DRA*LCPPGWSARSQHTVVSTFLGS SKFSLGLPPELPGDHRHAPPCPANFFYFS *RWGLPMLLVSNSQAQAILPSPFQKGW DYRAWGHHTWGSYLNFE |
| 704 | 8755 | A | 1655 | 1 | 2325 | |
| 705 | 8756 | A | 1656 | 3 | 128 | |
| 706 | 8757 | A | 1657 | 203 | 2698 | SANMGKKRTKGKTVPIDDSSETLEPVCR HIRKGLEQGNLKKALVNVEWNICQDC KTDNKNVKDKAEEETENKPSVWLCLAKC GPQGFGRNFSR/EQHALKHYLTTPRSEPH CLVLSLDNWSVWCYVCDNEVQYCSSNQ LGQVVDYVRKQASITTPKPAEKDNGNIE LENKKLEKESKNEQEREKKENMAKENP PMNSPCQITVKGLSNLGNTEFFNAV MQN LSQTPVLRRELKEVKMSGTIVKIEPPDLA LTEPLEINLEPPGPLTLAMSQFLNEMQET KKGVVTPKELFSQVCKKAVRFKGYQQQ DSQELLRYLLDGMRAEEHQVRVSKGILKA FGNSTEKLDEELKNKVVDYEKKKSMPSPF VDRIFGGELTSMIMCDQCRTVSLVHESF LDLSLPVLDDQSGKKSANDTPALTKTVTY AECYSEEKYHTDCCYI*RSDISSGTRKHL QKKATKQAKKQAKNQRRQQKISGPALH LNDIRTIDHPEDSEYEAMSLQGEVNITS NHISQEGVMHKAECVNQKDLNGQAKM IESVTDNQKSTEEVDMKNINMDNDLEVL TSSPTRNLNGAYLTEGSNGEVDISNGFK NLNLNAALHPDEINIELNDSHTPGTKVY EVVNEDPETAFACTLANREVNTGECQIQ HCLYQFTRNEKLRDANKLLCEVCTRQ CNGPKANIKGEVRKHVYTNAKKQMLISL APPVLT LHLRFQQAQFNLRKVNHKHF PEILDAPFCTLKCKNVAENTRVLYSLY GVVEHSGTMRSGHYTAYAKARTANSH LSNLVLAHGDIPQDFEMESKGQWFFHISD THVQAVPTTKVLNSQAYLLFYERIL |
| 707 | 8758 | A | 1658 | 992 | 1863 | GIWRNVHRQPQLESCEPTACSGRACAC CPVSCGWSHGQDWMVPVAGRCTRAQR CCTGGASLPTVHKSTLSSCSAPPADSAA CVFIYFIIF*QSLNSVAQAGVQWRNL KLLQPLPPAFKAFSCLSLCNWDYRRVP PGLANFCIFSRDGGFTMLVVRLVSN*PC DLPASASQSAGITALSHHAWLLFFETES RSVVQAGVQWCDLGLSQAPPPGFTPFSC LSLQSSWDYRRPPRPANF/CVFLVETGF HC*PGWSRSPDLMIPPGLSLPKCWDCCR DTKHPASKF |

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| 708 | 8759 | A | 1659 | 318 | 1681 | SPRMHALVLLLCIGALLGHSSCQNPASPP EEGSPDPDSTGALVEEEDPFFKVPVNKL AAAVSQTSAYDLYRVRIQA*APRPNVLP VSLFKCGPTALSA\LSLGKRSKRKNPIIH RVALYYDLIKQAPD\HGYLIRKLP*HGHF PPQKNLKSASR\VFEEKLRIKSSFVAPLE KSYGTRPRVLTGNPRLDLAQEINN\WVQ A\Q\MKGKLARSTKEIPDEISIVLL/GV*AH FKGQ\WETKFDSRKT\LEGFLLGMKERT REGPP*LSDPKGCIFYAMGLGFRFSACKIC PACPLTGSMISIIFFLP\KVTQ\NLT\NEES LTLRS*FMTIDPRT*KTVAGGPSLSPKLL LSYEGEEHPKFLAGR*SLQSLV*FHPDFS KNTGK\PIKLD\FRVEH\RLAFEWNE\GGA GNHPPSPRGLQPAHL\TFPLDYHLNQPFI LLRDTDTGALLFIGK\LDPRGP |
| 709 | 8760 | A | 166 | 283 | 397 | NWQEKCSFQIIGGRKRMSFRILINFFHN* DRTVCYVP |
| 710 | 8761 | A | 1660 | 3 | 340 | |
| 711 | 8762 | A | 1661 | 2 | 500 | GKPD PSTKKQHTIWSPHQQNSPDLEVY NVIRKQSDVSLAETRPDLKNISFRVCSGE ATPDDMSCDYDNMAVNPSESGFVTLVS VENEIYGY*DI*KTETDNNKGEMISKILLF SIRKIHRRSMNKLRSQPVDEHVPTTSC WTPTFWL\YPLSQPVIQLDLMRRYL |
| 712 | 8763 | A | 1662 | 3 | 52 | |
| 713 | 8764 | C | 1663 | 92 | 244 | MRCEIHLVLIPIVYFYFYSNKLCSRLXXXX XGGAVLKNPWGGQSLPGLAR** |
| 714 | 8765 | A | 1664 | 336 | 413 | |
| 715 | 8766 | A | 1665 | 233 | 400 | GGAVLKNPWGGPSLPGLAR**FFPYRGA Y*NLPGNFWKEPLFLGGDILGQPPFGNL |
| 716 | 8767 | A | 1666 | 194 | 360 | GGAVLKDPWGGQSLPGLARK*FFPYGG PN*NLPGNFWKGPLLWGGDILGQPPYRN |
| 717 | 8768 | A | 1667 | 319 | 391 | |
| 718 | 8769 | A | 1668 | 313 | 542 | ALKQPT/PQTKEERAFDPRVHAE*IPYVF EIHIRST*KTT*NGNPTAPLPVRAPTARV RTWPNPGHSCAGSHSSR |
| 719 | 8770 | A | 1669 | 143 | 1316 | ERLEIGKELQLVWDEPHLTPGNDLLPSS CCVTAASDLDRGGQPVCRRGTQRPCY KVIYFHDTSRRLNFEVVKFSCRRDGGQL GSIESEDEQK\IEKF\IENLLPSDGD\FWIGL RRREEKQSNSTACQDLYAWTDGSIQFR NWYVDEPSCGSEVCVVMYHQPSAPAGI GGPYMFQW\NDDRCNMKNNFICKYSDE KPAVPSRRS*GEETELTTPVLPEETQEED AKKTFKESREAALN\LAYILIPSIPLLLLLV VTT\VCWVWICRKRKREQDPSTKKQH TIWSPHQQNSPDLEVYNVSKKTNAKSF LSETRPDLRNISFRVCSESPDDMSCDY DNMAVNPSESGFVTLVSVESGFVTNDIY EFSPDQMGRSKESGWVENEIYGY |
| 720 | 8771 | A | 167 | 2 | 1012 | AEALVESFWKAKQHTKEELKSLQAKDE EKNENEKAKAACSAAMEEDSEASSST GDSSQGDNNLQKLGPD\DVSDTDSIRRV YTRLLSNEKIEIAFLNALVYLSNVECDL MYHKVYSQDPNYLNLFIIVMENRNLHSP EYLEMALPLFC\KAMSKLPLAAQGLIRL WSKYNADQIRRMETVQQLITYKVISNE FNSQNLVND\DDAIVAASKCLKMIYYAN AYAVTKNLGLY\DNRIRMYSERRITVLY SLVQGGQLNPYLRLIVRCDHIIDALVRL EMITMENPADLKQFY/RGI*RRTRWVAA FWDRASEPKANSIGFGGSQLWMPTPVAS YT |

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| 721 | 8772 | A | 1670 | 18 | 686 | SPPPPPPAREMNFVRAANRRPRRVSRRP VQQQQQQPPPPPPPPPPPPPPHQQPSS PPQ*QQQQHPPASSPPPPPLQERNVGE RDDDVPADMVAEESGPGAQNSPYQLRR KTLLPKRTACPTKNSLEGASTSTTENFIG HRAKRARVSGKSQDLSPAAPAEQYLQEK LPDEVVLKIFSYLLEQDLCAAACVCKRF SELANDPNLWKRLYMEVFYTRPMMH |
| 722 | 8773 | B | 1671 | 155 | 310 | MAAIRKKLVIVGDGACGKTCLLIVFSK QFPEVYVPTVFENYVADIEVDGKQ* |
| 723 | 8774 | A | 1672 | 162 | 877 | AMAAIRKKLVIVGDGACGKTCLLIVFSK DQFPEVYVPTVFENYVADIEVDGKAGRS LACGDTAGQEDYDRLRPLS*PDTDVILA MCFSIDSPDSLEWIPRKSWTPEVKHFC PNGGPSILVGELRRVLSGIDGATQGRGLR PRLKAGSPVET*RKGRDMGKQGLALFG YIGSCSSQRPKDWEVEEEVF*KWATESL LWQA*TLGKKKSGVPLSLVKPLLQAQPL MRLIFEVLFINLSV |
| 724 | 8775 | A | 1673 | 1 | 711 | |
| 725 | 8776 | A | 1674 | 1 | 2647 | MGVTSAAAGLVGSAPQCVALPSEGWT AVWPVAACTCSGVGSSPKLTPGSFVHCP WFLLLTEATRAEIKRPFASKAELKASVRP MEGSHCWGGEARRTSQGHTEQKGELRA RRQAQNEDEDVKEVWVGKTKKEESDKL GCQGAWVPPRVPSPWIGRFEWVVGWYE QPAVSWQMRVVRLLRLRAALTLLGEVP RRPASRGVPGSRRTQKSGARTDSAWR RALTVISTSPGTSRMDPVALVAVGGPRR FPGGHTLQRLPVALRTLIPADQAHQAPN STTWLGSRAGLLALAAGLGIRDAAHG PLQVGGMGGYTGMGSEVRWEKEKHED GVKWRQLEHKGPYFAPPYEPLPDGVRFF YEGRPVRLSVAEEVATFYGRMLDHEY TTKEVFRKNFFNDWRKEMAVEEREVIKS LDKCDFTIHRFYVDKAAARKVLSREEK QKLKEEAELQQEFQYCLDGHQEKIGN FKIEPPGLFRGRGDHPKMGMLKRRITPE DVVINCSRDSKIEPPAGHQWKEVRSDN TVTWLAAWTESVQNSIKYIMLNPCSKL KGETAWQKFETARRLRGFVDEIRSQYRA DWKSREMKTQRVALYFIDKLALRAG NEKEDGEAADTVGCCSLRVEHVQLHPE ADGCQHVVFEFDLGDICIRYNNKVPGE KPVY*NLQLFMENKDPDDLFDRLTTS LNKHLQELMDGLTAKVFRYNASITLQE QLRALTRAEDSIAAKILSYNRRANRVVAIL CNHQRAATPSTFEKSMQNLQTKIAKKEQ VAEARAELRRARAHEKAQGDGKSRSVL EKKRRLL*KLQEHHLAHLVQATDKEEN KQVALGTSQNLNYLDPRISIAWCKRFRVP VEKIYSKTQRRERFAWALAMAGEDFEF |
| 726 | 8777 | A | 1675 | 2002 | 2238 | KGDFTKLPC/LC*SVPAFY*RLKICCSIY LV*YMSVSVIESICYKYTVFCRSRG |
| 727 | 8778 | A | 1676 | 3 | 428 | |
| 728 | 8779 | A | 1677 | 263 | 899 | ISYQEGTSAIQRK*QEVTLRK*TQESE/SA GNDSASTAPRSTEESESDVFTESELSPIR EELVSSDELRODKSSGASSESQTVNQA EVESLTVKSESTGTPGHLRSDEHSTNEV GTLCHKTDLNNLEMAIKEDQIADNFQGI SGPKEDSTSIKGNSDQDSFLHENS LHQEE SQKENMPCGETAEFKQKQSVNKGKQGGK EQNQDFTGQRAG |
| 729 | 8780 | A | 1678 | 1165 | 1530 | VKNGGNEVIIHCHFLTFGIYLLFFETEFCS CRPRLECNGAILAHCNRLRPGFKRFSCF SLPCC*DYRHLPVRPVKFFVVLVETGFHY LGQAGLKLTPGDL/PPPLGLPKCVSHCA QPRVSTF |

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| 730 | 8781 | A | 1679 | 197 | 843 | RLFSSNQTVDSQKNVDITLKGTPQ*SC KGPRGTLRWRDFMHIKCGTSALLGKEKK RGFRVDKWWGSRRELGYPGTTCSHV QDHDPRGVTTGASRYQDEGPVYASPSPH PTVGLSQENGSSLLKSRNFFGVKKYIPQG FRMRPGCLLVSVSQGPRKE*INPLKGNDI *ALLQIPAALNPASPTRLKTGIRKFFGW VSMSLEKGTVPQGLIE |
| 731 | 8782 | A | 168 | 966 | 3172 | |
| 732 | 8783 | C | 1680 | 27 | 218 | MLMADIRKEERNHLCRSSRRTWTILDRA EYSDHVVLQAGAGVGWGTSSXSPFLYSFEI PYGAQVA* |
| 733 | 8784 | A | 1681 | 490 | 773 | HPQIFVPGQESFNDRIKQPVEGLVVLRE HERHSPSLRLHLEATQRLRHPGLRLRG ELLWLIIRFIQTLPFPAAGPTRGAGIY PRGKQPVEGLVVLREHERHSPSLRLHLE ATQRLCHPGLRLRGELLWLIIRFIQTLP LPFAAGPTWAGIYPRGKQPVEGLVVL REHERHSPSLRLHLEATQRLCHPGLRL RGELLWLIIRFIQTLPFPAAGPTWGA GIYPRGKQPVEGLVVLREHERHSPSLRL HLEATQRLCHPG/LPQAQGRAPSLAHHQI HPNTPSSFCSGQTYAGGWDLPGQQAAC |
| 734 | 8785 | C | 1682 | 48 | 80 | MGLWLFHEY* |
| 735 | 8786 | A | 1683 | 858 | 1055 | |
| 736 | 8787 | A | 1684 | 1 | 103 | VFFLFGGDGVSLSCHPGWSAVA*TQEAE PFVQII |
| 737 | 8788 | A | 1685 | 451 | 785 | CSQDGGRLRDLVRHPQTFVPGQESFND RILKQPVEGLVVLREHERHSPSL/PASS*G HTASPPRSPQAQGRAPSVAPPTTPQICP TTPSSFSKRRTYAGGWDLPGQQAAC |
| 738 | 8789 | A | 1686 | 1 | 1335 | MNDDIRSDLPDWRDTPCVQKKAMD RTKTRFRKRGQITGKITTSRQHPQNEQS LQRSTSGYPLQEVVDDEVLGPSAPGVDP SPPCRSLGWKRKKEWSDESEEEPEKELA PEPEETWVVEMLCGLKMKLKQQRVSPIL PEHHKDFNSQLAPGVDPSPPHRSFCWKR KREWWDSEESLEEEPRKVLAPPEEIIW VAEMLCGLKMKLKRRRVSLVLPHEHEA FNRLLEDPVIKRFLAWDKDLRVSDKIPSE PTI/HGSITQNPSSGFDLHPTFEYPSIPQFP NEYSHPNTEGGCQS*ARDSPLPS/VSGKL TSAGGLSWWCP*APT*FLSSATWPMTW RRTRTPNKTSTSCMRPALAYPWSVT VGSSYAVA*TPCVQKKAMDRTKTRFRK RGQITGKITTSRQHPQNEQSLQRSTSGY PLQEVVDDEVLGPSAPGVDPSPPCRSLG WKRKKEWSDESEEEPEKELAPEPEETWV VEMLCGLKMKLKQQRVSPILPEHHKDF NSQLAPGVDPSPPHRSFCWKRKREWWD ESESLEEEPRKVLAPPEEIIWVAEMLCG LKMMLKRRRVSLVLPHEHEAFNRLLED VIKRLAWDKDLRVSDKIPSEPTILGASP KTLPLASQICRPSNTPPSRNFQMSVTPT LRVGASPELGTVPYLPWEADLSRRPLL VVPLSTNLISVLSYLANDMEEDDEDPKQ NIFYFLYGKTRSLPLVRNRRFQLCRCLN PRARKNRSQIALFQKLRFQFCSMSGRA WVSREELEENTGPRGDVDFQQELYSNA NGRQQERGEEPFVQII |
| 739 | 8790 | A | 1687 | 385 | 889 | LEPTLTEQGYARAVLPQIEVEDVLFGLV VLLHVIGQVESQEEMNALVLPGEAGP AEIRYDHSQEILVRHPQIFVPGQESFNDRI LKQPVEGLVVLREHERHSPSL/PASS*GH TASPPRSPQAQGRAPSVAPPTTPQIGPT TPSSFSKRRTYAGGWDLPGQQAAC |

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| 740 | 8791 | C | 1688 | 1 | 1869 | MDSPTPHDPAAPLLVTVLESVQKKTDR TETSFGEIGQILGKIMTSHQPPQEEQSPQ RSTSGYPLQEVVDDEVSGPSAPGVDPSPP RRSLGCKRKRECLDESDEPEKELAPEP EETWVAETLCGLKMKAKRRRVSLVLP YYEAFNRLLAPGVDPSPPRRSLGCKRKR ECLDESDEPEKELAPEPEETWVAETLC GLKMKAKRRRVSLVLPYYEAFNRLLA PGVDPSPPRRSLGCKRKRECLDESDEPE KELAPEPEETWVAETLCGLKMKAKRRR VSLVLPYYEAFNRLLAPGVDPSPPRRSL GCKRKRECLDESDEPEKELAPEPEETW VAETLCGLKMKAKRRRVSLVLPYYEA FNRLAPGVDPSPPRRSLGCKRKRECLD ESDDEPEKELAPEPEETWVAETLCGLKM KAKRRRVSLVLPYYEAFNRLLDPVIL RFLAWDKDLRVSDKIPSEPTILGASPKTL PPASRICIRPSNTPPRNFMSTVTPMLSY LANDMEEDDEAPKQKIFYFLYGKTHSHI PLRPKHWFQLCRPMNPRARKNCSQIALF QKRRFQFFCSMRCRAWVSPEELEENTGP RGDVFQFQELYSANGRHQEGGEEFV QII* |
| 741 | 8792 | A | 1689 | 520 | 1235 | WTDFRSIGLMALAGSVLEFSARSKDATP DPP/LGTGKVPSTAPTGAAPPGLPTAAFD VVLHPFRAGRKKYFPSLLFA*WLCQRSS P*RGADPVIGLYLVHRGGACQPTLGNR QTPRLGIHARPRRRATTSLTLLAFGKN AVRCALIGPSLTSRTRPLTEPLGEKERR EVFFPPRPERVEHNVESRWEPRRGAC GSRGGNFPSPRGGSGVASLERAENSSTEP AKAIKPIDRKSVHQICSGPVVPSLRPNV KELVENS LDAGAH |
| 742 | 8793 | B | 169 | 1 | 2187 | MAGKASESWRKVKDTSCMAVTRENEK DAKAETPDKTIRSRETYHKNMSWETAP MIQIISQGVPTTHENYGSTIQDEIWCLTN FCLDDMLSFVLESCNHCAYCLNVWYR KRAAAKHILIERYYHQLTEGCGNEACTN EFCASCPTFLRMDNNAAIKALELYKIN AKLCDPHPSKKGASSAYLENSKGAPNNS CSEIKMNNKGARIDFKDVTYLTEEKVYE ILELCREREDYSPLIRVIGRVFSSAEALVQ SFRKVKQHTKEELKSLQAKDEKDEDE KEKAACSAAMEEDSEASSRIGDSSQG DNNLQKLGPDVSDIDAIRRVYTRLLS NEKIETAFLNALVYLSNVEDLTYNHV YSRDPNYLNLFIIVMENRNLHSPEYLEM ALPLFCCKAMSKPLAAQGLIRLWSKYN ADQIRRMETFQQLITYKVISNEFNSRNL VNDDDAIVAASKCLKMVYYANVVGGE VDTNHNEEDDEEPIPESELTLQELLGEE RRNKKGPRVDPLETELGVKTLDCRKPLI PFEEFINEPLNEVLEMDKDYTFKVVETEN KFSFMTCPFILNAVTKNLGLYYDNIRRM YSERRITVLYSLVQGGQQLNPYLRLKVRR DHIIDALVRLEMIAMENPADLKKQLYV EFEGEQGVDEGGVSKEFFQLVVEEIFNP DIGMFTYDESTKLFWFNPSSFETEGQFTP IGIVLGLAIYNNCILDVHFPGLSTGS* |
| 743 | 8794 | A | 1690 | 2176 | 2641 | RKTIEEKADPKLQGFVCLFVLETESCSA SQAGMEWPNLNSLQPPPGFTQFLC/SQP PE*LGLTGVPPhQAHCIFSRDGASPC*P GWSPTPGLKRSTCFSLKWCWDRHEPPR LAYFLALFNRDEGLAMLPRPVNSWPQVI LLWPPSVLGFQA |
| 744 | 8795 | A | 1691 | 112 | 410 | |

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| 745 | 8796 | A | 1692 | 2148 | 2510 | SQHFGKLRQEDHLRSGVREQPGQHGKT PYLLKIQKLVAGHGGMCLYSQLLMLRQ ENGVNPGGACNEPRLRHCTPAWVTEQ DSVSKKKTVHKKLNWGSVHRGET*RT SPCVALDTAHL |
| 746 | 8797 | A | 1693 | 178 | 730 | IFFFFFFKMECSVAQAGVQWRDLGSLQ APPRGFTPFSCSLPSSWDYRRPLRPAN FFYF**RRGFTVLATMVIS*PHDLPTLAS QNAGITGVSHHTQPVYALFFSFETEFCS\ VAQAGGQWRDLGSPQPPPRFKQFSHLS LPSSWDYRHAPPSLANFFCIFSRRDRVSPS WSGWSRTPDLR |
| 747 | 8798 | A | 1694 | 2 | 780 | CWGLRRQRSQDVTMTAWALLITLLTQ GTGSAQASALTQPPSASGLGQSVTFSC SGTSSDIGNYNVSWYRQHHPGKAPKLM YEVTKRPSGVPEARFSGSKSGNTASLTVS GLQSEDEGDYCCSMARHHS/VGWVF GGGTQVDPGLGQPKRAALGSLCFPPSLG EASSQPRPTLVCVISDFLPGKP*TVAKA\ DSSPVKAGVETTPPSKQSNNNYAATS YLTLTPEPLKVPQEATAACRVTPEGGTLE KTVAPECS |
| 748 | 8799 | A | 1695 | 103 | 532 | |
| 749 | 8800 | A | 1696 | 112 | 1158 | SCGLGHRKTFSFVSLPARNETQPKACRE QNMEGDFSVCNRC*RHVVSANFTLHEA YCLRFLVLCPECEEPVPKETMEEHCKLE HQQVVGCTMCQIMHKSSLEFHKANECQ ERPVECKFCKLDMQLSKLEHESYCGSR TELCQCGQFIMHRMLAQRRDVCRESQ AQLGKGERISAPEREIYCHYCNQMIPEN KYFHHMGKCCPDSEFKHFPVGNPEILP SSLPSQAAENQTSTMEKDVRPKTRSINRF PLHSESSSKKAPRSKNKTLDPLLMSEPKP RTSSPRGDKAAYDILRRCSCQGILLPLPIL NQHQEKCRWLASSKRKTSEKFQLDLEK ERYYKFKRHF |
| 750 | 8801 | A | 1697 | 343 | 586 | KQKQTSFSSLPRRVNCNSHLVLL/RCDFK NCNLAFETKICQFIKST*EYMGFIFLCFF LLYNIPFHICGPRVKSSFCYRH |
| 751 | 8802 | A | 1698 | 217 | 360 | |
| 752 | 8803 | A | 1699 | 1 | 390 | WEEIQELNEVARHRPRSTLVMGIQQENR QIRELQQENKELRTSLAEHQSALEIMSK YREQMFRLMASKKDDPGIIMKLKEQHS KELQAHVDQITEMAAVMRKPLKLTNR VARNKNEYFNLNKKTKA |
| 753 | 8804 | A | 17 | 214 | 464 | FCGLLLLHPVSADF*PAELINTQEPQERC QLDTGESSRVQHTLPSCPVCQGGTAELS RNVMIASELKCLHPSPKLEYILPGN |
| 754 | 8805 | A | 170 | 270 | 497 | MHFLKAGRGGURL*SQHFGRRPRWADHE/ RSGDRDNRG*HGETPSLLKNTKN*PGT VAGALVASTREAEAGEWREPG |
| 755 | 8806 | A | 1700 | 386 | 790 | NSIMEEQELNEVARHRPRSTLVMGIQQ ENRQIRELQQENKELRTSLAEHQSGLGN L**AKYREQMLRLMASKVDDPGIIMK LKAEQHSYD*HWYIVTSPKDSSLMHLDTS LKHLNMDWREGTWKQIRMYTK |
| 756 | 8807 | A | 1701 | 1089 | 1295 | CPPLFFFEFEFRSCCPGWSNSSLHRPPG FKQFILNFG*K/PSYPYLFQAQSCARMCV CVCVCIIFTET |
| 757 | 8808 | A | 1702 | 2 | 367 | RDNTSPISVILVSSGSRGNKLLFRYPQRS QEHFASQT/RFSVILATILATKSEMCGQ KFELKIDNVRFVGHPTLLQHALGQISKTD PSPKREAPTMILFNVFALRANADPSVIN CLHNLS |

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| 758 | 8809 | A | 1703 | 1 | 452 | RCQYSTREAKLI/LALQD/EVSAMAD/GN E/GPQSPFHILPKCKLARDLKEAYDSL TSGVVRHLHINSWLEVSFCLPHKIHYAASS LIPPEAIERSLKAIRPYHALLLSDEKSLL GELPIDCSPALVRVIKTTSVKNLQQLAQ DALLPPRLP |
| 759 | 8810 | A | 1704 | 1 | 468 | |
| 760 | 8811 | A | 1705 | 2 | 118 | |
| 761 | 8812 | A | 1706 | 1 | 671 | DADSRFSEVF/LATILATQFEMCGQKFEL KIDNVRVFGHPTLHRHALGQISKTDPSPK REAPTMILFNVGFALRANADPSVINCLH NLSRRIATVLQHEERRCQYLTREAKLILA LQDEVSAMADGNEGQSPFHILPKCKL ARD/PQLWLPNQQR*HDPHQPHGQLQR RATSQRGLATEPEDDGEPAGQPVGA*TR SHPQCTRSPEP*GPPHVCQAPSLPRP |
| 762 | 8813 | A | 1707 | 230 | 345 | |
| 763 | 8814 | A | 1708 | 464 | 763 | |
| 764 | 8815 | A | 1709 | 3 | 156 | GRHHL/EEEIMYNENTRGSQLLMLF*QSF AACWMVTTTHEDPVIAVFQALLP |
| 765 | 8816 | A | 171 | 2 | 421 | PAWLSRFTCAATYIKMPEE*ETHYQPM EEEADTFTY/EAKMAPLML*IINTFYSSKE ISLRELISNSSD/AK*LINQSDFGFRVNL GVLNA*INIFC*QALDKIRYESLTDPIKLD SGKELHINLIPNKQDRTLITVD |
| 766 | 8817 | A | 1710 | 1 | 1878 | FRGTWAPSASGSVLLRLPPPPAPSSSGPL RPRPRPHGMRDNTSPISVILVSSGSRGN KLLFRYPFQRSQEHASQTSKPRSRYAAS NTGDHADEQDGSFSDVILATILATKS EMCGQKFELKIDNVRVFGHPTLLQHAL GQISKTDPSDEGKAP*TMILF*CWLFALA RANADPSVINCLHNLNRRIATVLQHEER RCQYLTREAKLILALQDEVSAMADGNE DPKPPFHILPKCKLARDLKEAYDSLCT SGVVRHLHINSWLEVSFCLPHKIHYAASS LIPPEAIERSLKAIRPYHALLLSDEKSLL GELPIDCSPALVRVIKTTSACERTCRQLA QDADLALLQVFQLAHLVYWGKAIIY PLCENNVMYMLSPNASVCLYSPAGPSSSS HQFPFSWTWPSVLAKFSLPVFLCQNFN PLAPRCARRTQLH/IQMVVWMLQRRLL IQLHTYVCLMASPSEVEPRPRIEDDVPF TVARVGGRLSTPNALSFGSP*SSDDMT LTKPQAWTTPSAELLPSGDSPLNQRMT NLF/APSLSEHERAAILSVPAQNPEDKN MFA/RGILHYFRGRHHEEIMYNENTRRS QLLMLFDKFRSVLVVTTTHEDPVIAVFQ ALLP |
| 767 | 8818 | A | 1711 | 1 | 613 | PLKRS DGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPVEKSAVTALWGQA*TW MKVGGKALGK/RWVVLPPWDPKRSFEV LWGNLSQLPDAVNGANP*R*KASMAKE KVLGCPLSEWPLAHLADNLKGHPLPHE VNLNCDKILHRGSLKNFRLLGQTCLVC VPGPINFQKNSTPTSCACLIKKSOLA WCWLNALGPTSIT |
| 768 | 8819 | A | 1714 | 97 | 424 | SPALWEAYDGWITLRSGVQDQSGQHGE MPSLLKIQLAGHDGECL*SQLLRRLRR ENHLNLGGRGCSELSRYCIPAWAPEIAP LHSSLGDLNKTLSQKKTKTVSFI |
| 769 | 8820 | A | 1716 | 18 | 367 | SPPPPRTTRWWPLRRPRLSLGTRAASLR FSSRKPCQNKPDYGLRSEKFR*SRK/A*G RQRP/PREKFPLPFPKKPIEPGEAKPGEIV NGSVRPNNMPLYIPTSIAPYFTFLAVLT L |

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| 770 | 8821 | A | 1717 | 47 | 409 | NSYIYMCIYSYINTIYIHIYLESNISLPLNI YISTPT/HIY*RHTV*VHTKAYVHML*HV YIHFLCLVHKSFKGTIYRDASFLESCSKV NTECHKLRKVKRKYSRIHHTGIHQSSFIM RKMS |
| 771 | 8822 | A | 1718 | 89 | 1560 | IMKHTNPEPGSFSRFYSLKVAPKVKATA APVAGAPPQPDLEFTKLPNGLVIASLEN YSPVSRIGLFIKAGSRYEDFSNLGVTTHLL RLYIQS*RTKGASSFQDNPNVIGRQLGGQ IKC*PQQGENMGLYWWECARGDVDI MFEFLIVTTAPEFRSLGK*VNLQPQLKV DKAVAFQNPQTHAIGNLHAAA/YTGN ALANPLYCPDYRIGKVTSEELHYFVQN HFTSARMALIGLGVSHPVVKQVAEQFL NMRG\GVGLSGWQRANYRGGEIREQNG DSLVAHAFVAKSAVAGSAKPNAFVVLQ HVLGAGATMSRGAATTS\HLHQ\AVSQ ATQQP\FDVSAFNARYSDLG\FGIYTISQ GHQLAGDCIKAA\YNQVKPIRSKKPFFP TQGVSAAKNKG*KAGIPLMVQWKSFLK CSPGRKSGSPGLLV/GLVPYMPHTPTVPS SQMDSSGLMLDIN\ARAKKFVFWARSS MGSKFGKFGDITPFCLMEL |
| 772 | 8823 | A | 1719 | 53 | 420 | |
| 773 | 8824 | A | 172 | 1 | 267 | CSAGGPWRAPQPRRFHRRRRPAQLPPPL PLPPLASPRIHNRTFPRPSQRTPPPAALG CPEPGS/RSQGRGHARPPGSGEGDPTVSS PGY |
| 774 | 8825 | A | 1720 | 1 | 1260 | |
| 775 | 8826 | A | 1721 | 403 | 1334 | DTMALTSDLGKQIKLER/EVEGTLQPAT VDNWSQIQSFPAKPDDLLICTYPKAGTT WQEIIVDMIEQNGDVEKQCRV\IQRH\HP FIEWARPPQPSGVEKAKAMPSRILKTSP FHFSWLPPSFWEENNCKF/LFMLASEIAK D\CMVS*YHFQORMNHMLPDPVTWKEY F\ETFINGK\VFWSWFDHVKG\WW\EM KDRHQ\N\LFYEDIKRDPK\HEIRK\VMQ FMGKKVE*TVLDKIVQETSFEKIKENPM TNRSTVSK\SILD\QSIFPPFMRKGTVG WENHFTVA\QNERFDEIYRRKMEGATSV NFCMEL |
| 776 | 8827 | A | 1722 | 2 | 645 | HGIAHQIQPSYKTIIGGRDDSFHTFFSET GAGKHVPRLLL*NWKPTVMDEVRTGTY CQLFHLEQFITARKIAANNYARGHYTIG KEIIDLVLDRIKLADQCTGLQGFLVFHS FGGGTSGGFTSLLMERLSVDYGKKSLE FSIYPAPQVSTAVVEPYNSILTHTTLEHS DCAFMEEGEFSEAREDMAALEKDYEEV GVDSVEGEGEEEGEEY |
| 777 | 8828 | A | 1723 | 87 | 1531 | SLATMRECISIHVGQAGVQIGNACWELY CLEHGIQPDGQM/TQVTRPLGGGDDSFN TFFSETGAGKHVPRAVFDLEPTVIDEV RTGTYRQLFHPEQLITGKEDAANNYARG NYTIGKEIIDLVLDRIKLADQCTGLQGF LVFHSFGGGTSGGFTSLLMERLSVDYCK KSKLEFSIYPAPQVCTAVVEPYNYILTD HTTLEHSDCAFMDNEAIYDICRRNLDI ERPTYTNLNLISQIVSSITASLRFDGALN FTLTNFGTKLVFPFRIPLPFCPIMPPVHFA *ERPPMNSFSVAREITQMLCFEPSPTRLVK \CDPRPWVKS\WPCCLVATGGDVVPKRC QMLPIAHPSPKRTIQFVDWCPTGFKVA GINYQPPH\WVPGGNLA\KVTR\EA\VCML SKHHSPFAEAWARPPTSFDLMLCQACP FVHWYLG\EGMEEGEFSEGRER*GCPFR KDYEK\GVDSVEGEGEEEGKILIIHSLF G |

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| 778 | 8829 | A | 1724 | 84 | 1560 | EATTSPLRLRHQLGSREAATMRECISIHV GQAGVQIGNACWELYCLEHGIOPDGQM PSD/RKPLGEGDDSFNTFFSETGAGKHVP RAVFVDLEPTVIDEVRTGTYRQLFHPEQ LITGKEDAANNYARGHYTIGKEIIDLVLD RIRKLADQCTGLQGFLVFHSLGGGNWV LVPPPPCLQLGGGGAGKRLSVDYQGQEV SWEFSIYPGAPRFPQPVVEPYNFHPTNPT PTLGAL*LCPSWVDNEAIYDICRRNLDIE RPTYTNLNRLLIGQIVSSITASLRFDGALN VDLTFQTNLVPYPRIHFLGHIMPPVIFA EKAYHEPAFL*QRSQMLCFEPANQOMV KCDPRPGKYMLCCLLYPAGDVVPQRISF LPLPTIKTQ/RLTHFLDWSPTDFKLVINY QPPTVVPGGDLTKVQRAVCMLSNTVTAI AEA WARLDHKFDLMYAKRAVFWHYVG EGMEEGEFSEAREDMAALEKDYEVEGV DSVEGEGEEEGEEY |
| 779 | 8830 | A | 1725 | 153 | 380 | EYKTONRFELRSPRLDCSGAISAHCNLC LPGSNSHSAVASK*AGITGMHHAWDN FCILFSRRWGFCHVGQGW |
| 780 | 8831 | A | 1726 | 14 | 322 | IFSSEPLEGRPGRPGGARAACQEGAGK AGAAGD*PSP/PG*GHAAAPKCREFGHN QIDAGWNQRP/GKPGLVPMWEPCQPSC PLELSEFPPGAHSSWTSNSIY |
| 781 | 8832 | A | 1727 | 605 | 3133 | DSRGQEG*RTGAPHMGDKGPGVSGPPG FQASIKFCGQNFSPITLGPFGP/WGGC GQALSPSGVPGLEGVSPTRAKGWRFP KAPETLNERQIYPNAPPS*AG*GHADTE GQDRTPHLLGANSSGHLCCQLPF*SASIG GAGRD\SQGLSRAFSSASKHVPASAGTF *HSFSKG*VSKTTTTNAGNALFPMGSSK TKKPNSHQRGQMGS*GRNPPSLGRAPAP LPEREAPIAPQLGPSAAGTSRQVGQKSS TSP/PPGRGGNIEP*TQEERRKEKMKKAT GLSKHQPAQFIQNE*NLKGAGEF/GP/SGL AGSQNPSSKLQQLGGKC*EQRL**GAG PDCSPLGKHTP*RSPSPLPRTGDASRGIS* GFSGKEASFGPGQPSTCLSGIRPSLGS*P LGQ*RTL/PCSNLPAGK/RNCLG/PPGLGR GHGRCSDSLQHGQSQT*AGANWRKRQ/PP VPAGLLDPGLTAQQAQVTRSPWEGAQ RGGEQPVGLCWG*ACAKCRLQSGRFT AGGRQGSRGVWVGSEVMAPRKRPPAG PPGHKEGTAEAVSSQTVTGRIPEAVWP HHHQGKGTTEQEPCC*DVTKASAPGVS GDTG/MRGPLQPQASPNI*GAAACPFSSQR AGSSLQQRSLPAPSCPQAA/RGPPGLPG LPSSGSEENIHSGAWALVQGEPSMDGR GNGMMLRGVWTGVHGGGMDMWRRG DLKGKVPHGMIQVWTP/G/DKQDSSPAR TPAPQWLSITTGS*TPE/GDPGGKLDAAQ RGRAIAAHEQPEVAVLGVA/GHL*SPGS ARSSPRWHPHRSACRPPRSGGSPPSPSSA *KSDRTDAGAGVAAAASPGAGAPAHCP QGPPRSCQGPQR |
| 782 | 8833 | A | 1728 | 1096 | 1748 | ELFPPTSTIALAQLRALTAQAGQPLTQVN QGAFSMPLWVLDPRERGDLEKIPSFLLL WGWAHLGFQHEALWALGCAFIERGG REAFLGPEMFWSGGFAHPCP*THQFWPG EPQ/EV*GGRHCGKAPREKWPALAPTFQ KEKPVVPVTPEAIPVCQEGAPPGTAKSIH CPPEIHTKEACVPVPGKEENVPGKRKIWS KKRDRQGRAQESRIQGSSEIP |

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| 783 | 8834 | A | 1729 | 162 | 788 | QKLFFLAENIIRSFRTVKLSFVLNQMM CFISVFDVFSFFSPGFTSFVISLCFGFAAN LIGLGLAAKALDSGAFFSFVLSPSFPLPS CPHHFTLLKVMNTRSEIPFLAPSTLGFFE MESHCVTQ/CSGA/ISAHCSLHLP*SNFP VSAS*VAGTTGASHDNWLIFLFLVETGF HHADQGGKLF*PQIHLPLGLPKWLGLQC EPCGWL |
| 784 | 8835 | A | 173 | 218 | 430 | |
| 785 | 8836 | A | 1730 | 158 | 468 | TGAGHGGLMPVIPSHFGRPWADHLRS GVRDQPGQH*NPVSTKNTKIGWA*WR APVIPAT*EGLRQGESLEPGRAEGARRC HYIPAGGDRVRLCLKKKKLN |
| 786 | 8837 | A | 1731 | 1 | 1161 | |
| 787 | 8838 | B | 1732 | 1 | 1380 | MDKFLDTYTLPRINQEELESNRPITASEI VAIINSLSSKKSPGPDGFTAIFYWSVGS GQAIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAPNLLKLISNFSKVS NVQKSQAFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLIRDVKDLFKENYKPLLKE IKEDTNKWKNI PCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTILEKNTLKFIWN QKRARIAKSILNQKNKAGGITLPDFKLY YKATVTKTTWYWHQNRDIDQWNRTEPS EITPHIYNILFDKPEKNKQWGKDSLFNK WCWENWLAICRKLKLDLFLTPYTKINSR WIKDLKVRPKTIKLEENLGITIQHIGMG KDFMSKTPKAMATKAKIDKWDLIKLS FCTAKETTIRVNREPTWEKIFATYSSDK GLISRIYNELKQIYKKKQTPSKSGRRT* |
| 788 | 8839 | A | 1733 | 1 | 293 | |
| 789 | 8840 | A | 1734 | 1 | 1183 | MKLKRNNEMSGKALDPREGFCDASYEI QTTIREYYKHL YANKLENLEEMDTFLDT YTLPRLNQEEVESLNRPIGAEIVAIINSL PTKKSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASILIPKGRDT TKKENFRPISLMNTDAKILNKILANRIQQ HIKKLIHHDQVGFIPGMQGWFNIRKSINV IQHINRAKDKNHLIISIDAFAFDKIQPF MLKTLNKL GIDGTYFKI/Y/RDRHFSKEDI YAAKHKMKCSLSLAIREMQIKTTMRY HLTPVRMAIKKSGNNRCWRGCGEIGTL LHWCWDCKLVQPLWKS VWRFLRDLEL EIPFDPAIPLLGVYPKDYKSCCYKDTCH/ IMFIVALFTIAKTWNQPKCPTMIDWI |
| 790 | 8841 | A | 1735 | 66 | 1392 | QVLLSFGTPLVLTTKREKNQIDAINDK GDITTDPTIEIQTSEYYKHL YANKLENLE EMDKLLDTYTLPRLNQEGVESLNRPIG SEIEAIINSLRPISLMNIHAKILNKILGN*IQ QHIKKLIHHDQVGFIPGMQGWFNIRKSIN VIEHINRTKDKNHMIILIDAFAFDKIQPF FMLKTLNKL GIDGTYLKIIRAIYGKPTVN IILNRQKLEAFPLKTGTROGCPLSPLFNI VLEVLAKAIRQEKEIKGIQLGKEEVKLSL FADDMIVYLENPIISAQNLKLTGNFSKV SGYKINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLVKENY KPLLKEIKEDTNKWKNI PCSWVGRINILK MAILPKVIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRACIAKSILSQKNKAGGITLP DFK |
| 791 | 8842 | A | 1736 | 1 | 432 | |
| 792 | 8843 | A | 1737 | 1 | 413 | |
| 793 | 8844 | A | 1738 | 1 | 1401 | |

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| 794 | 8845 | A | 1739 | 1 | 510 | MLEVLAWAVRQEKEIKGIQLGKEEVKLS L*LMSNFSKVSQYKISVQKSHAFVYTNN RQSESQIMSELPFTVATKRIKYLGIQLTR DVKDLFKENYKPLLNEIQEDTNKWKNIP CSWVGRINIVKMAILPKVIYRFNAIPKLP MTFFTELEKTKFIWNQKRAHIAKTIL |
| 795 | 8846 | A | 174 | 9 | 201 | |
| 796 | 8847 | A | 1740 | 1 | 2052 | |
| 797 | 8848 | A | 1741 | 1 | 762 | MNIDAKILNKILAKQIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHINRTEDKN HMIISIDAEKAFDKIQQPFMLKPLNKLGI DGTYFKIIRAIYDKSTPNILNGQKLELMS NFSKVSQYKISVQKSHAFVYTNNRQSES QIMSELPFTVATKRIKYLGIQLTRDVKDL FKENYKPLLNEIQEDTNKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPKLPMTFFT ELEKTKFIWNQKRAHIAKTIL |
| 798 | 8849 | A | 1742 | 1 | 1057 | |
| 799 | 8850 | A | 1743 | 1 | 1380 | |
| 800 | 8851 | A | 1744 | 1 | 862 | MDTFLNTYTLPRLNQEEVESLNRPTGSE IVAIINSLPSKKSPGPDGFTAKFYQRYKE ELVPFLLKLFQSIEKEGILPNSFYEGSIILIP KPGRDPPKKENFRPTSLMNIDAKILNKIL ATRIQQHIKKLIHHDQVGIIIPGMQGWFN PKSINVIQHINRAKDKNHMIISIDAEKAFD KIQQPFMLKTLNKLIGDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTROGCPLS PLLFNIVVEVLARAIQEKKIKGIQLRKE EVKLSLFADDMIVYLENPIVSA*RLNQEE VESLNRPTGSEIVAIINSLPSKKSPGPDGF TAKFYQRYKEELVPFLLKLFQSIEKEGIL PNSFYEGSIILIPKPGRDPPKKENFRPTSL MNIDAKILNKILATRIQQHIKKLIHHDQV GIIPGMQGWFNIPKSINVIQHINRAKDKN HMIISIDAEKAFDKIQQPFMLKTLNKLGI DGTYFKIIRAIYDKPTANIILNGQKLEAFP LKTGTROGCPLSPLLFNIVVEVLARAIQ EKKIKGIQLRKEEVKLSLFADDMIVYLEN PIVSA |
| 801 | 8852 | A | 1745 | 1 | 1551 | |
| 802 | 8853 | A | 1746 | 1 | 947 | |
| 803 | 8854 | A | 1747 | 179 | 887 | |
| 804 | 8855 | A | 1748 | 1 | 1074 | |
| 805 | 8856 | A | 1749 | 1 | 1060 | MDTFLDITYTLQRLNQEEVESLNRPTGSE IVAIINSLPTKKSPGPDGFTAIFYQRYME ELVPFLLKLFQSIEKEGILPNSFYEASIIIP KLGRDTTKKENFRPISLMNIDAKILNKIL AKRIQQHIKKLIHHDQVGFIIPGMQGWFN ICKSINVIQHINRAKDKNHMIISIDAEKAF DKIQRFMLKTLNKLIGDGTYFKWKNIP CSWIGRINIVKMAILHKALYRFNAIPKLP MTFFTELEKTTLKFIWNQKRACIAKSILS QKNKAGGITLPDFKLHYKATVTKTAWG PYDR/DID/SWNQTDLMCAVLPSRYVTL QDSSIL*KMR*VKKLQKSLQADLVQG LRKDVSIT |
| 806 | 8857 | A | 175 | 1453 | 1936 | EVEKHLCCQG*ELLRAQHN*AAACRRPRP PAPGPQCSAGGPMARAPAPQVPPPPPCS A/PPPLPLPAS/HAHPQPHFRHGRSA LLPRPPWAVRSRGALAGPRTRAAAGLR GGAGAAPAPADARFPASSPAE*PKFPQN SARALTGFPRCTDPTVSSPGY |

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| 807 | 8858 | A | 1750 | 1 | 1401 | MSELPTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSWVGRI NIVKMAIMPKVIYRFNAIPIKLPMPFFTEL EKTTLKFIWNQKRARIAKAILSQKNKAG GITLPDFKLYKATVTKTAWYQNRD IDQWNRTEPSKITPHIYNLYIFDRPEKNK QWGKDSL FNKWCWENWLAICRKLKLD PFLTPTKINSRWIKDLNVRSKTIKLE NLGNTIQDTGMGKDFMSKTPMATKD KIDKWDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELQIYK TNNPIKKWARDMNRHFSKEDIYAAKKH MKKCSLSLAIREMQIKTTMRYHLTPVRM AIIKSGNNRCWRGCGEIGTLLHCCWDC KL VQPLWKS VWRFLRDLELEIPFPAIPL LGVYPKDYKSCCYKDTCT/R/MFIVALFT IAKTWNQPKCPTMIDWI |
| 808 | 8859 | A | 1751 | 1 | 1410 | |
| 809 | 8860 | A | 1752 | 1 | 1559 | MDTFLDTYTLPRLNQEEVESLNRPTGSE IVAIINSLPTKKSPGPDGFTAIFYQRYKEE LVPFLLKLFQSIEKEGILPNSFYEAHILIP KPGRDTTKENFRPISLMNIDAKILNKIL ANQIQQHKKLIHHDQVGFIPGMQGWFN IRKSINVIQHINRAKDKNHMISDAEKAF DKIQRFMLKTLIKLGIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTROGCPLS PLLFNIVLEVLARAIQEKEIKGIQLGKEE VKLSLFADNMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTNNRQTES QIMSELPTIASKRIKYLGIQLTRDVKDLF TSVISQVWVGSGLDTSLLQLWVGSGLDISV ILQLWVGSGLDTSVISQLWVRSGLDTSVISQ LWDIAFLSHVPGMLS*KSQVSLATLMQR MSSHGLGQLQPCGSAGYSSHGCFHRLAL NACGSSSAQCKLLVDLPFWGLDGGLLLT AARGHSPGALCVRVPTPHFPSMLP |
| 810 | 8861 | A | 1753 | 1 | 1575 | MNTDAKILNKILANRIQQHKKLIHHDQV GFIPGMQGWFNIRKSINVIQHINRTKDKN HMIVSTDAEKTFDKIQQPFMLKTLNKLGI DGTYLKIIIRAIYDKPTANIILNGQKLEAFP LKTGTROGCPLSPLHKFLDTYTLPRLNQ EEVESLSSPITGSEIVAISS/FTNEKESRTR WIHSRILPEV*GGT/RIKYLGIQLTRDVKD LFKESYKPLLKEIKEDTNKWKNIPC*WV GRINIVKMAILP/KELEKTTLFIWNQKR ACIAKSILIQSKAGGITLPDFKLYKAT VTCTAWYQYQNRDIDQWNSTEPSEIMP HIYNLYIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLDPLTPYTKISSRWIK DLNVRPKTIKLEENLGNTIQDIGMGKDF MSKTPKAMATKANIDKWDPIKLKSFCT AKETTIRVNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKTNNPIKKWAKDMN RHSSKEDIYAAKKHMKKCSLSLAIREMQ IKTTMRYHLTPV |
| 811 | 8862 | A | 1754 | 468 | 4080 | RVRSGTDSIASGPRVLCSTRERRRRRSY LVHRRCVPCGPAVDGVFNLTNDRWFL HINRAKDKNHMISDAEKAFDKIQQPFM LKTNLKLGIDGTYFRIIRAIYDKPTANIIL NGQKLEAFPLKTGTROGCPLSPLLFNIVL EVLARAIQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLISDFSKVSG YKINVQKSQTFLYTNNRQTESQIMSELPF TIASRIKYLGIQLTRDVKDLFK |

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| 812 | 8863 | A | 1755 | 1 | 2882 | MDKFLDXYTLPRNLQEEVESLNRSTGSE IVAIINSLPTKKSPGPDGFTAIFYQRYKEE LVLLLLLKFQSIKEATLPNSFYEAHILIP KPGRDTTKKENFRPISLMNIDAKILSKIL ANQIQQHIKKFVHHDEVGFIPRMQGWFN IHKSKNVIQYINRTKDKNYMIISIDAEGA FDKIQQLFMLKTLTKLIDGTYLKIRAIY DKPTVKIILNGQKLEEFPLKTGTROGCPL SPLLFNIVLEVLARAIQEK |
| 813 | 8864 | A | 1756 | 1 | 1746 | MIISVDAEKAFDKIQQPFMLKTLNKLID GMYFKIIRAIYDKPTANIILNGQKLEAFPL KTGTROGCPLSPLLFNIVLEVLARAIQEK KEIKGIHLGKEEIKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSQYKINAQKSQA FLYTNNRQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYNPLNEIKEDTN KWKNIPCSWSVGRINIVKMAILPKNWKK TTLKFIWNQKRACIAKSILSQKNKAGGIT LPDFKLYYKATVTKTAWYWYQNRDIDQ WNRTEPSEIMPIYNYLIFDKPEKNKQW GKDSLNFNKCWENWLAICRKLKLDPFPL TPYTKINSRWIKDLNVRPKTIKLEENLG ITIQDIGLGKDFMSKTPKAMATKAKIDK WDLIKLSFCAEKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKTNNPI KKWVKDMNRHFSKEDIYAACKHMKKC SSSLAIREMQIKTMRYHFTPVMAIHKK SGNNRDMDEIGNHHSQQTIAMTKNQTP HVLTHRWELNNENTWTQEGEHHTLGPV VGNLKLRLKPKISLS |
| 814 | 8865 | A | 1757 | 1 | 2866 | |
| 815 | 8866 | A | 1758 | 1 | 1285 | MLEVLAWAVRQEKEIKGIQLGKEEVKLS LFADNMTVYLENPIVSAQNLLKLISNFSK VSGYKVSQKQSQALLYTNNRQTESQIMS ELPFTIASKRIKYLGIHLTRDVKDLFKEN YKPLLKEIKKDTNKWKNIPCSWSVGRINI VKMAILPKDIIQENFPNLRQANIQIQR KTPQRYSSRRATPRHIIVRFTKVEMKEK MLRAAREKASHHTYSKIDPILGSKPLLSK CKRTEIITNYLSDHSAIKLEFRIKNI |
| 816 | 8867 | A | 1759 | 2 | 231 | PPSAS/CVQTGPPCHSLAFPPSAPGQEQE GHQLPSHVIPCHLALGTAFPPQPAAMAG WGVSQATYCQELEPPQFPVSSS |
| 817 | 8868 | A | 176 | 5 | 711 | FEALRMIGHLFAKSPYHKGINSKIVART NIKLMVKVVMWKNGEIDTLQIVYGDN APKKSVAVYKCITSLRRSKVLDEACSSR PVTSICKGKINLVYANISIGSAYTILM/EK LNLSKLSTHWMPQ/PVHPDQLKTRAKLS ME/ILNKWDQDPKGFL*KIVTRDRTWLY *YTFEDKAQSKQWLPKGGSGPVKAKAG WSRAKVKA/TTGFWNAQIVLLVDFLEGQ RTITSAYESILLKKK |
| 818 | 8869 | A | 1760 | 1842 | 2096 | CHSQKPQVPPPKPWGSLERPNT*VPAC VLPAPAPARPGQIARQ*PWVAPGTSGQ SRVGRTPGVSSGHGQTLTCPMALLQPLL |
| 819 | 8870 | A | 1761 | 37 | 288 | WGNTGSQVMTTVLNTALLPPKPSMPLPI KHYAIPPPSY/SPHP*PIIPSPTANLESAPP ASAP/PPPLPPPAQLGEAHAPPE*YAIPPP SYSHTRSHPSPAQQQTLQSRHQPLHLSSS ASTLPSWGKLMHHLNNIPQ |
| 820 | 8871 | A | 1762 | 397 | 506 | SFLEDLTGLSNQPATAGANWITRLCTGS P*NV*PPWHMSSGHPEAVSRVCIFNLVG FGI |
| 821 | 8872 | C | 1763 | 291 | 491 | MGADRQTHPQDRWFSHLHLKLLRRSYRI EQPASHSRGRDLNTSLHRLSLCPCHPPLF LTLFLGIMF* |

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| 822 | 8873 | A | 1764 | 630 | 1159 | SFYSALMLSDRKNRGRGRHGLSRRIKR QRKLVEAEAASQACLAGKPGPTPASHP/ PGDGLPCPLSAPTLSPAT/ALPLP/SP* RSP NHSAN/PNPLSPTSSVKHSRCSPPHSALPL STPKATPPSPNHRAGLFSSPLAPMSTS*L LQKNCVLVRAPAPTSYIPVFFMTPAQCP VFLSAQ |
| 823 | 8874 | B | 1765 | 1 | 1359 | MGIKNSKRGSLPLAAPALLKPDTLWSCIF GEGDLGEEDMPPDPQAPSPAILPPNHAF GLWPFYRTQTHPQEAADPAAAYHPEP PPLILAGVRFERSNPALPENGKGAWRGDG VAEGHAALWVLGLRCERSVTAALAART REHDGRWREGAEKGPRRRWVVRAIQTP RLGKALIHCVWTRGSLWVNSSVSAGSER DQRADHAAAQTSACAGAVACGLLLLLLV RGQAWVKKQNLSPETRTKELVVSLMPL PHPGQGHNLASRAKARTQPPVPSGPTHGA GAGESCPCEGRQAGVQTLGIPFAKPPPL VRCDLHPLSPLNLGVVWGNHPSGHIY TPAHSHEGSNLPWHRQARNRQLGYLDQ VAALRWVQQNIPTLEATLTVSPFLASLR WHECVFACCVPHIPRTFHGAIMESGVAL LPGLLPAQLMSSPRFGPCVFYEFQHQP S WLKNIRPT* |
| 824 | 8875 | A | 1766 | 2 | 597 | RWLIPKVMRIYDTQKKMDREASQAALQ KMLTLLMLPPTFGDLLREEYIGDNGDPQ TLQAQFQEMMADSMFVIPALQVAHFQC SRAPVYFYEYFQHQPWLKNIRPPHMKAD HVKFTEEEELSRKMMKYWANFARNG NPNGEGLPHWPLFDQEEQYLQNLQPA VGRALKAHRLQLWKKALPQKIQELEEP EERHTEL |
| 825 | 8876 | A | 1767 | 3 | 1867 | IHPSPRLGKALIHCCSFPQPLGEQQRV RRQRTETSEPTMRLHRLRARSAGACGL LLLLVRGQGQDSASPIRTHTGQVLGSL VHVKGANAGVQTLGIPFAKPPPLGPLR FAPP*SPLESWSGVRDGTTHPAMCLQDL TAVESEFLSQFNMTFSDSMSDECLYLSI YTPAHSHEGSNLPVMVWIHGGALVFGM ASLYDGSMLAALLENVVIQLPPGGV LGFFSTGDKHATGNWGYLDQVAALRW VQQNIAHFGGNPDRTVTFGESAGGTSVSS LVVSPISQGLFHGAIMESGVAL/LPGLIA SSADVISTVVANLSACDQVDSEALVGCL RGKSKEEILCN*TSLFKMIPGVGGMGVF LAQGTPRELLASADFQPPVSIQVNNNE FGWLIPKVIEDLIDNPEGKLGQERASQV VLQKMLTLLMLPPTFGDLLREVYIGDNG DPQTLPKRKFKQKMMADSMFVIPALQV AHFQCSRAPVYLTSSQHQPWLKNIR PPHMKADHGDELFFVFRSFFGGNYIKF TEEEELSRKMMKYWANFARNGNPNG EGLPHWPLFDQGGAITLQNLQPAVGP GL*KAHRLAQFWKALPQKIQELEEP RHTEL |
| 826 | 8877 | A | 1768 | 2 | 288 | CPNSSPGSASEVGCARSQSSLLRSLPRC DGWPWAEAGA/MCAGRNLTSVGRY/ YSSR*QDEES*TARHLLCAPQTGHQRRR PCRQGRNFCCHIPC |
| 827 | 8878 | A | 1769 | 1017 | 1463 | PRGPWSQGEPKWLLARQAAGCCPPGAC LWGHSPAGACSPCAAKGSRYSRVPASS GTPAGK\GWQLLAREGEQEAGLCIEASQI GVPNSSPRKRQR*DVPDRGSPVC*EVFP RCDGWPAEAGASVQGGTSPPVSFNRM TSASTPNIW |
| 828 | 8879 | A | 177 | 1 | 152 | PGAMAVLLETTLSDVVIDLYTEERPRGE A*APLTCRRGPRACLPTFPSLR |

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| 829 | 8880 | A | 1770 | 1 | 1181 | MAAYKLVLIQHGESMWNPENRFSSWYN TDLSPAGHKEAKCGRQHSGLIGLNKAE TAAKHGEAQVKIWRHSYDVPPPLMEPD HPFYNISKDRRFANLTEDQLPSCESLKDT IAKALPFWNEEIVPQIKEGKQPKYPFEKR LEVVNHYFTTDDGYRIISARFGVPRTQV RTWVALYEKHGEKGLIPKPGVSDAPEL RIKVVKAVIEQHMSLNQAAAHFMLAGS GSVARWLKVYEERGEAGLRALKIGTKR NIAISVDPEKAASALELSKDRRIEDLERQ VRFLETRLMYLKKLKAHAHPTKKAEEIP RSTFYHKLKALSKPDKYADVKKRISEIY HENRGRYGYRRVTLHLHREGKQINHKA VQRLMGTLSLKAIAIKVKRYRSYRGEVG QTAPNVLQRDFKATRPNEKWVTDVTEF AVNGRKLYLSPVIDLFNNEVISYLSERP VMNMVENMLDQAFKKLNPHEHPVLHS DQGWQYRMRRYQNILKEHGKQSMSRK GNCLDNAVVECFGTCLKSECFYLDSEFSNI SELKDAVTEYIEYNSRRISLKLKDLIAS CLTVQLFGVSTLEGLSEEAIMELNLPTGI PVVYELDKNLKPIQFLGDEETMRKAME AVAAQVEDEYNLYGDVTTVSSLTPEKL APEVKENVPERLNLQVGGRSRTNLNR VRVPIHKHPSIRDPSQASLNKLTDKMD SLWLKSKNRPKGPWKGEAVKLFVSLE NAAKPVFLQPSQRRVPGNNGSWEFPS*S RKSGISIGAVKRPTH*GS*KASSIS*NAAY VSKKAESLSSSHEKGCSDTAQYVLLSSK GSQQA*QVCGR*KAY**DLSRE*RPRIIP* GNAVSSSRRETD*P*SCSAPDGNPLT*SS D*GOAIPLLQRRGRANRP |
| 830 | 8881 | A | 1771 | 362 | 551 | DRLDPHSAAH*GAKSSPLAATSQWHL ALSRGSGSLYKCTEVKQMSNS*PASRSA CPPPSPPR |
| 831 | 8882 | A | 1772 | 2318 | 3200 | FMPLHLDDGGYCSAEGFSSRYEHGLMK DLSRGSLSPPGERACEGVPSAPQNPQR KKVSLLEYRKRKQEAENSAGGGGDSA QSKSKSAGAGQGSSNSVSDTGAHGVQG SSARTPSSPHTKFFPSHSSMSHLEAVSPS DSRGTSSSHCRPQENISSRWMGSHISRTT P/SKEGASPRSSEAA*G/SAQKGESPTWE SNITEKSDPADGEGPETLSSALS*RSNSF TALSRYSYQT/PLAPFTGTPGYFSSQPHS GNSTGNSLPRRSCPSAASPTLQGPSDSP TSDSVSQSSTGTL |
| 832 | 8883 | A | 1773 | 53 | 1025 | GTRHLEAVSPSDSRGTFLSHCRPQENISS RWMVPTSVERLREGGSIPKVLRSSVRVA QKGEPSPTWESNITEKSDPADGEGPETL SSALSKGATVYSPSRISATSSCSVIVLGQN HKASFSRVPPSEDIPTQSPGYSYRTTAL RPGNPPSHGSSSESSLSTSYSSPAHPVSTD SLAPFTGTPGYFSSQPHSGNSTGNSLPRR SCPSSAASPTLQGPSDSPTSVSFVSVAQE L*ASTS/SSSEI/PRSSLAIRLTD*SVCPVLG QSAGYQGLQGICGFQFTALPHTVGVGFS TQYRIPSPLQGSRSQDSRRGLFLGLLGF GKQN |
| 833 | 8884 | A | 1774 | 1 | 414 | AENTILSLMFSGKSWGSLSECCALLPGT PTATRLQSLTRRSSLKRG*GPQIPAARP REGSRIGTCTSS*PGLRTEAHRSLRNRQA GVSSPFQLSPALKPRKSPQATGQRP*G QWGQKSGSALLPTNTTHVEA |
| 834 | 8885 | A | 1775 | 1 | 458 | ENTILSLMFSGKSWGSLSECCALLPGTP TATRLQSLTRRSSLKRG*GPQIPAARPR EGSRISQNVGDGGKENRYRGFGGPPGT KSDPGHQHG*GGEGLWGSWRSGKSGPAI ATGAIASPATQLLRVNPDTGDWDVYFLL TLVSGRLRTGA |

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| 835 | 8886 | A | 1776 | 1 | 1387 | HSMGWKEHVDREGGHTKGMVFVSLQPA CWLPRERPFQLRLCLIEDPLRLCGQGR GRGQETTSGLILLSHVGTFLRDRWTLTSL WPCPRALLVFLSHSCEVMGAGAPGVSLP EGQLSPLPWLVQGRSSRRAPDSGGPLG PPGLADVSMRGRAPGTSMCGS/RSTPVPP QSPGG*VSMPATPGIGFLCRLPHKSAPEG P/GGFGFLFFIKHLKQHCSLPSRGLSITA STCVVLVGSKADDPDFCPHCPHPLTSS LRGAFSR/PSEQGRAGRGLESSRLSVSQ SCEASVLRPESRGSTHP/ISPVSGFTLRW VAGEAIAPVAIAGPAGAGLRIGLRGALRP AHGHPRL*SPGNPISPSSTSPCLMPQGH CLPAGPPNPRCLSSFPSPTLVLTNPASLS GPGCRDLGSLKSLKSNFCGSDSEAELL VGVPGRAPHSLLKLPQLFPENIKLRIVFS AKKKKK |
| 836 | 8887 | A | 1777 | 46 | 591 | LSPPKPQKQSQEQNPFCQRWALGKQLGP PQGGQEG/QGPPDSLVLPGV/PPVPLFVG GNLPHPPPPVQPQRNKGRQTEGSCSPFF KGQHNS/PCGPQPS*AHPLRHGSGDQAQ PTSAP/PPCR/PES*PQADEMPTPCCHNTG KALGPPSQEGMEPGGPQPGPSRSTQSSV AHLTSGTAVRPGLGSP |
| 837 | 8888 | A | 1778 | 1412 | 1673 | KRCPINRFPLECLPLPHLMGIPPEGHFHH PLMGE**NPPCSIQDPHCVTYFETPPVNL CPSTRPEVGVWEGGPSSPFAFEAPGLKG |
| 838 | 8889 | A | 1779 | 646 | 1098 | MVELLVTFPPFSQLQLYFQLTYSFTELL KVPLMVLFGMPMKKHFLKPTVSDQW ENNRKLRRI*SR*FSCRKV*V*IACHKF CLVLREA/HMHWLILCAKKRF/PPLKKLT WLGVMVSHTCNPSTLGG*GR*TA*TQEFK TSLDNMVKPHLF |
| 839 | 8890 | A | 178 | 1112 | 2085 | RHSHAVQKKPLSGGGAGAMAVLLETTL GDVVIDLYTEERP/RCQLYGDQASFEAE KVPRIKHKKKGTVMVNGSDQHGSQF LITGENLDYLDGVHTVFGEVTEGMDIHK KINETFVDKDFVQDIRINHTVILDDPF DDPPDLLIPDRSPEPTREQLDSGRIGADE EIDDFKGRSAEEVEEIKAEKEAKTQAILL EMVGDLPDADIKPPENVLFCVCKLNPVTT DEDLEHFSRFGPIRSCEVIRDWKTGESLC YAFIEFEKGGGAYGKTPATRPFGSWPF AGLLTCSFLRYPLILWITVLPPLSELPL AAAERPSAASQ |
| 840 | 8891 | A | 1780 | 109 | 943 | WAKLGKGPAPK*PQALGASAPSAlyPR HVAPARAPGRTKGAGSSCRNSPRQVVRP QPWQWGGGAQSDVSP*GQTPRGGSFER SSSCSGHTGLVGKERRPLSLEGP*/SPEDP PRARHGGPQGREHPPWFSRPLCPEAGP EPRAPAWTSDSIGERSTGG/PSRPASKGP VPSAQRAGQTPGNPEAAGSLSLPCRALP QGREAPQPQPPPYLPLKLERGILVFALSK IFKN |
| 841 | 8892 | B | 1781 | 98 | 195 | GLCLGQEVGQEDLVMQTLPGVGLGLDR DEEVTG* |
| 842 | 8893 | A | 1782 | 2 | 1556 | |

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| 843 | 8894 | A | 1783 | 2 | 1928 | ARGAPRLRAAGAPSSSARVSLSVSPSPA MAALTRDPQFQKLQQWYREHRSELNLR RLFDANKDRFNHFSLTNTNHHGHLVDY SKN/LLVTEDVMRMLVGLWPKSRGVEA ARERMFGVEKINYTEGRAVLHVALRE TGFKTHPILG*NGKDVMPEVNKVLDKM KSFQCRVRSGLKGYTGQRPFTDVINI WIGGSDLGPLMVTEALKPYSGGPRVW YVSNIDGTHIAKVTLAQLNPESLFIASK TFTTQETITNAETAKEWFLQAAKDPSPA VGEDFLFALSTNTTKVKEFGIDPQNMFE FWDWVGGRYSLWSAIGLTSIALHVGF NFEQLLSLAHWMDQLFRDAPGRKNAP VLLALLGIWYINCFGCETHAMLPYDQYL HALLRTSSRAITWSPMGNTSPNLEPVWT TRQAPLCGGSQGPMSMLFTSCIHQGT KMIPCDFLIPVQTOHPIRKGLHHKILLA NFLAQDRGP**GGKSTEEGPKGASRVAG KSPEDFERLLPHKGL*KGNRPVTFYVFT KVVTPIQLGAWSPMYEHKILRFRVIWADI NSF*PSGELELGKQPGRLKLEPELDGSA QVTFQDVSTNGLINFIKAAAARGPRVPINS VLICSLCDSHFFSSLSFSPKPELIVP |
| 844 | 8895 | C | 1784 | 127 | 435 | MAASXNPEVLDITEETLHSRLEGVRNV ASVCLQIGYPTXASVPHSHNGYKRVLAL SVETDYTFPLAEKVKAFLADPSAFVAAA XLGCCHHSCSXCCCSPS* |
| 845 | 8896 | A | 1785 | 112 | 1161 | RTAVMPREDRATWKSNYFLKIIQLDDY PKCFIVGADNVGSKQMQQIRMSLRGKA VVLMGKNTMHAQAPFEGTL*NNPSLWR KLLPHIRGEFGLLFHPGRTLTEIRDMLL AQ*GCPAAARPGAICPHVKVTVASPRTL GLGPEKTSFFPGL*VSPTKNLQGAPIENP EVNVPAESRTGDQSGEPSESHGWLNML NISPFLLGWVIPARCSTNGQHSKPLK VLGLFTGGKLLQFSAFLGGVSRKCLPSV CLPELAYPNCCNQYPSIINGYKRVLAL SCGDGITPFPLAEKVKAFLADPSAFVCC CNLWVAATTACFA/AAAAAPAKVEAKE ESESEDEDMGFGFLD |
| 846 | 8897 | A | 1786 | 2 | 355 | RSITCKTEARMMLLAWVQAFVLSNMMLL AEAYGSGGCFWDNGHLYREDQTSAPAG LRICLNWLDAQSGLASAPVSGAGNHSYC RNPDEDPRGPWCYVSGEAGVPEKRPCE DLRCPGGRI |
| 847 | 8898 | A | 1787 | 1 | 771 | MLLAWVQAFVLSNMMLLAEAYGSGGCF WDNGHLYREDQTSAPAGLRCLNWLDAQ SGLASAPVGYCRNPDEDPRGPWCYVSG E/AGVPEKRPCEDLRCPETTSQALPAFTT EIQEASEGPGADEVQVFAPANALPARSE AAAVQPVIGISQVRMNSKEKKDLGTLG YVLGITMMVIIIAGAGIILGYSYKRGKDL KEQHDQKVCEREMQRITLPLSAFTNPTC EIVDEKTVVHTSQTTPVDPQEGTTPLMG QAGTPGA |
| 848 | 8899 | A | 1788 | 48 | 375 | KGLIKPFGHRTPERKK*LAQGRKQATGM ARAQLPDGAQHFTALC*QLSRASNL*C HTQEALAPSHKASFSEPHLPMGRRVN GAFYGAIWFGDLNLKWSGCGNDAG |
| 849 | 8900 | A | 1789 | 6 | 902 | LQGWDEAEPPPRGPRNLNTRGSITCKTK EARMMLLAWVQAFVLSNMMLLAEAYGSG GCFWDNGHLYREDQTSAPAGLRCLNWL DAIQAGLASAPVSGAGNHSYCRNPDEDP RGPWCYVSGEGGVPEKRPCEDLRCPVE TTASKALPAFTTEIQGNVLKGPSADEVQ VFAPANALPARSEAAAVQPVIGISQVR MNSKEKKDLGTLGYVLGITMMVIIIAG DGILGYSYKRGKDLKEQHDQKVCERE MQRITLP*SAFTSPTCEIVNEKTVVHTS |

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| | | | | | | QTPVDPQEGSTPLMGQAGTPGA |
| 850 | 8901 | A | 179 | 3 | 492 | GGGAGAMAVLLETTLFYVAIFLYTEKR PRACGNFLKLCRIKYNYCLIHNVQRDFI IQTVDTTGTGRG*ESIFGQLYGDQASFFE AEKVPRIKHKKKGTVSMVNNGSDQHGS QFLITTGENLDYLDGVHTVFGEVTEGMD IKNINETFVDKDFVPYQDIRIN |
| 851 | 8902 | A | 1790 | 1 | 1995 | LGRPTRPAPTFWAVAVRTRCLAERRQE LMGALCYPPQGDRLQKSWIFRPVMA DKLTRIAIGNHDKCKPKRRQECKKSCP VVRMGKLCIEVTPQSKIAWISETLCIGCG ICIKKCPFGALSIVNLPNLEKETTHRYC ANAFKLHRLPIPRPGEVLGLVGTNGIGKS TALKILAGKQKPNLGKYDDPPDWQEILT YFRGSELQNYFTKILEDDLEAIKPQYVD QIPKAAKGTVGSILDRKDETKTQAIVCQ QLDLTHLKERNVEDLSGGELQRFACAV VCIQKADIFMFDEPSSYLDVKQRLKAAIT IRSLINPDRIIVVEHDLVLDYLSDFICC LYGVPSAYGVVTMPFSVREGINIFLDGY VPTENLRFDRASLVFKVAETANEEVK KMCMYKYPGMKKMGFEFELAIVAGEF TDSEIMVMMLGENGMGKTTFIRMLAIGS LKPDEGGEVPLNVSYKPKISPKSTGS VRQLLHEKIRDAYTHPQFVTRL**KPLQI ENIIDQEVQTLSSGELQRVTLAL*LGQN LPDVYLIDEPPAIYLDSEQRMAARVV KRFIPHAKKTAIFVVGWTFIMATYLAAD RVIVFDIGVPSTKNTVANSPTLLGWA*I NFWSSAWKFTFQEELQNTYWPRINKLI SLEDVDQKKSGMYFFLDD |
| 852 | 8903 | A | 1796 | 1217 | 2829 | GARSEAAEFQSSASCRRLRGGGGPGTPG RGGALLASLLPPCRTPPDPPDGSCCTR LLSPLGKLSAPPRPRPLFVVAQAGHAPQ GLLPTSRPAAPATAGSRNMSTLLSAFY DVDFLCKTEKSLANLNLNMLDKKAVG TP/VAAAPSSGFAPGFLRRHSASNLHALA HPAPSPGSCSPKFGAANGSSCGSAAAG GAVGGRRTALLNKENKFRDRSFSENG RSQHLLHLQQQKGGGGSQINSTRYKTE LCRPFEESGTKYGEKCQFAHGFHELRS LTRHPKYKTELCTFHTIGFCPYGPRCHF IHNADERRPAPSGG/ASGDL/RPTSRTPPP PSCSSASSCSSASSCSSASAATPSGAPT CCASAPAAAAAALLYGTGGAEDLLAPG APCAACSSASCANNAFAFGPELSSLITPL AIQTHNFAAVAAAAYYRSQQQQQQQGL APPRAP/APPSATLPAGAAAPPSPFSFQL PRRLSDSPVFDAPSPDLSLDRDSYLSG SLSSGSLSGSESPSLDPGRRLPFISRLSISD D |

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| 853 | 8904 | A | 1797 | 731 | 2553 | GARSEAAEFQQSASCRRLRGGGGPGTGP RGGALLASLLPPCRTPPDPPDGSCRCRTP LLSPLGKLSPPRPSVIRGGSPATPPQG LLPTSRPAAPATAGSRNMWTLVSAFYD VDFLCKTEKYLANLNLNNMLDKKAVG TPVAAVAPSSGFAPGLRRHSASNLHAL AHPAPSPGSCSPKFGAANGSSCGSAAA GGPTSYGTLKEPSGGGGTALLNKENKFR DRSFSENGDRSQHLLHLQQQKGGGS PDQIPTRYKTELCPFEERARAQYGEK CQFAHGFHELRLTRHPEVQDRSCAAP FHTIGFCPYGPRCHFIHNADERRPAPSGG ASGDLRAFGTRDALHLGFPREPRPKLHH SLSFSGFSPGHHQPPGGLESPLLLDSPTS RTPPPSCSSASSCSSASSCSSASAASTP SGAPTCCASAAAALRLLYGTGGA*DLL APGAPCAACSSASCANNAFAFGPELSSLI TPLAIQTHNFAAVAAAAYYRSQQQQQQ QQQGLAPPAQPPAPPSATLPAGAAVAPP SP*PFSQLPRRLSDSPVFDAPPSPDLSLSD RDSYLSGSLSSGLSGSESVPFDPGRRLP IFSRLSISDD |
| 854 | 8905 | A | 1798 | 146 | 403 | RKLDVYFEYEEKIMSKTTLDKSLDDIISD PDAGTPEDKMRVFLIYYISTQQAPSEAF TKMASAPASYGSTTTKPMGLLSRVMT G |
| 855 | 8906 | C | 1799 | 47 | 235 | MXVXCNIQXLVSRAINRPDITDTEME TVMDTIVDSLFCFFVTLGAVPIIRCSRG SSKKW* |
| 856 | 8907 | A | 18 | 246 | 730 | SSIMTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPE/RS*VFINSAGQKSADT GWSSSKPQN*QLSSTGAALPLASLSRER AWVDDGKHRLTTPMTVPQRAVQQL*E TSG**DWRQKVQIFQQA*VGMIPSHSQ FLOREDVIMLRPFGLHLSWEENG |
| 857 | 8908 | A | 180 | 1 | 451 | MGFRHVGQAGLELLTSGDLPASAYQSA GITDVSHCAQPASPLSYFLQALKHEFVV RHLTPGHLDTQTPDTKKPGHPDTQTLDT QTPSHLTSRHPDTQTADTQTPDTQNLTP GPPDT*HPDTWHLTPDTQTPGHPTLRHP DTQIPRHPET |
| 858 | 8909 | A | 1800 | 48 | 2100 | PAPGLPVLPRVEVFLEEPGSGSWEPRWR RRRQRQQQQQPSFRKDSQLSCVYCLS MCLILKTAQEHYPYGRYSMLMHRFGQDIFS PLLSVRELDMGITLHLLHSDRDPIDV PAVYFVMPTEENIDRMCQDLRNQYES YYLNFISAISRKLEDIANASVRGLSAIVT QVAKVWDQYLNFTLEDDMFVLCNQN KELVSYRAINRPDITDTEMETVMDTIVDS LFCFFVTLGAVPIIRCSRGTAEMVAVKL DKKLEENLARDARNSLFYRVDTLGAGHF SFQRPLLVLVDRNIDLATPLHHTWY*A LVHVDVDFHLNRVNLEESSGVENSPAGA RPRKRNKKSVDLTPVDKFWQKHKGSPF PEVAESVQQELAESYRAQEDVKRLKSI MGVLEGEDEGAISMAF/SDNTAKLTS SLPELLEKKRLIDLHTNVATAVLEHIKAR KLDVYFEYEEKIMSKTTLDKSLDDIISDP DAGTPEDKMRLFLIYYISTQQARS EADL QQYKKALTDAGCNLNRSYIKQ*RAFT KMASA*AGYGSTTTKTMGLLSRVLNT GSQFVMEGVKNLVKQQLNPVTRILD NLMEKKSNNPRKLMYRYFDPKNACGG NDSSVVPQKLKIPFPRGHSFFVGGEENYI NEYQNLCDYIKGKQKHLAYGCASELFN ATQFIKQLSQLGOK |
| 859 | 8910 | A | 1801 | 1 | 394 | |

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| 860 | 8911 | A | 1802 | 3 | 536 | RIYIFRV/PMASCD/FSIRT/YTNADTPDDF QLHNFSLPEEDTKLKIPLIHRALQLAQR VSLASPWTSPTWLKTNGAVNGKGS LKGQPGDIYHQTWARYFVKFLDAYAEHKL QFWAVTAENEPSAGLLSGYPFQCLGFTP EHQGGSLKAAAGVPRHPDDSYGTSQEK WQLLKEKMFEPPK |
| 861 | 8912 | A | 1803 | 192 | 2035 | GRYLHPCFCLVDPLSFRDSGTPVVFSSSN DPEGMEFSSPSRECPKPLSRVSIMAGSL TGLLLLQAVSWASGARPCIPKSFYSSV VCVCNATYCDSDPPTFPALGTFSTRYGE /STRSGRTGWSLSMGPIQANHTGTGLLL TLQPEQKFQVKVGFGGAMTDAALNIL ALSPPAQNLLKSYFSEEGIGYNIIRVPM ASCDFSIRTYTYADTPDDFQLHNFSLPEE DTKLQDTPGFHRALQLAQRVSLASPW TSPTWLKTNGAVNGKGSLLKGQPGDIYH QWARYFVKFLDAYAEHKLQFWAATA KNEPSAGLLSGYPFQCLGFTPEHQDRIA RDLSPTLANSTHHNVRLMLDDQRLLLP HWAKVVLTDPEAAKYVHGIAVHWYLD FLAPAKATLGETHRLFPNTMLFAEACV GSKFWEQSVRLGSWDRGMQYSHSIHQ QTSWYHVVGWWTAGNALNPEGAGPNW VRNFVDSPIIVDITKDTFYKQPMFYHLGH FKQSSIPEGSQRVGLVAISQKNDLDAVVA LMHPDGSAAVVVVLNRSSKDVP LTIKDP VGFLETISPGYSIHTYLWRRQLDGADYS RRHWGSAGAFKGTESAHTLSVTKEGTA GPV |
| 862 | 8913 | A | 1804 | 113 | 1799 | PSAYSYGRYLHPCFCLVDPLSFRDSGTPV LFSSSDPEVMEFSSPSRECPKPSGRVSI MAGSLTGLLLLQAVSWASGG/RPCIPKSF /SYSSVVCVCNATYCDSDPPTFPALGAFS RYKSRSSGHWMELSTG/PIQANCTGTGL LLILQPEFQVKVGFGGAVTDAGALNILA LSPPAQNLLKSYFSEEGIGYNIIRVPM AS*DFSIRTYTYADTPDDFQLHNFSLPEE DTKLKIPLIHRALQLAQRVSLASPWT SPTRLKTRGAGNGKGPLKGQPRDIYHQ TWARYFVKFLDAYAEHKLQFWAVTAENE PSAGLLSGYPFQCLGFTPEHQDRIARDL GPTLANGTHHNVRLMLDDQRLLLPHW AKVVLTDPEAAKYVHGIAVHWYLDFLA PAKATLRETHHLPNTMLFAEACVGSK FWEQSVRLGSWDRGMQYSQSIKKLPV PMWVGWEPNW/ITPSL*NITQATRFNKQ PMFLPPLANFSKFIPVGSQRVGLVAISQ KNDLDAVALMHPDGSAAVVVVLNRSSK DVPLTIKDPVGFLETISPGYSIHTYLWR RQ |
| 863 | 8914 | A | 1805 | 22 | 424 | ALGMAHITLFFFLLFCDSLALSPRLQC SGTISAHCNLPVPGFKQFSCSLGSDY RCMPPC/RWLTFFVLFVETGFHHVQAGL ELLTSGDPPALA/FPKC*DYRRDPRAWA LFVFLT*FFSKLYHKAKEKWS |
| 864 | 8915 | A | 1806 | 14 | 253 | LIPCGPQLFNCLSL*PGFWAMVKFAWVQ YVRSCLSSSGCLKESRSSCESGGDHHPL SSTSLPLSLFMLCKEVLLESGR |
| 865 | 8916 | A | 1807 | 318 | 455 | |
| 866 | 8917 | A | 1808 | 1960 | 2150 | CFVTSNLKCSK*GRAWWFIPVISTLWEA KVGGSLPRSLRLQCAMIAPLYCSLGD VRPYLLK |

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| 867 | 8918 | A | 1809 | 2 | 1345 | GVVPPGLLAGEGVCQLLRHSSPGRCLLK SRARGSVIMSRYGRYGGETKVYVGNLG TGAGKGELERAFSYGPLRTVWIARNPP GFAFVEFEDPRDAEDALRGLDGKVICGS RVRVELSTGMPRRSRFDRPPARRPFDPN DRCYECGEKGHYAYDCHRYSRRRRSRA ENLRR*SP*Q*IWLTIGAPLRFKRNTRLT TFPTRKIFLRQSSLTWLIWLSV*SSLD*RK HLDAAIGYRYF*IV*Y*TMGQRGSTCKL ARFMLNTHYSVLYVVMSCNSAFNKSF FR**KKKYSTTNRPVYFQMRH*I*IVLR FDFSRGTQTLKNELLSLFFL*LEK*SR RSHSRSGRRYSRSGRRSRSGRRSRASPR RSRISLRRSRASLRRSRSGSIKGSRYFQ SPSRSRSRSRISPRSSRSKSRSPSPKRS RSPSGSPRRSASPERMD |
| 868 | 8919 | A | 181 | 143 | 647 | LRSRCVQIQGSPATEPVSGSHCADTGLVI RGGALSAHAIAPEGQRLSHALHTASAYIN SGRMWDTVHLPQKRCVRPRPQGRV RTP RTRATH/NRVVGARRGTPQRYTG/WGRD *EPSLSQLPQNGDLLAARRREHPACSTG CTSGARVRSRVWRAGQALVPGCAGCAY ILH |
| 869 | 8920 | A | 1810 | 1 | 840 | VVPPGLLAGEGVCQLLRHSSPGRCLLK RARGSVIMSRYGRYGGETKVYVGNLGT GAGNGELYRVIR*YGPLRTVWIARNPPG FAFVEFEDPRDAEDAVRGLDGKVICGSR VRVELSTGMPRRSRFDRPPARRSFDPN GCYECGEKGHYAYDCHRYSRRRRSR FRSHSRSGRRYSRSGRRSRSGRRSRAS PRRSR/SPISLRRSRASLRRSRSGSIKGS RYFPIPRRRSRSKIPGLFHGPRSSRSKSR PSPKRSRSPSGSPRRSASPERMD |
| 870 | 8921 | A | 1811 | 20 | 701 | DHASGQSTASSGPDVSGQLQPSQPNAD QGKLTMTMRIA VICFLLGITCAIPVKQAD SGSSEEKQLYNKY PDAVATWLNPDPSQ KQNLAPQNGCVL*RNQ*L*TRITLPSKS NESH DHMDMDDD\EGD\DDHVDSQDSI DSWDSDDVDDTD\DSHQSDSHHS\DES DELVTGFSTDLPA TEVFTPVVPTVDTYD GRGDSVVYGLRSKSK\KFRRPDIKYPDA TDEDI |
| 871 | 8922 | A | 1812 | 121 | 1206 | LIAGSTHACAHASGRAQHRRDQTRLKAS CSLLSQTPTKENSLPRELPVICFLLGITC AIPVKQADSGSSEEKQLYNKY PDAVAT WLNPDPSQKQNLAPQITLPSKSNESH HMDDMDDED\DD\DHVGTARDSIDSND S\DDVDDTD\DSHQ*WSLHHS*WNLDE LVTGFFPTGPCGNRSFSIPVCSPTVDY DGRGDSVVYGLRSKSK\KFRRPDIQYPD ATDEDITSHMESEELNGAYKAIPVAQDL NAPSDWANRGKDSYGTSKLD*QSAETH R\HQQSRLYKRKANDESNEHSDCDW*A RTFPKVSRE\FHS\HEFSS\HGDFACL*PPK SKEEDNTPLEFRYSPGIRMWHFWGSI |
| 872 | 8923 | A | 1813 | 171 | 459 | |
| 873 | 8924 | A | 1814 | 1 | 235 | |
| 874 | 8925 | A | 1815 | 292 | 1396 | AQATGPYSRICACAKGAMAASCVLLHT GQK\MPLIWSWGTWK\SEPGQVKA AVK VLPLALGYRH\DCGVY\GNELEIG\EAL KGRTVGPGKAGCLGRKPGFVTSKLWA NTKHHPEGMWSLPLRKDSGLTFQLEYL DLYLMHWPYAFERGDNPFPKCDWNI WLDSPHYKET*RALKALVAKGLVQA/V WGLSNFNSRQDDILSVASVRPAVLQV EHPITGLKMRLIA\HCQGTWAWR*TAF NPLGLPLNRAWDPDEPVPAGGNPVVL GIGLKKYGRSPSESCLRWPGPSGKV\CI PKSITPFSNPFRTFKVDFTFSPPEEMNQ |

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| | | | | | | LNALNKNWRYIVPMLTVDGKRVPKD AGHPLYPFNDPY |
| 875 | 8926 | A | 1816 | 133 | 402 | LLTSLVNSRILILFINSKKIFAIHIFSTRGGIL RITAVIWNNISVTHGNGDMALAQYSMP VPA*AIGRRILVMLYPSRTEAFEKFLIRC |
| 876 | 8927 | A | 1817 | 356 | 463 | |
| 877 | 8928 | A | 1818 | 81 | 728 | TRGPPPAEEMDEDGLPLMGSGIDLTKEVP AIQQKRTVAFNLQFVVHTVQFLNRFST VCEEKLADLASLRIQQNETTLNILADAKLS SIPGLDDVTVEVSPFKLSPSVTNGVAHP* RPLSEIQQPEPVPPGLLDLQES*SIQAGN FL*L*PKDPARYARYLKMVQVGVPMMA IRNKMISEGLADPDLLERPDAPVPDGEIS EKTVEESSDSESSFS |
| 878 | 8929 | A | 1819 | 1214 | 1565 | LKEITDEM VYRTLHSHRIKMVSPPIFFS TNTVPFFPCYNPFFMNIQEMTKVTASRLF LFFVDLLQGVQPCFLCCCLCSIWFCNEH LDL**ASDFVMCMCVYMHYITPIHV*YI HYIYVDTY/MEVCIHLYII*CV |
| 879 | 8930 | C | 182 | 225 | 335 | MLARLGSNSWTSSDPPTSASQTAGITGV SHRAGPLT* |
| 880 | 8931 | A | 1820 | 1 | 1044 | MAEKFDCHYCRDPLQGGKYVQKDGHH CCLKCFDKFCANTCCECRKPIGADSKEV HYKNRFWHDTCFRCAKCLHPLANET/FC GQQQDPCNKCTTREDSPKCKGCFKAI VAGDQNVYKGTVWHKDCFTCSNCKQ VIGTGSPFPKGEDFYCVTCHETKFAKHC VKCNKAITSGGITYQDQPWADCFVVCVT CSKKLAGQRFTAVEDQYYCVDICYKNFV AKKCAGCKNPIT/GEKDCVKSEPPSL*S* EAPSVPRETLASHPVSQRQPPQASGWR EDLSLVGGGSL*KKSKLSSSSWPGFGK SSVVAYEGQSWHDYCFHCKKCSVNLAT KRFVFPQEQVYCPVCAKKL |
| 881 | 8932 | A | 1821 | 235 | 1119 | GPSSYKVGTMAEKFDCHYCRDPLQGGK YVQKDGHHCCCLKCFDKFCANTCCECRK PIGADSKEVHYKNRFWHDTCFRCAKCL HPLANETFCGQGGQRSCATSCTTREG PPSAKGCFAIYAIGDQNVYKGTVWH KD\CFTCSN\CKQVIGTGSPFPKGDYF VTCHETKFAKHCVKCNKAIASWGVTY* DEPWHAEGFVCVTCSKKLAVQHFTTVE DQ*YCVDCYKNFVAKKCAGCKNPITGF GKGSSVVAYEGQSWHDYCFHCKKCSVN LANKRFFVHQEQVYCPDCAKKL |
| 882 | 8933 | A | 1822 | 222 | 622 | KCSSSKHFTKEDSQITNKHIEKCSS*LLV REMQUIITKSVAIHQNG*NENTKQTCQ/ DIDNDMQQWEFMR*EWANW*N*KTNW Q*LLRLDKCVSYDPAIPFLDISPTEH AYHKTCIRMFKATLFKIAPNI |

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| 883 | 8934 | A | 1823 | 75 | 1402 | VRRRTLSSRRWHRLSHGPRWLPQVLTAS PPLQARGAFRSFPHSWGEDFLASLMFKI QLEPLKLRAWTLNGFVKFRNKETSAGPV AVMGKDYYKILGIPSGAINEDLIVCAYRT MALKYHPDKNKEPNABEKFKEIAEAYD VLSDPKWRGLYDQYGEGLKTGGGTSG GFRGFHYTFYGDPHATFASFSGSNPF DIFFASSRSTRPFSGFDPDDMDVDEDED PF/GALFGRFGFQWG*VGGPRRAPGTIV TLGRQGCRRDPVVVHELRSLEEIYHGST KRMKITRRRLNPDGRTVRTDKILHIVIK RGWKEGKTITFPKEGDATPDNIPADIVF VLKDKPHAFRRDGTNVLYSALISLKE ALCGCTVNPLFDVGRGIPPCNDVIKPG TVKRLRGEGLPPFKVPTQRGDLIVEFKV RFPDRLTPQTRQILKQHLPCS |
| 884 | 8935 | A | 1824 | 245 | 486 | |
| 885 | 8936 | A | 1825 | 63 | 1820 | RVDKGGGLAAGLRPLGRGSRACVREER EREGRLRGDFQPASLLSRGAINAPNFPAC LKEEDLSKAMSQDGASQFQEVIRQELE LSVKKKELEKILTASSHEFEHTQKKTWM DFRKLFRHFLQKKGAFWNLGEKFQRP P*DSIQPYEKIKARGLPDNISSVLNKLWV VKLNGGLGTSMGCKGPKSLIGVRNENTF LDLTVQQIEHLNKTNTDVPLVLMNSFN TDEDTKKILQKYNHCARVKIYTFNQSR PRINKES/LYFPVAKDVSYS/GENTEAW YPPIGHGDIYASFYNSGLLDTFIGEGKE YIFVSNIDNLGATVDLYILNHLMNPPNG KRCEFVMEVTNKTTRADVKGGGDNLQ YGRANLRTWWEIAQVPK/AHHVDEFKS VSKFKIFNTNNLWISLAAVKRLQEQNAI DMEIIVNAKTLGGGLNVIQLETAVGAAI KSFENSLGINVPRTRFLPVKTTSDLLV MSNLYSNLAGSLTMSEKREFPTVPLVKI RPVLFKRVQDYLKGFKEIQNRLELDHLA TVSGRCDHLEKNGFIKGEPIVHPLQIHGD RMDIPTWEPVFREPRLVSGNLARILDH |
| 886 | 8937 | A | 1826 | 48 | 239 | GRAETMSDIEEVVEEYEEEGQEEAAVE EEEDWREDEDEQEEAAEEDSEAEA*D/T RETRAEEDE*YEDASDAEDGPMEESELK PWS*RPNLVLP*VLI*FIVVYVDLHRLC ME*DE |
| 887 | 8938 | A | 1827 | 78 | 357 | |
| 888 | 8939 | A | 1828 | 3 | 327 | |
| 889 | 8940 | A | 1829 | 1 | 429 | RAEVALKKKKALSSMRAHYSSYLAKA DQKRGKKQTAREMKKKILAERRKPLNID HLGEDKLKRDKAKELWETLHQLEIDKFEF GEKLRKLYDITLRSRWDSTSSSPHNP VRGSLTVLGVERPSRGVPRVCVLAAPFIP WGL |
| 890 | 8941 | A | 183 | 1108 | 1627 | PMDQVMCRT*KG*MGGQRDVSPASEQ VSTARPGPRAVIDYSKADAWAVGAIAY EIFGLVNPFGYGGKAHLESRSYQEAQLP ALPESVPPDVRLVRLALQREASKRPSA RVAANGVLHLSLWGEHILALKNLKLDKM VGLAPPKIGRHFVGTGSQEEVVVLETK NEDALFG |
| 891 | 8942 | A | 1830 | 3 | 986 | HTPATQSLANGLGRSNVTITRGCEPGA SACSRCCPQGAPALLTDPQKPPTFTMS DEVEQVEEQYEEEEEAQEEAAEVHEEV HEPEEVQEEKPRPKLTAPKIPEGEKVDF DDIQQKRLNKDLMELQALIDSHFEARKK EEEELSALLERIEKRAEVAEQQRIRAEK ERERQNRLAEEKARREVEDATRAEDD LKKKKALSSMGANYSSYLGPRLDQKR GKKIQTAREMKKKILAEVRRKPLQPSIHL GERQN*GDQGRSFWETLHQLEDLTKF EFGKELKRQKYDITTLQEPECRCWPES |

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| | | | | | | TSKEGLGPPAKGKVGGGRWK |
| 892 | 8943 | A | 1831 | 7 | 1382 | PPGLEARPAPARLAGSGVCSGGRGRGAG RRSRQSMRGAARAAWGRAGQPWPRP PAPGPPPPPLPLLLLLLAGLLGAGAQYS SDRCSWKSGSLTHEAHRKEVEQVYLPC AAGAVEWMYPTGALIVNLRPNTFSPAR HLTVCI RSFTDSSGANIYEKTGELRLLV PDGDGRPGRVQCFGLEHGGVLFVEATPQ S/QDIGRRTTGFQYELVRRHRASDLHEL GECPARSSSSSSSSSSSPPARAANSHLK WRWSQRCLDVDTLPLDALLSVRIL*RW WAAFQSLSRPGCFLTLPFFSAPCRPCSDT EVLLAVCTSDFA*VSPRQLSSSSSSSSSS SSSSPHLLPRTAVRGSIQQVTHEPERQDS AIHLRVSRLYRQKSRVFEPVPEGDGHWQ GRVRTLLECGVRPGHGDFTGTHMHFG EPRRLRCAPKASRTFQRMRYDAIQUERGL NPLVGWQRN |
| 893 | 8944 | A | 1832 | 1 | 433 | NNPDFKAGV/MALPTL/LQIQRHDDYLV MLKAIRILVQERLTQDAVAKANQTK EGL PVALDKHILGFDTGDAVLNEAAQILRL HIEELRELQTKINEAIVAVQAIHFHVW KSKCHILGGSPENWVCSRDLPLLIAFF FNKV |
| 894 | 8945 | A | 1833 | 1 | 459 | |
| 895 | 8946 | A | 1834 | 2 | 1108 | SFRSDSAPARPLAASPVPAPPAPRFFSPG RGP GDQSEKRWTFMFRRLTGSSTTYSP FVFNRRDETEFRNFIVWLEDQKIRHYKI EDRGNLRNIHSSDWPKVLEKYFKDVN CPFKIQDRQETIDWLLGLAVRLEYGR* WLKNTKDLVP**FQNLNDNATKNAEPF DPFWDVNNP*F*GLVLLALG*TWLQIQR HDDFLVMLKANS GFVWQEP*PPGMP VCLRANSNKRGA*PVAFRQTHILGFD/TG DASSLMKLEILRIACT*EELRELTQKS TKAIVAVQAIYC*SKRQDHLGKSLEDE HFEDLQLTYFRYMLGNHTLLACFGKSK CHNSRGEKSPEKLGYSRGFYHHWLIAS CFFL |
| 896 | 8947 | A | 1835 | 1 | 891 | |
| 897 | 8948 | A | 1836 | 1 | 984 | |
| 898 | 8949 | A | 1837 | 1 | 1917 | |
| 899 | 8950 | A | 1838 | 2 | 1411 | FVGKGPRQAEDSRCGAGRRTGRTLGE QRACVWCVPKGRKVAKGGESEWVEGG EGREEKKVGGPGGRVAHSGPTGSSA MRRVTLFLNGSPNNGKAGAGYGTLSL LSGGSSKPGIKATNVYNGKGLIDIALI RDDDDVLFVCEGEFIDPQTDSPPEGLL FHTDWLTLNVGGRYFTTTRSTLVNKEPD SMLAHMFKDKGVWGNKQDHRGAFLID RSPEYFEPILNYLRHGQLIVNDGINLLGV LEEARFFGIDSLIEHLEVAIKNSQPPEDHS PISRKEFVRFLATPTKSELRCQGLNFSG ADLSRLDLRYINFKMAQFKPL*FAHANL C*ANLERTDLYGSVLD CANLQGVKMLC SNAEGASLKL CNFEDPSGLKANLEGANL KGVDMEGSQMTGINLRVATLKNALKN CNLRGATLAGTDLENCDSLGC DLQEAN LRGSNVKGAI FEEMLTPLHMSQSVR |

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| 900 | 8951 | A | 1839 | 1 | 320 | |
| 901 | 8952 | A | 184 | 56 | 335 | TGFCFFSRVKCNGTILGPCNL*IS/GSKYF SGL/SLPSKWDFRAPPNGNLF**TRF SPVYQDGFDFLTSCPPGLPKLLEFRGA PPLPSE |
| 902 | 8953 | A | 1840 | 1 | 1430 | MAAAEAAANCIMELPRAFGIRPSGGSYP SHVEEGWGRFRPGPHVAAAAPPPRPGP HTPWGVIDLGPSTMWGVSWEEQCFSAL YQPPSELRGHLLGYRTRFCFVWSCGQA ESSEKPNADMTSKDYYI*LHTHTFGIHE EMLKDEVRTLTyrNSMFHNRHLFKDK VVLDAVSGTGILACMFCCQGPWPRKVIG IECSSYSS*LWR*RCVQANKLRPRRTSI KGKGGKVELPVGERWDIIHQRVGWGY CLFLTESMLQHRALMPRDKWLAPDGLA IFPDRAQLYVTAIRGTGRYKDSRSHLLG ENVYAGFDMSCIKADVPIKEPLVDVDPK QLVTQRLAFIKEVDIYTVKVEDLTFNL PRFCPCCLKRN*LTCTALVTLLSTFEFTH CHKRTGGTGFFHQPPRSPYTHWKQTVF YMEDVYLTRERRAEEIFGTIGMRPNAK EQPGTLDFTIDLDFKGQLCELSICSTDYR MR |
| 903 | 8954 | A | 1841 | 1 | 45 | |
| 904 | 8955 | A | 1842 | 2 | 580 | GRVGGRVGCEPPAWIDIYKAAGRSSF E*ARKMSS*AAFRTSFVLGAEDGCISTQ GSWGKVMRMHGPPEHPMRELQEMIDE VDEDGSGTVDFDEFLVMMVRCMKDD SKGKF*GRSLDLLPACFDQKMLDGYA DLVELED*LLQATGRDPFTEDDDIEELAM KDGDKNNDGRIDYDEFLAEFMKGVGVD A |
| 905 | 8956 | A | 1844 | 2 | 368 | |
| 906 | 8957 | A | 1845 | 28 | 479 | |
| 907 | 8958 | A | 1846 | 4 | 458 | |
| 908 | 8959 | A | 1847 | 90 | 769 | |
| 909 | 8960 | A | 1848 | 231 | 909 | HCSQHPSLWISFCFIIPANQFIFRLCTSEA MGKISSLPTQLFKCCFCDFLKVKMHTMS SSHLFYALCLLTFTASSATAGTGDGSAG AELVDALQVPCVEDRQGFYFNKPTGYG LPAVRRAPQTGVVDECCFRISCADLRLE MYCAPPQACPSQLRSVRAQRHTDMPQD PERKYI*RTQVEGVQETRTTGLLEDPGG VKSMDMPQDPLLCTSYLLNFGTPTKK |
| 910 | 8961 | A | 185 | 523 | 817 | SQHSVGPRQADRLRSQVVDQPGQHGET PSILKVIQKLPRGGACL*SQLGLSLRREN CLNPGGRGCSEPRSHHCSPAWMTE*DSI SKNK*INKNEIKKK |
| 911 | 8962 | A | 1850 | 141 | 439 | |
| 912 | 8963 | B | 1851 | 851 | 1807 | MAIKSIYAALRSIYHSEGHRLFSGLTAT LLRDAPFSGIYLMFYNQTKNIVPHDQGP PLGMFLGQAIHKAQRSCKPALPGPEELP TQGNWK* |
| 913 | 8964 | A | 1852 | 913 | 1375 | SIFPGVVIEHLTLTFIYYHFIINRTSQGIDS QILSLFLFFF/CFFETESRSVTQAGVQWR HLGSLQPPPPWFKRFSCLSLQSSWGYRH VPPHPG*FLVFLVGDGGFTMLGQGSQ NSCTSRSTRRLRLAQPLFSQFKNCFKNC KSSIGLIPLYYY |
| 914 | 8965 | A | 1853 | 1295 | 1679 | KCINCKVYFTGVFFLIPTCQMQUIHIFVCL CLVIISIHISFFYFIYFYDIIS*MCNL*VLLD YFNPLEITHAFCIQFM**LIYL/CFKILFC GFLGCFLLKIYRF**S*FSFSLKCIYS FYSLV |
| 915 | 8966 | A | 1854 | 2 | 410 | |
| 916 | 8967 | A | 1855 | 3 | 322 | |

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| 917 | 8968 | A | 1856 | 1 | 666 | SGRDDQGRRAQCSAARCGRPSGGVMED ERSFSDICGGRLALQRRYYSPSCREFCLS CPRLSLRSLTAVTCTVWLAGYGLFTLCE NSMILSAGIFITLLRPLGVSPSVKNDQETL LUIDSLGVQMTSSYSGKESTTFNEMGK VK/EIFVNNEAIYMVSI*KHKAIIYLVNL FEKIPVÆPHGDIPKYVPVFQSAKPRLADC LÆEVYRSCQEILAHQKATSTSP |
| 918 | 8969 | A | 186 | 49 | 1357 | RTPERCLREV GKATGWPECILT*QTIIPRP /YPSVGTAASDTKKKKINNGTNPETTTSG GCHSPEDAQVQTIRILTQCKTELQMALY YSQHAVKQLEGEARDLISRLHDSWKFA GELEQALS AVATQKKKADRYIEELTKER DALSLELYRNTITDEELKEKNAKLQEKL QLVESEKSEIQLNVKELKRKLERAKLLP QQQLQAEADHLGKELQSVSAKLQAQVE ENELWNLNQQEEKMWRQEEKIQERE EKIQEEKIREQEEKMRRQEEEMMWEK EEKMRRQEEEMMWEKEEKIRELEEKMH QEKIREQEEKRQEEKIREQEKREQE KMWRQEEKIREQEEKIREQEKMMWRQ EKIHEQEKIREEEKRQEEEMWRQEEKI REQEEIWRQEKMHVRTDEISVCSIFQGF ISVGLCKFAYPFDCFTL |
| 919 | 8970 | A | 1861 | 20 | 465 | VACCVRI PGPRRS GPAMAVTITLKT QQTFKIRMEPDETVKVLKEKIEAEKGRD AFQNMQRVQIQNPALLPALLQQLGQENP QLLQQISRHQEQFIQMLNEPPGELADISD VEGEVGAIGKEAPQMNYIQVTPQEKEAI *RLKALG |
| 920 | 8971 | A | 1862 | 6 | 448 | |
| 921 | 8972 | A | 1863 | 391 | 1610 | VAMCVEIPGAASLGPRHWPVTITLKT QQTFKIRMEPDETVKVLKEKIEAEKGR DAFPVAGQKLIYAGKILSDDVPIRDLFA FDGGRNFVVRWVTKTKAGQGYLQAP PGGSPSHLPQSPLTSFPFPCPHLQACSIPP LAGQRRHKSPSEESGPKTFPESVASGSVP SSG/SGSGREEDAASTLVNGAFEY*GR WLTEIMSMGYERERVVAALRASYNNA HRAVVEYLLTGIPGSPEHGSVQESQVS EQPATEAAGENPLÆFLRDQPIQFQNMRI QVIQEEPLRCCPALLPASWAQENPQLLT AKSARPPRSQFIQMLERSPPGEAWADIS DVEGEVGAIGEEAPQMNYIHGDARRRK EAIER*KALGFPESLVIQPYFACEKNED LAANFSLSQNFDE |
| 922 | 8973 | A | 187 | 1 | 408 | ASDRPESRATHASGKSPVFSDESDLD DISKLEQQSKVQNTGHGKPREKSIIDEKF FQLSEMEAYLENREKEEERKDDNDDES KSSRNVNKDFDFPVESEDEDIASDHDE LGSN/EDDEIAEEEAEEGSISEI |
| 923 | 8974 | C | 1870 | 293 | 448 | MXKTLQELRAHENEITXVRKVTFNGLN QMIVIGLPPSLTELHLGWQQNQSS* |
| 924 | 8975 | A | 1871 | 1 | 475 | SYIRIADTNITSIPQGLPPS/TELHLDG ISRVDAASLKG LNNLAKLGLSFNSISAVD NGSLANTPHLRELHLDNNKLTRVPGGLA EHKYIQVVLHNNNISVVGSSDFCPPGH NTKKASYSVGS/LFKNPQYWEIQPSTFRC VYVRSAILGNYKKK |
| 925 | 8976 | A | 1872 | 1 | 636 | |

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| 926 | 8977 | A | 1873 | 196 | 1274 | IMKATIILLLLAQVSWAGPFOQRGLFDF MLEDEASGIGPEVPDDRDFEPLGPS/V CPFRCAQCHLRVVQCFILGLADKVTGI FSPNLNTLLDLQNNKITEIKDGDGFKNLKN LHALILVNNKISKVSPGAFTPLVKV/EER LYLSKESA*RELPEKMPKTLQELRALED* /EFTKVRKVTFNGLNQMIIVELGTNPLKS SGIENGAFQGMKKLSYIRIADTNITSIPQG LPPSLTELHLDGKNISRVDAASLKGNNL AKLGLSFNSISAVDNGSLANTPHRELHL DNNKLTRVVYLHNNNISVVGSSDFCPA GHTPKRASYSVSLFSNPVP/QYWEIQH PTFRCVYVRSAILGNYK |
| 927 | 8978 | A | 1874 | 248 | 1393 | IMKATIILLLLAQVSWAGPFOQRGLFDF ML*DEASGIGPEVPDDRDFEPLGPMCPF PLQCHLRVVGQSDLCLEQMPKDLPPDT VTLADLQNNKITEIKDGDGFKNLKNLHAL ILVNNKISKVSPGAFTPLVKLERLYLSK NQLKVELPEKMPKTLQELGAHEEWDHQ KWRKS*LFNGLNPMIVHRNWAPIPLKSS VGIENGAFQGMKKLSYIGIADTNITSIP QGLAPPSHTKLHLADGKQKSSRVDAASL KGLNNLAALKGIEFSNSISAG*TNGLSGP TRPHLRELHLGQQQALPRVPWWGWAE H*VHPRLS*PFITNQYLCRLGSSDFCPPG HNTKKASYSVSLFSNPVQYWEIQPST FRCVYVRSAILGNYK |
| 928 | 8979 | A | 1875 | 81 | 137 | TMAFPAGFGWAAATAAYQVEGGWDAD GKGPCVWDTFTTHQGGERVFKNQTDGVA CGSYTLWEEDLKCIKQLGLTHYRFSLSW SRLLPDGTTFINQKGIDYNNKIIDDLLK NGVTPIVTLYHFDLPQTLEDQGGWLSEA IIESFDKYA/QCFSTFGDRVKQWITINEA NVLSVMSYDLGMFPHARSHFGTGGYQA AHNLIKAHARSWSYDSLFRKRQKGMV SLSLFPARLEPADPNSVSDQEAAKRAITF HLDLFAKPIFIDGDYPEVVKSQIASMSQK QGYPSRLPEFTEEEKMIKGTADFFAV QYYTTRLIKQYENKKGELGTLDAAIEFF PDPSWKNVDWIYVVPWGVCKLLKYIKD TYNNPVIYITEDGFPQE*PSAFWMDTSTL GSIFRQTFQELFKAIQLDKVNLQVYCAW SLLDNFEWNQGYSSRFLFHVDFEDPAR PRVPYTSK*YAKIHRNNGP*RTRGAWLL WPKGALLAAEDPSRQLLKPWLSLQDL DGRQPLQLIK |
| 929 | 8980 | A | 1876 | 243 | 1126 | FQQRLYRAARRFTMVKIAFNTPAVQKE EARQDV EALLSRTVRTQILTGKELRVC HPGKKEGSSGEMLWFTLFRAFQFILGGL YLFGGACIYK/YTFMPKRHHFTVGEMCF FDESDPANFPFGGGE*LSCLVT*/EADI REDDNIAIIDVPVPSFSDSDPAANYFMTF EKGMTAYLADLLGNCIYLMPLQYFYF LWPPKKIWVELFGQTGRVGRYLPQTYV VRLEDLVAVSRKIRDVSNLGIIFYQLCNN RKSFRLLRRDRLGFKRAIDKCWKIRH FPNEFIVETKICQE |
| 930 | 8981 | A | 1877 | 985 | 1401 | DFA*V*RDRVKFKGTCFLFV*WFLKFF KMEFLPRLECNGKJHCNLLMGSSNSP TSASQVAGDYRHVLWWFLIEMEGFPML VRAGLKLLYLEWIGSAF |
| 931 | 8982 | A | 1878 | 184 | 481 | SPRCNPSPLPQAFQSGDCPLPCTAAGL MCAWRSAREPCLLPHCLPRVWHRDP/ CSQPTSQG*TEALPILCK*KPPWPPQEIS PSQWIHQSPADPAL |
| 932 | 8983 | B | 1879 | 148 | 194 | XNILSVIAVRKLFTAAX* |

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| 933 | 8984 | B | 188 | 1 | 1995 | MSKETRQSKLAEAKEQLTDHHPQTNPSV GTAASDTKKKKINNGTNPETTTSGGCHS PEDEQKASHQHQEALRRELEAQVHTIRIL TCQKTELQMALYYSQHAVKQLEGEARD LISRLHDSWKFAGELEQALSAVATQKKK ADRYIEELTKERDALSLEYRNTITDEEL KEKNAKLQEKQLVESEKSEIQLNVKEL KRKLERAKLLLPQQQLQAEADHLGKEL QSVSAKLQAQVEENELWNRLNQQQEEK MWRQEEKIQEWEEKIQEQUEEKIREQUEEKI REQUEEKMRQEEMMWEKEEKMRQEEM MMWEKEEKMRLEEMMWEKEEKIREL EEKMHEQEKIREQUEEKREQUEEKIREQEK RQEQEAKMWRQEEKIREQUEEKIREQEKK MWRQEEKIHEQEKIREEEKRQEQEEMW RQEEKIREQUEEIWRQEKEMHEQEKIRKQ EEKVWRQEEKMHDQEEKIREQUEEKMW RQEEKIREQUEEKIREQUEEKIREQUEEKIREQ EEMMQEQUEEKMGEEKMQEQUEEKMR QUEEKIREQUEEKIREQEKIREQUEEKIWEQ EEKIREQUEEMMQEQUEEKMWEEKMC RKRRCKNRRRKYYVFARIIQRVYLLNHIIR NRKSVQILVLSCDFLNSKNSHLLPDTL MLEDKAYLQIESCLIPNEEEYQYLAE* |
| 934 | 8985 | A | 1880 | 2 | 1508 | PESVGGGKTLQQUEEKQLQPCMQMDNRL PPKKVPGFCSFRYGLSFLVHCCNVIITAQ RACNLNLTMMVMVNSVDPHGLPNTSTKK LALDNKNPMYNWSPDQGIHLSSTSYG VIIIQVP/VLGYFSGIYSTKKMIGFALCLSS VLSLLIPPAAGIGVAWVVVCRAVQGAA QGIVATAQFEIYVKWAPPLERGRLTSM TSGFLLGPFIVLLVTGVICSLGWPMVY IFGACGCAVCLLWFVLFYDDPKDHPCISI SEKEYITSSLVQQVSSSRQSLPIKAILKSL PVWASIGSFTFFWSHNIMTLYTPMFINS MLHVNLIKENGFLSSLPYLFADWL/CGNL AGQLSDFFLTRNLSVIAVRKLFTAAGFL LPAIFGVCLPYLSSTFYSIVIFLILAGATGS FCLGGVFNGLGYCSPDILGFIKACSTLT GN**GGLIASITLTGLILKQDPESAWF*N LQSLMASPLMVTGP*FSHPYRLPTARNS RDWAKEKQHHTSPEV |
| 935 | 8986 | A | 1881 | 90 | 458 | HFSRGYLEAFSEISNIRFVPPHSVTVVVV FGACFLCILGIWPWACLPGPGGEGSGGF GEGRGSEAGRLGSVELTPATLPLQAPEA YPVFEPVPPVPEAAQGDTEDEGAPPLK RJCNPADP |
| 936 | 8987 | A | 1882 | 15 | 796 | PGSTISWRPGLARSLSPDGRPRRGLGP GPSPASMAGRTRVRAETRSRAKDDIKV MATIEKVRKWKKRWVTVAATPFRILNW VAIVVDPQEEER/RREAGGGAERSRGRE RRGRGASPRGGGPLILLDLNDENSQON FHSEGLQRGTEVSPGGITPKPNRPCVTL PDPPEGGP*EGLSPPRLGQEERSPPGGITV GSTYEPPMLTKEEPVPELLEAEAEAYP VFETVPPVHETAQGDTEDEGAPPLKRI CPNPADP |
| 937 | 8988 | A | 1883 | 566 | 831 | ARSFFLITILIQRTDWRKNKFPPSNFPSNL RTNFLDQFLKETILRKH/RVGLGVLAHT CNPSTLGGRGGWSP*QGEFENSLTNMVN HFS |
| 938 | 8989 | A | 1884 | 534 | 1835 | GSSYMHFQGEWVIAQCFKKLHRGVVCV VCL/CLYTHICIF*YITKAILMNY/ACI*KN SCHLAHRFVCMCIYICMYVWCYIVLKI TQ*CMY |
| 939 | 8990 | A | 1885 | 60 | 395 | |
| 940 | 8991 | A | 1886 | 1 | 193 | FRLARGENLEHLRNKTEDEATSEHFKT TSQKVARKFWWKNAMIVL/VFIILFIV LFATGAFS |

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| 941 | 8992 | A | 1887 | 1 | 280 | |
| 942 | 8993 | A | 1888 | 1 | 396 | |
| 943 | 8994 | A | 1889 | 85 | 410 | DMEASEGGGNDVRNQLQSEVEGVKNI MTQNVERILARGENLEHLRNKTEDLEK PTSEHFKTITSQKGGSEKFWWKVVKDD CPLICRDCF*SSLLQLWLFAVTGAFS |
| 944 | 8995 | A | 189 | 386 | 1321 | RTLERCLTEVGKATGWPCILTYARRSL APVLLGSH/HGRGLQTPGKLWSWGKSEE QECEEDGSETETGGQEDLEDLQEEEEEVS DMGGDNPEVGKKARNSSKFELRKSPVF SDESDLDLDFDISKLEQQSKVQNKGGQKP REKSIVDDKFFKLEMDLYLENIHKR*E ERKDDNDDELDSPPQTSFVGTGATDT KKKKJNNGTNPETTTSGGCHSPEDAQVH TIRILTCQKTELQALYYSQHAARQLEGE SRDLVSLHDSWKFAGELERALSAVTTQ KKKADRRQTGAESA AVGELGDTGDTVG SEHWT |
| 945 | 8996 | A | 1890 | 122 | 975 | AARPTRHLCCGQQQVLVCGPSAVGRL PLQWGLGLGPTMSSLGGGSQDAGSSSS STNGSGGSGSGPKAGAADKSAVVAAA APASVADDTPPPAGVGTAVSSVSPSTRA CA/GSRPLSHYSSFGSSGSGGSGMMGG ESA*QGHCGCSRGLPVGQWA*PGGGHG GGQKQPYLKAQKWCCGQPAEQGRAGH GAGSRGTADAAVFAVHRDAEARGAG ASPADERGGLACLDMEA VAGAEALNG QSDFFYLGRFPSTQGLLSLLTPAGVVS WAEKRAAHGRAWA |
| 946 | 8997 | B | 1891 | 1 | 8736 | MPGQILVKAQLFQKAKSFHRMVLEQ LGIYWETNKPFPFHPITHENEFEMNHRG ECKTKNYKTSRRKYRRTSLTPRGQQSFL RIQKIGQRYLQYIYQAKASNPECTKNSC KPKDKQPDNRMGKKTLES DKEGLRPKA PIPAPDPVAGRTLIGKEHVPLWGGVLAS GTSCSLSPAGSPVHPTTLRDHQLGPPQPL WSCLELQPHQTHNKFVGRGGAKERDRN LARACPLSQGWQRPLNTTINIPAGE NLNL |
| 947 | 8998 | C | 1892 | 377 | 463 | |
| 948 | 8999 | A | 1893 | 753 | 3000 | KLEPCGGTPGPRAGSGPCQDPHIPPEGVG GSPDGPAGWAPNTHSASWSWGPHEPC PPPA*AADCRGTDRESFASPVCPLSPNS QRPPHLEAPGYLPGGSSRTQPAV/PTCSP PGIP/AVPALCP*PG*KTT/PIYTEAGKLAT SAPGT/PPRQLSPGNAVYCLPPDTHQPG RAGLAESAPYPEAQPAGVGQEGDAGTE/ PGPSCQTQH*PPQEPLLGPPQL/PPTSQQ PEGGALHSWPQRWPRKFPDP/PL/PVRP VWSAKPWNT*RRSPPGAPSPTRTAMGT TTPCPRPSPDSKHVPLALPGAP/VPAQILD LLPRQALRTEPSAPEPLAGYGDSPWLCG MAVSTGPVLPWLRNGPRTNHSC/CRSRN FASALHGAAPSKSFIRR*WGRTP*PAGC PF/PGLGIVPRSTSSAPTQLGSGNAVAVG HVRVLP SFHSDGFLQPMSSSGSLAQSV WASLGSEQQQVPM LPPASPGTPAARAGP VQFEQCLLSPTWKPY/PAFAQAVP*S RMVCPEAGPRSQQ/PA*QPPGLPPPPAT RVG/PPDVKGGRGLGSPGRPA/PPACMSF EQLPIGLLAWGLQDARPA GAGGRAFE* PPGGSSQRFPPSGT*EAE**QF/VNGDGPA PTFSCPMGKPASPCPVRAVPPALPDVLT GNTAALGGLKAFGNLQPSLDNSPVP* LLEGPTQPPTTSAPKECSSSPTMPGV GPWVTGTSGRPTFLSPFFSYEEHFKVLLF KEITVQQAEDGFHHRPFPRNKQ |

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| 949 | 9000 | A | 1894 | 3 | 576 | LTRIPFLGAKYAPVIFA/EGA/YQ*QRS*T EIQMACFKQATRWWKC/DPRHGKYMAY CCLLYRGDVFPKDVNAAIATIKTKRSIQ FVDWCPTGFKVAGINYSPTTVVPGDLA KVQRAVCMLSNNTAIAEAWARLDHKFD LMYAKRAFVHWYVGEEMEEGEFSEARE DMAALEKDYEYVGVDSVEGEGEEEGEE Y |
| 950 | 9001 | A | 1895 | 58 | 1636 | LVGDGNPGPGVCSCRLRLIPYPLCGECN SINHVGQAGVQIGNACWELSCL*HGIQPD GQMPK*PKPLGEGDDSFNTFFSETGAGK HVPRAVFVDLEPTVIDEVRTGTYRQLF HPEQVITGKEDAANNYARGNYTIGKEH DLVLDRIARKLADQCTGLQGFLVHHSF GGGTGSGFTSLDEWLSVDYWQESPSL EFSIYPGAPRFPQPVVEPYNSILTHTTLA EHSGLCPSWVENEAIYDICRRNLDIERPT YTNLNRLLSQIVSSITASLRFDGALNVDL TEFQTNLVPLPRHSTSLRPTYAPVNPPS* EKPTHEQAFCSRRSPKCFAFEPSQPRWL KCDPSPMGKYMACCLLYRIGDVVPKID VNAIAHPSKPKRSIQFVDWCPTGFKV VAINYQPPATVVPVGDIAKVQKTVCMML SNTAIAEAWARLDHKFDLMYAKRAV VHWYLGEGMEEGEFSKA REDMAALR KDYEYVGVDSVKGEEGEEGKGLIHL FGPCSMSCSNFSLTDRR |
| 951 | 9002 | A | 1897 | 2 | 350 | SQVDR*QSEPEIRICREDHMERLQAFDA NSRKQAEWKEKAIKELEEWYARQDEQ LQKTKANNRVAEKLSTNNPSLT*LVMS EEAFVNDIDESSPGTEWVARLCDFP KSLD |
| 952 | 9003 | A | 1898 | 2240 | 2492 | |
| 953 | 9004 | A | 1899 | 1 | 906 | ATAVSVGRLVVFVSTGCVRAVQLPAMA ELDPFGAPAGAPGGPALGNVAGAGE EDPAAFLAQGESEIAGIENDEAFAILDG GAPGPQPHGEPPGGPDV DGMNGEYY QESNGPTDSYAAISQVDRLOQSEPSIRK WREEQMERLEISLDANSPEKKQSWKEK AIKGA*KEWYARQDEQLQKTKANNR VADESFLQTTLR*RDWLCHKHKPSLLQP RTGQPEEALFKDLEGLSPSNEWERVAR LCGL*PPSLSKQAKDVSPHGASVLISLK AGPRWGHLKSHPVETLHLQYLNTQ |
| 954 | 9005 | A | 19 | 12 | 288 | FGGGYIPTWGKGEGILALELNHDISREFC SAPALASRPPPTPPPLLPPT/PPLPAPRSPA DATPRRVGGPLR*ALKPRAPGPGWSRRR CRSWW |
| 955 | 9006 | A | 190 | 792 | 1061 | GSGV*DQPGQHGTPSLLKIQLAERGG GHL*SQLLRRLRQENHLNPGGRCCSEPR LLHCTPAW/VNESKTSSQTNKISQEW CVPIVL |
| 956 | 9007 | A | 1900 | 29 | 852 | PSRSLVRVVEFAPQRWLPVSVVSGRLVF VSPVGVRAVQLPAMAE LDPFGAPAGAP GGPALGNVAGAGEENPAAFLAQGES EIAGIENDRAFAILDGGAPGPQPHGEPA GGPDV DGMNGEYYQESNGPTDSYAA AISQVDRLOQSEPSIRKWREEQMERFG KPFANSRKQAEWKEKAIKELEEWYA RQDEQLPENQKANNR/AQTEARPL*NDI DESSPRPLKWGNWGPRAV*TLNPPKS*A KQAQKMSPPHDASVLILPLKAGPRWCH |
| 957 | 9008 | A | 1901 | 1 | 585 | |

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| 958 | 9009 | A | 1902 | 2 | 537 | GTLRRDFNHNVELSLLVKKKKRLRVDT MLGQQKRNWPTSRGLFGSHVQDHDQG VLPLGFPLPRMRVLCMPHFPOSTVVIPGR MGSSLLKIRNFLGVKNTIRRVVRMRPGC CLVQYPQAQKDELILEGNDELIVSNSAG LIQQATTV*KQGISGNFLDGIYVSEKGT SCRLMNKI |
| 959 | 9010 | A | 1903 | 560 | 898 | KCNTECFGSLMHFVVVLFIIIIIFLRQOGR SVTRLECSGAILAHCNLRPLGLSNPAS ASRVAGTTGTCTYRIQLIFVLVETGFHYV GQAGHKLLT*VIHPPQPPKVLGLQV |
| 960 | 9011 | C | 1904 | 224 | 379 | |
| 961 | 9012 | A | 1905 | 1249 | 1642 | LGCYPGPFHVPKWMIFPDPCISVTGVC VC/G/GVCSCGVCG/CG/CGCLPGGKICK YI*ICSQIL |
| 962 | 9013 | A | 1906 | 415 | 656 | SLPRSPLGRGTPSPQHLSSNLNLASLYHP HEITPWIISSSGSSI*TPI/TPSFYPSPTNCD PQIFDPQTPVSGCRLASSQGPSLNPSTNL SGPQIPFASYPCLLLAPHPLPASRPQSCP SPKTWAPPS |
| 963 | 9014 | A | 1907 | 1 | 417 | TISWNTGPRARSRARGSSSTGLDGCVGGG SGGNSGLPCPDLEPLGGLQSKCRLCAPT EARGLWS/KVPLFRQVRHLALHACGCRE AWPPPGPPLLVALCFHLKALPSRGSRA GREAVSKHLKFAMLAGGRVCGSRRVLS M |
| 964 | 9015 | A | 1908 | 1 | 438 | QCTPSSAADCELTACYGFSS*PS*GPSPL PWRPRMCESWVLHLPPTQCFSWDIGPS EVMVRPLGWDTLRGSMPLPW*GAGERA GKPLPAPADASPHRSGTGFDRAAGGRGR RRCNRSEEGVIPFAAPRLPPHAFWRVFP HWETT |
| 965 | 9016 | A | 1909 | 113 | 704 | |
| 966 | 9017 | A | 191 | 2 | 343 | LLFFFFFEMESCSVTRLECSGVISAHCKL C/LPGFKRFSCSLPSSWDYRRM/PPRLA NFLYFVEMGFHRVAQAGLKLSSGNLP ASA/F/PKY*NYRRDDASLAACSTFLGLG LLWV |
| 967 | 9018 | A | 1910 | 317 | 470 | NYPMSVVPQDMWRKSHAA/HILREMSS KITAAQL*WNNAYFGSSKGLSCVWP |
| 968 | 9019 | A | 1911 | 147 | 850 | MAASGAGAEVSGR*GREPPALPPAPCG PARRRRSPP*LPKTYRFFSLWQGRGPRDRSS APIGNSGLPCPDLEPLGRAARSKCRLCA PTEATKACWK*GPSCFRQVRHLALHA CGCR/EG/LGLPQGPPTSAGLLCAFTLKA LPSRGSPCKEELSASTSNFSHAGCGRVC GSRRVLSML*FSGCLKPLSVVPQDM*RK SHAAHLREMSSKACRSAFDGNALFLE VSKGLSCVWP |
| 969 | 9020 | A | 1912 | 119 | 1001 | GSRTKGRAVPECACAPVGAGEGRPAGV AVSDGVIKVFNDMKVRKSSTPEEVKKR KKAFLFLP*VRTKNNIIL/EEGKEILVGD VGQTVDDPYATF/VSKMLPDKDCRYAL YDATY/ETKESKEDLVFIFLGPPEAP PLEQNGFMPSSQGRPSKKGSWTGDSSHE FAKPNCLPKEGQGTACTLAREAGGQVP VYSPGRAKPFVSPFWPPCLGASGSPQHL APWGFAGCPFLQRPGRWGGSPAGGG EIPLNPCPKQTPPNPPGNFSPSNPLDGF WFFPKLLFESFDSSWG |

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| 970 | 9021 | A | 1913 | 361 | 1785 | LPLPRWKVLLPRDILGPRKINEVSSDDK DAFLCEQTSGLDKKTSEVVKSSPLGVTP LFMQSNVINSTAIKTLAATGTGDFDCAS KTDIQLCAESRGVPPERIIYKGSFVKQVS QIKYAANNGVQMMTFDSEVELMKVVA RGTFPKAKVWVLRJAATDDSKAVCRLSV KFGATLRTSRLLERAKELNIDVVGVSF HVRSGCTDPETFVQAISDARCVFDMGAE VGFSMYLLDIGGGFPGSEVDVKLKFEIT RP*STQPLDKYFPASN*KS*LEPGRY YVASTFDALQLISFAKKICIKRNQTS**P KIESELSRPLMYVYVNDGVYGSFNCILY DHAHVKPLLQKRPKPR*RRYSSSIWGP TCDGLDRIVERCDLPEMHVGDWMLFE NMGVAYTVAAASNVPMLPRGPTIYYVM SGPAWQLIQFQNPFGFPGRQPGCP APCPVFCAWESGMKRTRASPVPSG |
| 971 | 9022 | A | 1914 | 501 | 746 | ARSSLVLLFIYIFRDRVLLCHSGWSAVVQ SWFTAALISQA*VILK*FSLSLPSSWDY RQVSPHPANF/SYILFCRDR/SFTMLPRVG WNSWAQVLLLIQPPKVLQL*AGCHGSCL |
| 972 | 9023 | A | 1915 | 156 | 166 | VLFKRPYLVQDAVLWLFTAIISHSTLEL LGSSYPTTSAS*VKHSNSNIMKFKVPVLN ECTMQLGKTKMIKVLVKSIF |
| 973 | 9024 | A | 1916 | 452 | 1017 | SLHGSRPHLPTGRLLGPETCAGFSRFGQ NESLTPFVTSDRSKNRKRHFKAFFPHFE GKIMSSPLSKELRQDVQLCGSDARS*KD DEVQVVRGHL*GSAKLAKVVQVYRK KYVIYIERVQREKANGTTVHVGHFTPS KQVVIT*G*NWDQRPKRSLRTGKPKSR QVVGKGRGKYKERTIEKMQE |
| 974 | 9025 | A | 1917 | 3 | 474 | |
| 975 | 9026 | A | 1918 | 1 | 246 | |
| 976 | 9027 | A | 1919 | 373 | 560 | SOLKNAKFNLSPPLPNVY*DKGQYVTS QLYQNAAQPIFKQAFETCAHTNTIQD QAPRRI |
| 977 | 9028 | A | 192 | 2 | 447 | KEEIIPIL*NLFQNIKAEGILRISFNEARITL I/PKPN/RAITRKINPIDQSLMDRHAELNK ISAN*IR*RMKRIIPHGVRF*GMWGW NIRKQINVIHHTSLKKKNHMIISINAEKE FDKIRKLLKLRLNIYKRG*LT*VMVRNS |
| 978 | 9029 | A | 1920 | 837 | 1441 | IFFFHLSPSHSHARSHFLFAIMNRPAPVEI SYEDMRFLITHNPTNATLNKFTGT*GS MGVTDGFGVCGWLHMDKAPVWKKE GFHVLWDWPFDDGSSTPLIQVIGWIFK PV*KTKFSCSHGCCVAVHCVGRVGE APVL/VLALALDWNVGMKIYEDAVQFIR QKRRGAFNSKQLLYLEKYRPMRLRFR DTNGHCCVQ |
| 979 | 9030 | A | 1921 | 2 | 1059 | GRVGFFAGNPGSDSFGGLLGLTPVLR WVADGGTIPKRHELVKGPKEKVEVDK ETELVAQWNYCTLSQELRRPIVACELG RLYNKIEPVIEFLDKSAEKALGKGSISH* NALTNC*QS*KLSDNPCPGKIGKNTKG DKHDDLQAGASFI/CP/LVGGPGRWNGR HRFLPSGGCGLCCFS*AEPWKEIKAFC HTCGAGLSRRMMIIVLNGTKEDVDVLT RME/AEKAVERSFKRISKPKAAESVSKT QMSVEGSPRAHQKLRPGK*RSALDSR EKKTNLAPKSTAMNESSGKAGKASVW SHKEVHR*PVKNRKPNSLFTTHSFRQS APKEGVCPTGVHPTPTCF |
| 980 | 9031 | A | 1922 | 272 | 467 | |
| 981 | 9032 | B | 1923 | 131 | 268 | XFVTCNEKVAKEIARAVVEKRLAACV NLIPQITSYEWKGIKIEDX* |

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| 982 | 9033 | A | 1924 | 2 | 353 | GPPTQPSASDSGSGYVPGSVSAAFVT CPNEKVAKEIARAVVEKRLAACVNLIPOI TSIYEWKKGIEEDSEVLMSVHPYEA IALPVEHGNFPYLQWVRQVTESVSDSIT VLP |
| 983 | 9034 | A | 1925 | 70 | 357 | |
| 984 | 9035 | B | 1926 | 120 | 839 | MSGGRAPAVLLGGVVS DRPRPAPSGPRS LDRYPHPKSQRRFAKEIARAVVEKRLAA CVNLIPOITSIYEWKKGIEEDSEVLMMIK TQSSLVPALTD FVRSVHPYEA* |
| 985 | 9036 | A | 1927 | 259 | 935 | GASLLLSFVWMPALLPVGLPAFLFANPE SLLTMG/SLGSPSDPSRPASDSGSGYVP GSVSAVAVFTCPNEKGS PREIARAVGGR RRLAAACVQSSPQITIPSMKWKGKDSR EDS*GCWMDGFKTQKFPWVPSFWTDFV VRSVAPYEVVAEVI ALPVEQGNFPYLQW VRQVTESVSDSITILAMMSPVPAHHEDP RDTSKAFLTFQVMTWAPNKSRLWVKKK KKSRL |
| 986 | 9037 | A | 1928 | 285 | 476 | LLKHLINNMVSKTTWLGVL AHTCNPS/ TNFLGGRGRIS*GQEFESLGNMGRPC LYKNRQKTN |
| 987 | 9038 | A | 1929 | 218 | 602 | NGGQAVAHACNPSTLGGQWRVDHLRS GVRDQPGQRGETPSLLKIQKLAGRGGAR LWSQLLRRLRQENRLNLGGGCGSEPRW HHCI PAWGNKKE*NGNYAQRMGERWL TGLKHQRNGEDRTVREL SGR |
| 988 | 9039 | A | 193 | 128 | 363 | VHTWMLSSP*GPQPGVFHAQIRGCPFLSP *RVCQFQVFSLFYFDLLWVFILFFLEAE YHFVARLECSGLISAHCNLC |
| 989 | 9040 | A | 1933 | 2 | 355 | TSM LGCTVFLR/YCVYSYCNV LATVW SSLV*RSRLICHLVS/WSFVTDCKACYN TGMLFYSDY**FVYYF*YYCFFLCSLFFSI CLLMYFNIFFF/CNFMFDCYILL SFYFIIL YHYF |
| 990 | 9041 | A | 1936 | 139 | 782 | GLHHGCSLGMEEAAGRGDRSRSCRAP QHHRPPPLSCQPRLLGEAGRGGVGRK HGSL*KQAPPPRGRAETPGLANHTLPPR VPP/SEGQQHPREGQGLHGGPGKEGKPH RRKLKASVPCVSAERVNGPKGSSLQTAR IHPTGGHRKPTGAVCVCAAAHTSAAR GPLRPHHTACPAHVCTRRCRREHTPPSL CTRVPLSGPGGSSLLHVLSRA |
| 991 | 9042 | A | 1937 | 1 | 1878 | |
| 992 | 9043 | A | 1938 | 345 | 557 | LYMLIRMRLKEGRAKMVESIFR**FILE* SVLS/RIMKPGMYPVLNRVWKCGNSSSV SYPEEKVVGWLLKFI |
| 993 | 9044 | A | 1939 | 345 | 511 | ARDATFVNGLDYLITLPYCGWKDCKKK CPLRQFP*PFNCCFFLVFVRV*KHSLP |
| 994 | 9045 | A | 194 | 233 | 598 | |
| 995 | 9046 | A | 1940 | 827 | 2660 | |
| 996 | 9047 | A | 1941 | 478 | 1150 | SMPWQIGRSSVSAPPTITPTSSTASWTIVS STIWSPHVPATTKVSTLHWTVVRLLVII SKIIVISTSISSSIVVITTSVAPTLVAISRSS TTISSSSSITGATSKIATSRSSSSAGSRAE VLLAELFLEQRQFSLQRQDESGCSSAEI SLISLGCGKSG*SD*VRDGERKRNSSVSS LLVA*ALKPQKKV*GTTTNGESLQTVW **GILQAKDQEDLVL |
| 997 | 9048 | A | 1942 | 123 | 734 | LFKSAIKNGLQHELHCRKWEKKQNGKVS KKVQAEAPVESGVEKVLDRRVVNGKV EYFLKWKGFTDADNTWEPEENLDCPE LD*SRFLNFSRKAGQRKRWPKRKSLSD VSESDDSIHRRKRDAAADQPKEDFARGL DP*KK*LG AHRPASGEVLMFLMKWKDS DEADLVLAKEANMKCPQIVIAFYEEKP TWHSCPEDEAQ |

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| 998 | 9049 | A | 1943 | 1092 | 1285 | IDVCVCLALLRLECSSVISAHCSCS/SG SSDPPTSAS*VAGTTTACHHAQLIFGFFFF LKRWGF |
| 999 | 9050 | A | 1944 | 76 | 532 | LPRPRSRLTALPPPSFLQTPKSRALMAG LEVLFASAAPAITCRQDALVCFLHWEVV THGYCGLGVGDQPGPNDKKSELLPAGW NNNKDLYVLRYEYKDGSRKLLVKAITV ESSMILNVRTYKNSSEELRSRIVSGIPIH EQWEKANVSSP |
| 1000 | 9051 | A | 1945 | 109 | 1008 | ALPPPSFLHTPKSRALMAGLEVLFASAA PAITCRQDALVCFLHWEVVTHGYFGLG VGDQPGPNDKKSELLPAGWNNNKDLY VLRYEY*GWGPESFLVESHSPWESSIDSS MLLGIMGSQQSWQI*PLNLG*LFSMAEH LGDFHRTYKNSSEELRSRIGA\GIL\TPIHEQ WEKANVSSPHREFPPATAREVDPLRIPPH HPHTRSQPPWCDPLGPFVVGEDLDPF GPRRVGMNVADPLRSGLPRAFNDPSSG LPNRLPPGAVPQAGFDPPGPIGTSPPG VNP\DHLP\PPG\YDDMYL |
| 1001 | 9052 | A | 1946 | 152 | 991 | RKTKCVTRPAVVFQSP\TSRSSRASACE VAFPRGQPRKGPKRDNWILGTRPSWVA VCSSPRLGLSR\EYKLVMLGAGGVKSA MTMQFISHRFPEDHDPTIEDAYKIRIRIDD EPANL\DILDTAGQAEFTAMR\QYMR GEGFIIC*LLSRIRRSFHEVPESLNQLIYR VVRTDDTPVVL/VWGNKSDLQTA*DRF TKGRKGLALAPENSSCPLFWRTSGCHTR VYIDGCFPHAPVRE\RRKEKEAVL\AM EKKS*APKTSVWKEAKNHPFRKKKDSV T |
| 1002 | 9053 | A | 1947 | 305 | 406 | |
| 1003 | 9054 | A | 1948 | 372 | 501 | RPGAVAHSCNS\STLGGRGRWIT*GLEFE TCLANMVKLCFLHLY |
| 1004 | 9055 | A | 1949 | 441 | 812 | ITTHLYISKPLLCTPMKTYNNYLSIAKIF *FSLLRQGLALSPRECTSTITAHCSLNLP GFKQSSHSQPSE*LGTTDTHHHIQLVFLIL /AETEFCHVAQGGL/NIS*VQLIHLPTSK VLGLQM |
| 1005 | 9056 | A | 195 | 38 | 1222 | EPESCSVTRLECSGVISAHCNFR/LPGFKN FPASASQVHGTTGTPHHAQLNLYF*VEE QGFPMLAPGWILGSP*PLMDPAPSLALP QSAGDPQP*AHPHPGPSYLF\FKERENYE RPKII*LNPLPLAQGKKMEFALI\WVMKH TQ*IRNNHIFSKRQK/C*DL*SYMVAYFW VGKK*EKNITSLTGNDTF**KILLSFPTRM IHCKAKIY/IAKFFFWRRSLTSVTLGWSA VWHNLSSLQPPPSGLKRLSHLNLPNT/W DYRPPCPANLCFVVVVVLLFVFW*RW GF\TMLARLISNS*PQ/CDPPTSASQSAEIT GMS/HPCLAMGFVFH\TL*KPPFFKDYM KSFFQFFKYLIQG*CSLV*GVRYRSSLIFF F/CFFETESCLVTQAGVQWRDLGSLQS |
| 1006 | 9057 | A | 1950 | 2 | 370 | |
| 1007 | 9058 | B | 1951 | 209 | 524 | MLLSLAAFSVISVVSYLILALLSVTISFRI YKSVIQAVQKSEEGHPFKAYLDVDITLSS EAFHNYMNAAMVHINRALKLHRLFLVE DLVDSLKLAVFMWLM\TYVX* |
| 1008 | 9059 | A | 1952 | 3 | 463 | |

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| 1009 | 9060 | A | 1953 | 49 | 1129 | RDLEFSCRIILFPLPSLPPRISFHPSPTLAR VAMAEPSAATQSHSISSSSFGAEPSPGG GGSPGSLPRPWGPKSCSSSCAVHDLIFW RDVKKTGfVFGTTLIMLLSLAAFSVISV VSYLILALSVTISFRUYKFVIAQVQKSE EVGHPFQKPNWNVDITLSSKSFNNMNA AILHINMFLKLIIRLFLVEDLVDSLKLAVF MWLMTYVGAVFNGITLLILAELFISVPI VL*RYKTQIDHYVGIARDQTKSIVEKIP SKTPLGIAKKKGRIKYMETR NATSYLKH HLISYNVVTCTMKENTQCQLEPAFQAFF LIWCFLPSFFNPQSSSTKIDGLIKDLFLD LRRRNQIS |
| 1010 | 9061 | A | 1954 | 46 | 519 | SQTPMGHFEEDKATITSLWGK\VNVE DAGGETLGRLLVVYPMGPQRFL*PALG NLSSASAIHGQPPKSRAGQEGC*RLG DAIKAPGIDLQRAFAQA*SELALVDKLA MWDSLRFKASWGKFLVDPFLAIPFSA KEFHPLRCQVFLGQKDG |
| 1011 | 9062 | A | 1955 | 1 | 747 | |
| 1012 | 9063 | A | 1956 | 1 | 813 | MKEENLCQAFSDALLCKIEDIDNEDWEN PQLCSDYVKDIYQYLRQLEVGLQSNPH FLDGRDINGRM/RAILVDWLQVHSHKFR LLQETLYMCVGIMDRFLQLSLPAEDREA LGTSSPQHSAGLDVGYKSGFILSPHPC MSKIEPEDEKLSFLFIGPFLKNPSPRANG DPMFLCLNEDEAQQLEETKWTGCQKQL CDPLSEEVKTGEKLVQTKGERTSRIREV QFLAQNHITRRWQSWDLGTSSLTPEPVF SLEINVREQRDEDNIQVLRG |
| 1013 | 9064 | A | 1957 | 1 | 1390 | EATASKIPSAAGSESSPNGASYASVPPFS VRVPPWAGLALLPSPSLMALLRRPTVSS DLENIDTGVNSKVKSHVTIRRTVLEEIG NRVTTRAAQVAKESSGTPKFQVQPTKTT NVNKQLKPTASCQTQYQMGKVWLPKG PSPTPAEDVSMKGRESLPKLFSALLCKI EDIDNEDWENPRLCSDYVKDIYQYLRQ LEVLSINPHFLDGRDINGRMRAILVD WLQVHSHKFRLLQETLYMCVGIMGSD F*QVQPVSRKKLQLVGITALLAPKYEK MFSPNIEDFVYITDNAYPSISQIREMETLI LKELKFELGRPLPLHFLRRAS*AGEVDVE QHTLAKYLMELTLIDYDMVHYHPF*G* PAAASCLSQKVLDKGMEL*SQYYHK DTQENEVLEVHASTMAQECGAK*MENL NLNSIGHQRIKYAKQQT*KISMIPQLNS KAVKDLAASPILIGRS |
| 1014 | 9065 | A | 196 | 526 | 835 | FNLNFTVSLRTHSLPIPFSSNERIKPGKS TIDGPWTRRTRL*RKNLWMIQ*LWDFLF/ VLFETDSSSVARLECSGAISVHYNFHLP SSDSPDSRSMPIVDRO |
| 1015 | 9066 | A | 1964 | 33 | 513 | |
| 1016 | 9067 | A | 1965 | 1 | 503 | GHESDNLLFVQITGKKPNFEVGSSRQLK LSITKKSSPSVKPAVDPAAAKLWTL SAN DMEDDSMDLIDSDELLDPEDLKPPDPAS \LRA\ASC GEGKKRKACKNCTCGLAEEA EKEKSREQMSSQPKSAICGN CYRGAMPS GCASCPYLGMPAFKPGKVLSDSNLHD A |

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| 1017 | 9068 | A | 1966 | 29 | 1270 | PPFWPAVFQVCQYCTARMADFGISAGQF VAVVWDKSSPVEALKGLVVDKLQAF/TP GNEGRVSVENIKA AAVAILPTKNPSFGHY FVQ/CLVPGKAPLWHS A*DFWAGNPPGF LRPGWMFFFLKEPVETAVR*Q*AKWKT ASKLCSAL/TLGLV/EKLELQREPLTPE EVQSVREHLGHESDNL FVQITGKKPNF EVGSSRQLKLSITKKSSPSVKPAVDPA A KLWTL SANDMEDDSMCIFCGCSLTHRW PLEHV VQVE/IMMDQPKRRTRVDTFFTP RTPKFPSRSPASHFSFSIKQKT/TRPVSLIA LNTLAQDLIDSDELLDPEDLKKPDPSLLR AASCGEGKKRKACKNCTCGLAE ELEKE KSREQMSSQPKSACGN CYLGDAFR CAS CPYLGMPAFKPGAEKVLLSDSNLHDA |
| 1018 | 9069 | A | 1967 | 3 | 498 | LANRAIMSHKQIYYSDKYDDEFEYRLV LAREQLATGRELWPLRAQGISNRN*GDR IGACVRDMSCCPKDIKLVPRTHLMSES EWRNLGVQ/QRSGQWVHYMIHEPEPHI LLFRRPLPRPKEMKLGKLT FQPSFYT AGPYLPNIFLDNIYVGLLVFFTFDI |
| 1019 | 9070 | A | 1968 | 1 | 690 | RRKAFPKRLPKMAEVQVLVLADGQGH LGRLAIAIVAKIQVLLGRKGGCSYACEGI HISGNFLQNQVCSTLAFPLQA/RMNTNP SQGPYHFGAPSRIFWRTVVRGMLPHKT KAEARPLDRLKVFDGIPPPYD\KKKR MVVPAALKVVRFEAYTESFAYLGRLLA PEVGWNAIRPV TAPPGGERGKRKAKIH YRKKK*LMRLRKQAREETWRKKIDKY TEVLKTHGLLV |
| 1020 | 9071 | A | 1969 | 2064 | 2561 | KRFWSFALFYILKLL/CIDSIVRIGTILY STVLFFIFLKFV*LVLITFIQIFAIFGSET F*QVGV*FLIPNFFSRVLLILSEGKVI*VC QLIVLLGLNFHIVFTVYGEVVGIIYSILN K/AVIHFFIKV/YFHVKFLFLYVLLSYIT QLF*KSSFVEVLVK N |
| 1021 | 9072 | C | 197 | 7 | 276 | MQWRDHNYCIFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXLARPFI* |
| 1022 | 9073 | A | 1972 | 786 | 1502 | PPPTKKEMFVPYSPEQRIETSI PPFKGTG RP/PGQGR TWERPPFSLEGKAGALP LLS PRTTKGEDPSETLAQSGQEGDCLNRW QHLH*SAFRPSSAEPFTRKRLEGGPAPLR YPGAGNEPGRDAEGRP*GALAGRPRWP PSHGRPPAPCHPASRGGTARKTP/GRST KPPRFPPPLGDATSGKAIPANGRKGGA MSPHRGAGPASPSRFFSHIKQGRAIPHVS SRLHFSPPSSGSR |
| 1023 | 9074 | A | 1973 | 8 | 234 | SAQMAVTTADPRVRPRVRTQLCSLASLI QTL LVHLTPEEKSAVTALWGKVNVD E VGGKALGRLLVVL PWDPKRSFQSPLGES VPTP*MKVGGKALGRLLVVL PWDPKRS F |
| 1024 | 9075 | A | 1974 | 1 | 169 | NLYISNLPLSMDEQELENMLKPFQGVIST RILRDSSGTSRGVGFARMESTEKCEG |
| 1025 | 9076 | A | 1975 | 2 | 219 | |
| 1026 | 9077 | A | 1976 | 17 | 795 | HSTAKLY*HSTFAKRSHRNPQHPYV*IS KSLTSSINSSTSSNSGWDQLSKTNLYIRG LPHTTDQDLVKLCQPYGKIVSTNAILHK TTNKCKGYGFVDFDSPVAAQKAVSALK ASGVQAQMAKQEQDPTNLYISNLPLS MDKQELENMLKPFQGVISTRILRDASGT SRGVGFARTESTEKCEAVMVQSPSWTQ PQPYILQHPGAVLTPSMEHTMSLQFASM ISPLAQQMSHLSLGSTGYMPATSAMQG AYLPQY |

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| 1027 | 9078 | A | 1977 | 3 | 1421 | CLRRLHEFGTRPPPTPLPSSPERERQESP RLGNPKVSATLHGRLPSSFMGKVWVQQ MYPQYATYYYYPQYLQAKQTLVPAHPM APPSPTTSSNDNHRISISSNSRWDQLSRTN LYIRGLAPPHTTDQDLVKLCQPYGKIVIS TKGNFGIRTTNNCKGYGFLDF*QPMQQ LKKAVSALKASGGSSSKWAKQQGQDP TNLYISNLALSMDAEQELNMLKPFQGV ISTRULRDSSGTSRGVGFARMESTEKCE AVIGHFNGKFIKTTPPGVSCPHRNLL/CV LSFAGWEGQEKGDRTPNKYIPNGRPWA *EEGRGETLLGLTLT/YDPTTAAIQNGF YPSPIATNRMITQTSITPYIASTVHAFQ VQSPSWMQPQPYLHDPGAVLTPSMEH TMSLQPASMIPLAQQMHSLSLCSGTGY MPATSAMQGAJLPQYAHMQTTAVPVE EASGQQQVAVETFNHSPYTFQPNK |
| 1028 | 9079 | A | 1978 | 2 | 1440 | NSGPSSFMGKVWVQQMYPQYATYYYYP QYLQA/KVWKAFGNTK*KGRVKNRKMML VGWQTL*TLFLVGQKNQSLVPAHPMA PPSPSTTSSNNSSSSNSGWDQLSKTNL YIRGLPPHTTDQDLVKLCQPYGKIVSTK AILDKTTNKCKGYGFVDFDSPAQAQA VSALKASGVQAQMAKQEQDPTNLIS NLPLSMDEQELNMLKPFQGVISTRILRD SSGTSRGVGFARMESTEKCEAVIGHFNG KFIKTTPGVSAPEPLCKFADGGQKKR QNPKNYIPNGRPWHREGEVRLAGMTLT YDPTTAAIQNGFYPSPIATNRMITQTSI TPYIASPVSAQYQVAKETRENYRGSJK VQSPSWMQPQPIYFYQHPGAVLTPSM KHTMSLQPASMIQPFWPQQMSPSVH*G QHPEPYHALQPSLCKGALLGPQYCTYC RLTAVPC*GRQSGQTGRLAVRGRLNDPF SIYRFNPNK |
| 1029 | 9080 | A | 1979 | 104 | 340 | TGQSYKKRKFVKWLKQINRYLTSFLF/VF KEIRSHSVA*TLEHSGAIMAHCSLKLGL SNPPASASQVAGTSGVQYHTSLI |
| 1030 | 9081 | C | 198 | 2 | 28 | MIDTHTPS* |
| 1031 | 9082 | A | 1980 | 118 | 528 | |
| 1032 | 9083 | A | 1981 | 1 | 864 | |
| 1033 | 9084 | A | 1982 | 3 | 4258 | |
| 1034 | 9085 | A | 1983 | 44 | 1360 | VWDCPGLRWASFYLRSLSWRAHRPQCGT ISFVTVNAEEQEKQFVSSRTKQKAKEEK LEKCGEDDETIPSEYRLKPATDKDGKPLL PEPEEKPKPRSESELIDELSEDLDSECKE KPSKPTKTEESKAAAPAPVSEAVSRSTS MCSIQSAPPEPATLKGTVDDAVEALA DSLGGKEADPEDGKPVMDKVKEKAKKEE DREKLGEKEETIPDYRLEEVKDKDGKP LLPKESKEQLPPMSEDFLLDALSEDGSGP QNASSLKFEAKLAAAISEVVSQTPASTT QAGAPPRDTSSDKDLDDALDKLSDSLEQ RQPDPDENKPMEDKVKEKAKAEHRDKL GERDDTIPPEYRHLLDDNGQDKPVKPPT KKSEDSKPPADDQDPIDALSGDLSCPS TTETSQNTAKDKCKKAASSSKAPKNGG KAKDSAKTTEETSKPKDD |

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| 1035 | 9086 | A | 1984 | 159 | 2467 | EKKGSYKKAASLGSSQSSRTYAGGTAS VTKVSAFSGATSKSYSMNPETETKAIPVS QQMEGPHLPNKKKHKKQAVKTEPEKKS QSTKLSVVHEKKSQEGKPKEHTEPKSLP KQASDTGASNDAHNKKAVSRSAEQQPIS EKSTEPKTKPQDMISAGGESVAGITAISG KPGDKKKEKKS LTPAVPVESKPDKPSGK SGMDAGLAD\DLIDTLGGPEETEEENTTY TGPEVSDPMSSTYIEELGKREVTIPPKYR ELLAKKEGITGPPADSSKPIGPDDAIDAL SSDFTCGSPTAAGKKTEKEESTEVLKAAQ SAGTVRSAAPPQEKKRKVEKDTMSDQA LEALSASLGTRQAEPELDLRSIKEVDEAK AKEEKLEKCGEDDETIPSEYRLKPATDK DGKPLLPEPEEKPKPRSESELIDELSEDF DRSECKEKPSKTEKTEESKAAAPAPVS EAVSRTSMCSIQSAPPEAGTLKGTVQDD AVEALADSLGKKEADPEDGKPVMDKVK EKAKEEDREKLAGEKEETIPPDYRLEEVK DKDGGKATPCPKSLKEQLPPMSEDFLLD ALSEDFSGPQNASS\NFEDAKLAGAISE WVSONPRFSTT/TQAGAPPRDTSQSD\K ALGD\ALDKLSDSLG\QR\QPDPG*GTNQ WEG*S*REKAKAEHRDKLGRKRWTLFP PEYRHLL\DDNG\QDKPVEGHLTKKSEN QRNPGDDQDPIDALSEDLDS\CPSTTET SQNTAK\DKCKKAASS\SKAPKNGGKAK DSAKATEGTSKPKDD |
| 1036 | 9087 | A | 1985 | 2 | 788 | EFSASIVGICTMPWALLLLTLLTHSAVS VQAGLTQPPSVSKDLR\QTATLTCTGNS DNVGYQGAAWLQHHQGHPPKLLFSRN NNRPSGIHKRFYGSNSGTTATLTISGLQ AMDEGDYYCNSRDSSGNHLRVFGGIGT QVDPSLRVRQGMPPWVNFVPGPSSEEAS SPNKAHTGVVFISDFLTPGNP*QVAIWKA DSQPPFKAGVETPPHPKQSNKYTDSIS YLSLTP*PGGSPHRS LQLARVTH*RGAPL EKTVAPTRMFH |
| 1037 | 9088 | A | 1986 | 226 | 401 | TSGDHWNIAPAPHENS D L L L V Q G H D Y K YRYFGLIVCVL*QAIVTPEEPQSVPRLRT R |
| 1038 | 9089 | C | 1987 | 211 | 285 | MFYPPFNPRYFVS GF I A M N R H T D ** |
| 1039 | 9090 | A | 1988 | 107 | 192 | |
| 1040 | 9091 | A | 1989 | 1 | 285 | YIYIYIYIYIYIYIYIYIYIYNLDQSW FAPLLVCGP**AQVVTSELGNRN*SEKTF TWRICMRNIGRCSLGMLQDYFKPFDERS KVMLVV |
| 1041 | 9092 | A | 199 | 780 | 888 | NKRNQGSSRVGTHL*SQLL/RRLRQENH LNPEGRGCS |
| 1042 | 9093 | A | 1990 | 27 | 437 | IAEGNWCVYMPDIWVFPQAEAEEDCH SDTVRADDDEENESPAETDLQAQLQMF RAQWMFELAPGVSSSNLENRPCRARG SLAQKTSADTKGKQEQAKEEKLSDIVT NYIFFFWHMEIFTDTVSRHYNQTFGT |

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| 1043 | 9094 | A | 1991 | 25 | 1488 | GGSSAAASGVSSRADAPVLAQSPASAGN GRPSTPRVPGSRRHPSAPRSGPLPREDGC RTPGPQLPLPGA\LLRPRTLSSAAEDK ARSRHPDTQHPSSGGRCRGGTESPSSAA GRPASMAEAEEDCHSDTVRADDDEENE SPAETDVQALIPMIQAQWKLEPAPRVTS SRLENRPCRAARGSLQKTSADTKGKQEQ AKEEKARELFLKAVEEEQNGALYEAIF YRRAMQLVPDNEFKITFTRSPDGDGVG NSYIEDNDDDSKMADLLSYFQQQLTFQE SVLKLCQPELESSQIHISVLQMEVLMYIF RWVVSDDLDTSLAEQLSLVCRGFLTSC ARDP*KYARPGPALKVWGQKACIKLVS VTRPGREDVF*ERPPVS/RFDGVYISKTT YIRQGEQSLDGFYRA\WHQVEYYRYIRF FPDGHVMMLTPEEPQSIVPRLRTREYQ GLDAIPTGVITRLSPRHRTIRTQSIWLLIT KEKRKEKPL |
| 1044 | 9095 | A | 1992 | 242 | 433 | |
| 1045 | 9096 | A | 1993 | 243 | 549 | |
| 1046 | 9097 | A | 1994 | 81 | 436 | AKQGISPEGVMDVNTALQEVLKLA\LIH VWT*TRGNSRS*PKPLDKRQAHLCVLA SN\CDPE\MYVKLVEALCAEHQINLN*GL IDNNET/MGEWG*GLLLKFDRGGGKPRK SWFGCSCC |
| 1047 | 9098 | A | 1995 | 3 | 452 | |
| 1048 | 9099 | A | 1996 | 3 | 484 | PTLLVPTDSERTHPWLLSPADKTTVK/AP AWGKVGAAHAVRSMCAEALERMFLSFPT TKTYFPHFDLSHGSAQV*GPRARKVAD AL\TNAVAQRGTDAQRAVPPLSDLHAH KL\RVGPGSTFKLLKATGLLG*PWPGPPS PAEFNPWRLQRLPWDKVS\WVSC |
| 1049 | 9100 | A | 1997 | 797 | 1049 | SEEECCSCLPSPAGSDQRLCTHLP\CVI VNSEWGVARY*LNVCS*PVFFSVGPK QYPYNLYLERGGDPSKEPERVVH\YEI |
| 1050 | 9101 | A | 2 | 25 | 619 | EFHRLRENPPWCSSPADKTNVKA\WGK VGAHAGEYGAEALERMFLSFPTTKTYF HFDLSHGSAQVKGHGKKVADALTNA VAHVDDMPNALS\SDLAHAKL\RV PVNFQSS*SQLPCLGEPWAAHLPAEFQ LAVATSSLGTKFPGLSVEAPLLTFQITFK GWKPRVGHAF\WASPOQLLPFAPVP PWSLK |
| 1051 | 9102 | B | 20 | 103 | 282 | EDTAAQSSPGRGEEAEASAAEAQGGEQ AYLAGLAGQYHLERYPDSYESMSEPIA HLLRP* |
| 1052 | 9103 | A | 200 | 224 | 552 | KVLRVARCGGSLLSRPSTLGGQGGRLM RSGVRDQPGQHSETPSLLKMQKLAGHG G/RAL*SQLLGR\LRQENHLNPGGRGCSEL RSRHCIPSRVT*DSISKKRRKKVL |
| 1053 | 9104 | A | 2000 | 546 | 882 | CHVPPTLGTRGQGTQDPFPFPHSPGAP APCPPPA/LLGPPRPFPSPVPVPGGENRK PFTSAP*A*VFPRTP\LGALS\RG*GSPVVG RGATPSPTPSPACGPLKCWWHLIKN |
| 1054 | 9105 | A | 2001 | 43 | 311 | |
| 1055 | 9106 | A | 2002 | 178 | 817 | SPASGHCR\NGAAVAMFGCLVAGRLVQ TAI*QQVAEDKFVFDLPDYESINHVVVF MLGNNP\FPEGMGGSVYFSPDSNGMP VWKL\G\SVTNGKPSAIFKISGLKSGEGS QHPFGA/NEYCPNLHLLRLGISGELLDS MAQQT\VR*CCWYPQFDSFTQ\TKML DNFY\NFCSSFAVSQAQMT\PS/SI*KCSFR PNVVLKWYEA\FSVSNIAFYN |

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| 1056 | 9107 | A | 2003 | 283 | 840 | TLFAGFTDVISIHKTGENFCLICGNGRFA VHCITLEEAKYKLCVKRKIWFHDAHTIH YLDSEVVKVNDTV*TGKITDFIKFDTGNLG RIGVITNRKKHRGSFDDVHVVDANGNRF APWLSNIFVTGKCNKPWISLPRGKGIRLT IAFHSDKWFCSDISVQNLCKRFSQGDGTGI KNSEARRCSNLQV |
| 1057 | 9108 | A | 2004 | 1 | 966 | GRPAPEDGGPLSLPNAAMARGPKKHLK RVAAPKHWMLDKLTGVFAPRPSTGPHK LRECLPFIIFLRNRLKIYALTGDDEVKKI CMQRAFIKINDGQVRN*YNLPLLGFMDEV SNEKTGENFPF*SN*HPRGPLL*HRITP EAKYK/VCAKMRKIFCGPTKGIPHLVTS *CPAPHPAYPRNPLIQGEMNTHSRILET GQD/ITDFHSKFDHLVTLCMVTGGAWNL GRNWVLITQORRGTPGSFDRWFT*KDA NGNKLATSDFSNIWLLGKGNKPWISL VPRGKGIPPHHLEERDKRLAAKQSSWV KWGPWVTWSDLLVP |
| 1058 | 9109 | A | 2005 | 1 | 383 | RIRKLCNLICVGESGDRLTRAACKVLEQLT GQTPVFSKIVREYELRKNNFSDTGNFGF GQEHIDLGKIDPSIGIYGLDFYVVLGRP GFSIADKKRRTCIGAKHRISKEEAMRW FQQKYDGIILPGK |
| 1059 | 9110 | A | 2006 | 3 | 224 | |
| 1060 | 9111 | A | 2007 | 176 | 384 | |
| 1061 | 9112 | A | 2008 | 2 | 669 | IMAQDQGEKENPHAGNFAFRKLVNLIC VGESGDRPTRAQAQVLEPAQQGKTPCVF PKA*HTPVKSLWASRRNEKIAFPTATSS EGAKARRNLCRRGLKRFSEYGVQDNTT FSGYWETFGFGI/QEHIDLGKIDPSIGIY GPGTSYVV/LGVRPGFQHPQTKKPGQGG CIGAKHRISKEEAMRW/FQQKYDGIILP GQINSPFLSKSNKKFSVNKKNNKKITL |
| 1062 | 9113 | A | 2009 | 688 | 884 | CSCVWNLSFHGNFHLKTPYSRIKKAKH /WMAHVYSPITLGGRGGWIT*SQEFETSL SNIHKPCLY |
| 1063 | 9114 | A | 201 | 41 | 320 | |
| 1064 | 9115 | A | 2010 | 442 | 780 | IEFVIKKIFFPFSHCLICLAIDLQLQ*YMG VPRMQLKTCYVRGKYRGVLEEQNIL WK*IHIPQVREDGRPCLPLRKLGGKGG GGGEPLNQHGDPVQGNPPYFLFCHMRN P |
| 1065 | 9116 | A | 2011 | 136 | 219 | DPAREGHPVCCAGQRPCVDGHGQEKGF LKAALVELGASNPWS*DTEVKPQSALP QASALTIWVSQQGVLSATILYEILLGKA TLYAVLVLSALVLMAMVVRKDF |
| 1066 | 9117 | A | 2012 | 3 | 762 | TLRGAVLRGAAGRLGGGLLVLAGRAM GLSAVGRTRAESGTAERAAPVFLGLQA VSTDTQMFGPGTRLTLEDLKNVFPPEV AVFEPSEAEISHTQKATLVCLATGFPPD HVELSWWVNGKEVHSGVSTDPQLKEQ PALNDSRYCLSSRLRVSAFWQNPNNHF RCQVQFYGLSENDEWTQDRAKPVTOIV SAEAWGRADFGFTSVKSYQQGVLSATI LYEILLGKATLYAVLVLSALVLMAMVVR KDSRG |
| 1067 | 9118 | A | 2013 | 1 | 1010 | RYSFCKAVMGIRLLCRVAFCLAVGLVD VKVTQSSRYLVKRTGEKVLECVQDMD HENMFYQYRQDPGLGLRLIYFSYDVKM KEKGDIEGYSVSREKKERFSLILESAST NQTSMYLCASSLFNSGYQETQYFGPGT RLLVLEDLKNVFPPEVAVFEPSEAEISHT QKATLVCLATGIFPDHVELSWWVNGKE VHSGVSTDPQLKEQPALNDSRYCLSSR LRVSATFWQNPNNHFRQVQFYGLSGN DEWTQDRAKPVTOIVSAEAWGRADCGF TSVSYQQGVLSATILYEILARGRPTLYC |

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| | | | | | | LCW*APLVLMAMVKEKGFLKAALEVE LGAF |
| 1068 | 9119 | A | 2014 | 344 | 463 | |
| 1069 | 9120 | A | 2015 | 1075 | 2102 | QQKPGQPLFLGSISPKKSFKTRKQKSSSK AEYNLTACKCLLCKRKYSSQIMLKRHM QI/RPQDNSFWNKL*KRKR**YCQQFRN KS*S*TSRFCRIFTFFHYPFSTE/CN*REQII QMKKRTHRQHRKIKLNKTLK/CPKSTSP SAAGGQKTRKPKLSAGDFKQLYCKL CKRQFTSKQNLTKHIELHTDGNNIYVKF YKCPLCTYETRRKRDVIRHITVVHKSS RYLGKITASLEIRAIKKPIDFVLNKVAKR GPSRDEAKHSDSKHDGTSNSPSKKYEVA DVGIEVKVTKNFSLHRCNKCGKAFACK TYLEHHKKTHKANASNSPEGNKTKGRS TRSKALV |
| 1070 | 9121 | A | 2018 | 1 | 408 | SNPRVRGGGTHRSQGAFANMCRGGR MFAPT/KTWRRWHRRVNTTQKRYAICS ALAASALPALVMSKGHRIEEVPPELPLVV EDKVEGYKKTKEAVLLLKKLKAWNDIK KVYASQRMRAKGKK/RCGR*ERKEGC CWC |
| 1071 | 9122 | A | 2019 | 28 | 1437 | EERGCSLPLACARPLISVYSEKGESSG KNVTLP\AVFKAPIRPDIVELCSNPNLRK NNRQPYAVSELAHQTKAEISWGTGRA GGSKFPEVRGGGTHRS\GQGAFGWMCRR GGRMFAPTKTLGRRWNRRVNTTP/QK RYAICSVALAASALTSNWVMSKGHRIEE VPELPLV\VEDKVEGYKKTKEAVLLL KKLKAWNDIKKVYASQRLRAISKGKM RNRRRIPGAGGPCIYNEDNGINKAFRNIP GNYSAM*AKLNILK\APG\GHGGVRFCA WTEKCFSGKLDELGYGTWR*S/RASPQRS NYHSFPLHK\MINTDLSRILEKPQRSQRA PPGHHAKKIHR\VLKKNPTEKTLRJML KLKPHMQKTHAAGTTHSSPRNRNHKLR V\VDKGKLLHQRHLQAKSDEKAAVAGKK PAVG\KKGKKAP\VG\KKQKKPLVGKK\ AAATK\KPAPEKKPAEKKP\TTEKKPAA |
| 1072 | 9123 | A | 202 | 80 | 518 | VGPLTPNSVLPRGSV/LPTEVGLDALGEG LKGLCGPNPVVETTNQGFPMKQGVLT GRVR*ET*DQSTQDSASCYSTCPAAQTA AYCSE/ASSVPRKIKRLQNMLNFWPRE* RRLRRSARNKLRRDADFPLCELLLSLN PVRNKIF |
| 1073 | 9124 | A | 2020 | 1 | 2196 | |
| 1074 | 9125 | A | 2021 | 1 | 207 | |
| 1075 | 9126 | A | 2022 | 1 | 1062 | |
| 1076 | 9127 | A | 2023 | 171 | 476 | LPRFQTLRNTETEDHSCCCSGRRRFAAA VASRSQ*GNPASLAGSSTTGARSCAPVA RTQRCPRCAACGCWRWRTRWICSAKG WFAHSQFSARIDWLQFLEW |
| 1077 | 9128 | A | 2024 | 1 | 781 | |

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| 1078 | 9129 | B | 2025 | 1 | 1602 | MGYRARI RNHVWLATQNHSTLVTERSA VPFLPVNPEYSATRNQGRQKLGRFNARE FGNLIIDILSESKRRQQAARAEQPHSAAAA DGVTFSPVPTPHTRHSYAMHMLYAGIP LKVLQSLMGHKSISSTEYTKVFALDVA ARHRQPTRRKAPAVLGQCRAIATRERPG WFHVAEVRASRRGRSPTQCADPGWASI SRGVLVCDECCSVHRSLSGRHSIVKHLR HSAWPPTLLQSGFPGPSRRAAPRAARGP TPRTEEAAWAAMALTFLLVLLTLATLCT RLHRNFRRGESIYWGPTADSQDTVAGSP DHGLLAFAYHRLVRFLWVLCPGWAFF LVNSSRGGVFNPIHPCPRHGOARFAGV GRAEDVTFLYHPCAH PWLKLQALLAY ACMANPSLTPDFSLTQDRVDIEQLDPRG RTPHLATTLGHLECARVLLAHGETWA RENRSWTVLQEA VSTQDLELVQLVLR YRDYQRVVKRLASIPVLEKLRKQRSYL PGRPLARLRRSVNSSGAVGMIKSESOMR WVFGP* |
| 1079 | 9130 | A | 2026 | 2 | 692 | ENRSGFQSRRIYSISKQKKLTFFDVKD NT*SWNAVASREECYLG VIT*SRTLGRS *TKDRLRRT*SMPCYSDSM/ISMQELEFR HLNTIQKMRCELIRLQHOTELTNQLEYN KRRERELRRKHVMEVRQQPKGLKSKEL PNKKSSFQGYLQNSQTRQYKALRNHLE TTPKSEHKAVLKRLKEEQTRKLAILAEQ YDHSINEMLSTQAVSLLFLGQNKFSAPFL PPPE |
| 1080 | 9131 | A | 2027 | 1 | 2933 | MDDIPEARQYRHNQAYAYSIOGDGAE DDDERIVRFHTRVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFVDQIRKSD GTLQEHGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNPYAMRLY ESLCQYRKPDGSGIVSLKIDWIIERYQLP QSYQRMPPDFRRRFLQHIFVLRERPET |
| 1081 | 9132 | A | 2028 | 6994 | 7054 | LISTSDLYFL*DL*VRCKQTGVLPWFHTT TIPRSSLEVNPFRPTYHLCEL/SASYLTSW YLSFLIWTMG*LLHLHHTELL*G*SNKSC *VLCMEPDTVTAHSAVCTQFW/SNVDKN NNVISLRKSFLEFF*QSFALVTQAGVQWR DLGSLQAPPPGFTPFSCSLPSSWDYRRP LPRPANFLYF**RQGF PETGFHHVHHVG QADLELLTSGDPPTLASQSAGITGVSHH VQPEGEGFCNCCCVVESGPFKERVG |
| 1082 | 9133 | A | 2029 | 411 | 713 | TNSLYGLNIYLEIDQHFRNMKIYRSNSLI LILILLHLYCIFALSDL/CSH*PQVAI*KEIN WPGAVAHTCNPSTLGNRGRWIV*GQEFE TSLVNMAKARLY |
| 1083 | 9134 | A | 203 | 63 | 552 | |
| 1084 | 9135 | A | 2030 | 3 | 84 | SGSTHASGGLQASRWRRAGTSRCSVSSL TSTSTASLRGLPTVATGLRSGSWTSHHG VAG*GRPTRPVGSRRRDGGERVRVGAL CQA |
| 1085 | 9136 | A | 2031 | 3 | 519 | SRWRRAGTSRCSVSSLTSTSTASLRGLPT VATGDYPPPDQASSNLTLSPPPGHTHCG NRGQPWPVLGRGGANAAASSSSRPEQG GGS/SSFARLSSTHGTGGGEGVKAVSSA *GP/GGLPGTLNLVGGGDVTDASLSALT GGLEGILEKP*AGRCPITDGNPREEGREP RAG |

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| 1086 | 9137 | A | 2036 | 247 | 1294 | MPNTAMKEKRCLLMGERSGSGKNQAM/ RSIIFAKLPFARDTRRLGATIDVEHSHVR FLAGNLVLNLWDCGGQDTFMENYFTSQR WNIIFRNVGSFDFK VFDVESRELAEKDMH YYQSCLEGHPRTLPAKINFCLVHKMD/ LLVQEDQRD/LIFKEREEDLR/RLSRPLEC ACFRTSIWG*GRFYKAWVQAFVYQLD FPNVSAAGRLNLRDFAQINEAD/EVLLFE RSVTFVLVISHYQCKEQRDVHRFEKISNIN KIQFKLSCSKLPASFQSMEVNRNSNFAA FMRHLFT*NTYVMVMSDVPDPLGPL LINHSQCPCGNHFEETGRELNGPQATVFP YGVVEYCQNALSEKA |
| 1087 | 9138 | A | 2038 | 311 | 458 | |
| 1088 | 9139 | A | 2039 | 1271 | 1540 | |
| 1089 | 9140 | A | 204 | 1 | 69 | SGVKNGRGYVVGISGGTTNKVSP*SRVS *PMAVSACY*VKNGRGYVVGISGGTTN KVSP |
| 1090 | 9141 | A | 2040 | 176 | 552 | MRSSKQMKPNFPRCSSITVLSVRGMVLF LTLACPRFKMSSRTDFRFGNPQVT*GSTI CSIFRLPSILSMRTTK/DQGMFIWQFQGM RFHF*SSETHLVTFLLPGIM*E*FQSLKPE PFSFLLSCYCH |
| 1091 | 9142 | A | 2041 | 204 | 401 | WHEFTGAENHCKTLPKENF*WCLCKSH PSEPKNAAYNRTLCDLGISKSEVSLGTSF EMWTSQGOE |
| 1092 | 9143 | A | 2042 | 123 | 311 | PSRRLGHPRWALSPHLLLPQRFCWVS FAPASCPC/DLFISDRSSVSVGLMKHRM LGLAELL |
| 1093 | 9144 | A | 2043 | 2459 | 3030 | TSPSTSLRPAPIPSPSPSSRPSSSQTTSAA SSPSSAWPKAASRQGA*RCRE*LPSWTS QSSPPLKSWGLDSAPPPPLSTCLSASTTR GAGAAATPQCSAPCLHR/CDKVPGFAVA QCINQHSSPSLPHSRHPPAGAPAAAGA PATATLEAPARPPPPQPRVQQSGVAGK DADECSACRRPTVMAATGF |
| 1094 | 9145 | A | 2044 | 1125 | 1695 | DFFSKIDDHSLQVLFFENQLLILFFPHFLN DCSNSLFFFFSEMSRSVAQLECTG/AILA HCNLRLLGSSDFPALASRVAGTTGTCHH TQLIFVFLVETGFHHVQGAGTCMQSCLI KGLRENHLNPGGGGCNEPRSRPLRSSLG NRVRLSQREKQNP*DAQVSEKGLNTLEL QAKF*GVSHVFPGER/VSLISQNP*PFWK KVIKQVSRLRFKKPQDPFRASQSLRIFQS HH*KSWNTYSQQRQVILFLCLSSVYFVK SFSKQGPRTLQILCPWAWSTCCRSRLRE PCTNARVTHLPTLNPRIEDATKQDSFLH GMVPIVRQGGQHRM*ENAGEFFPWELGL WMRGCFAGHTIRLLSFL*PFLSSF*R*SR K*SSLKMLDKNSQNNKTHASTSLIKNLP HLAPKSMATATKSNFKELRFLQQR*FT SSSP/CLKISY*YYSSLISI*MTAAIVFCF/C FSEMSRSVA/QAGVHWCNLSLQSLPP GFKRFSCSLSSWDYRHAPPHPAHFCIF SRDRVSPCWPGWSQSPGPHGLPAWASP KCWDYSREPPRPQQYFSFVTRTSLSPIT LRLCIAPCPNQAFTDPSRVLHLFVPASSIP PNLKVTLY |
| 1095 | 9146 | A | 2045 | 1 | 577 | PLKRS DGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPEEKSAVTALWGKVNVD VGGKALGRLLVVPWTQRFFESFGDL STPDAYMGNPKVKAHGKKVLRGAFSDG LAHLADNLKGTFAHTEVSLHC*QACTW DPGELQGSWGNVLVCVAGPITFGKRIST PPVAGLPNQENWLAWCWLNALGPQVIT |
| 1096 | 9147 | A | 2046 | 16 | 370 | |
| 1097 | 9148 | A | 2047 | 1 | 1125 | |

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| 1098 | 9149 | A | 2048 | 1 | 1941 | MWKHLWNWVIGSGWKTLDVLEEDRKT KENLVLLRDFSSGCDQSIDRNMDESVQA DEFSDRNEEVIGNWSKGQPCYTLAKDLS ALCPYPKALWKVELKSDDLGEIPLELQR LVHGGQVNLDMEDHQDQEYIKPRLRFK AFSGEGQKLGSLTPEIVSTPSSPEEEDKSI LNAVVLIDDSVPTTKIQRILADGSRILQRF NSTHRRRAVNGPSNQLPDKPGSPSPFCL APLITVCPAADDPSPALWLHLVAARSTS QRNGQVLCYLPRKWGAVAVCTSVEACC WVFWLLERQNDSGMQLGGPPPSAIFRW LAAPAADAPAATSGAGCLATAGGAKTR KLALAELEYDEVKCKSSKSNRPKATVFK SPRTPPQRTVKNWFQLIAPNAGEDAEQQ ELAFIAGGTAKWYSHFGRPFGNLLQRAT WNVSRKLLRTTQISGSLRYWGFPGFQAK VAATLAKQEVIPPYLSLGRGAEFKGLSQ NSLQAPLHGTSGQKKNDYPETA VLPKLP REKVSRRERKLASSRCLSLGTCMSEEA FLVITNSSSCSCEGGFPYLIAGKYAQDFG LVEEACFPYTGTDSPCKMKEDCFRYYSS EYHYVGGFYGGCNEALMKLELVHHGP MAVAFEVYDDFLHYKKGIYHHTGLRND PFHPFEL |
| 1099 | 9150 | A | 2049 | 1 | 2077 | MTYPENIQIKKITGVQWMVPLKYKEEGS KVTTYCNETMTGWVHDVLGRNWACFT GKKVGTASENVYVNIHLKNSQEKYSN RLYKYDHNFKAINAIQKSWTATTYME YETLTLGDMIRRS GGHSRKIPSSVPLCSS APLDVQLLVSPAKILGLYGGRMGMA GQKAPFLRAPVIGVSFADSFQPSRLQDSP QLFNQGGQLLSAAQVGSSGSQRDVNCSV MGPQEKKVVVVYLQKLDYDLDLGN SGV HFTIYNQGFIVLNDLQVGLPFFKYKEG GAARVTTYCNETMTGWGA*CVWGRN WAICFTGKKVGTASENVYVNTAHLKN SQEKYSNRLYKYDHNFKAINAIQKSL TATTYMEYETLTLGDMIRRKWWATSR KIPR/PKPAPLTAEYSQKI/LLHLPTSWDW RNVHGINFVSPVRNQASCGSCYSFAS MGMLE/ARGIRILTNNSTPILSPQEVVSC ISQ/YAQGCEGGFPYLIAGKYAQDFGLV EEACFPYTGTDSPCKMKEDCFRYYSSSEY HYVG/GFYG/GCNEALMKLIELVHPWGP WEVCFLEVYDDFLHYKKGDPTPHTGLK RPFSTPFELTNHAVLLVG YGT* LKPLG MEY/WIVKNKLGAPAWGLRNGYFRIPR GTDECAIESIAVAATPQFLNFRGRLPSIFI NGSASSCKGGIGIFTDCRLSTSIFRSLQID FP |
| 1100 | 9151 | A | 205 | 379 | 540 | IKKVRNLGPKHPRFSVLLLVHSCSTNGG VLL*RSSVPRKIKKRLQNMLNFWPRE |
| 1101 | 9152 | B | 2050 | 59 | 466 | MSAAMRERFDRFLHEKNCMTDLLAKLE AKTGVNRSFIALGVIGLVALYLVWLPSL HLCGFLWCMAPSPSNGAELLYKRIIRPF FLKHESQMDSVVKDLKDKAKETADAIT KEAKKATVNLLX* |
| 1102 | 9153 | A | 2051 | 1 | 915 | |
| 1103 | 9154 | A | 2052 | 1 | 3180 | FRAAVAAPVYPALGTAPGGETVPEMTA AMRERFERILHDKNCTDLLAKLEAKT GVNRSFIALGVIGLEALYLVFGYGASLL CNLIGFGYPAYISIKAIESPKNKEDDTQWL ITYWVVYGVFVSHC*NSFSDIFLSWFPF* LHG*KCGFLVGWCMAPPELLNGG*NCS KRRIRSFSPGSTKSQIGQVLVKDP*RPR PKETADANH*KKPKKSLP*ILLG*KKKKK GGR |
| 1104 | 9155 | B | 2053 | 171 | 256 | XVDPASSQAMELSDVTLIEGVGNEVMV VAX* |

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| 1105 | 9156 | A | 2054 | 187 | 437 | PWS*LGS LPT*QTAVQPAPGRYCVSRRI RPPPGACGPPGGTANGNPELPHPSEG NDEKAEAEAGEGRGDSTWGGWSWGC |
| 1106 | 9157 | A | 2055 | 2 | 165 | NQHHHTLPPSPHYHPQ*G*HQRAPWP GCWQGPGRNKGQHQAEPEGLQPL |
| 1107 | 9158 | A | 2056 | 1 | 506 | SPASQCHHYPLMMGSSVVRGAFGLPP VGPHAPGVGRMCRLLTQ*RPAGAGCYRC LLRR*RAKLGPRLESAPHLPPSPHYHP PQ*G*HQRAPWPGCWQGPRTAR*GGV PHPFSEAKVPLLDGPIPSALDWGPWAHP NRRAAWPQPP**DQLSRPVRSRVG*GGH KP |
| 1108 | 9159 | A | 2057 | 496 | 1092 | QPAPGQLLCHLATHPAPPAGCGPPGAG QGGKPELPHPSEGNDKAEAEAGEGRG DSTGEAGAGGGVEP/RP*ASP*HPRPAQK TSRCRQQSRGPPEI*G*HLPPSQWPHH CAAQIPQ*YRGAGCG*ARGYRCPEEQI LPWTRKPDETDLPGPPATRPSPHTAFSEH YRQLCDSLPLTPRVCSRPLSLGLPLGH |
| 1109 | 9160 | A | 2058 | 155 | 701 | PGLFRRGLPHPGTGPVQSPFNFP*/PPR/GP EAPPP/RSPAPPSLRGVDGL*PP*PTLLT GRDNWSY/PEAGARQPFSGGPMDDPSA PRE*DHPKAESPQKKGAGPLLTVRSRY GQGRSQAEGQSKDP*GRTPGVLPGPSR EFPVSVPIVFVLCRRFFSCKSWIMTLTFL PSGVSCGCDK |
| 1110 | 9161 | A | 2059 | 1 | 506 | DRDAEFYKFLQENDQSQLNFSDDSSEE EEESFHSPLPYVLEEAFAAAVATT/RGD QESAEANKFQVTDASVFNALVFNALV TFCIRDLTGCLQKLLIGKVAKDSSRMLQ PSSLLWGKLRVDIKAYLGSVIQLVSCV AETVVLAAVLWHISVLVPCFLTFFPKQCS RE |
| 1111 | 9162 | A | 206 | 287 | 449 | IKKVRNLGPKHPRFVLLLVSCSTNGG VLL*RSSVPRKIKKRLQNMLNFWPRE |
| 1112 | 9163 | A | 2060 | 9 | 2295 | VGCTLRVGVMAAAGSRKRLAELTVDE FLASGFDSESESESENSQAREAREAA RSPDKPGGSPASRRKGRASEHKDQLSR LKDRDPEFYKFLQENDQSQLNFSDDSSE EEEGPFHSLPDVLEEASEEDGAEEGEDG DRVPRGLKGKNSVPVTAMVERWKQ AAKQRLTPKLFHEVVQAFQAAVATTG DQESAEANKFQVTDAAFNALVTFIRD LIGCLQKLLFGKVAKDSSRMLQPSSSPL WGKLRVDIKAYLGSAILMSCLSETTVL AAVLRHISVLVP*FLTFPKQCHMLLKR VVVWSTGEESLRVLAFLVLSRVCRHKK DTFLGPVLKQMYITYVRNCKFTSPGALP FISFMQWTLTELLALEPGVAYQHAFLYI RQLAIHLRNAMTRKKETYQSVYNWQY VHCLFLWCRVLSTAGPSEALQPLVYPLA QVIIGCIKLIPTARFYPLRMHCIRALTLS GSSGAFIPVLPFILAEMFQQVDFNRKPGR MSSKPINFSVILKLSNVNLQEKAYRGGL GWSSCYDLNPGSYLHSAHCIGFPELVL PVVLQLKSLRECKVANYCRQVQQLLG KVQENSAYICSRQRVSFGVSEQQAVEA WEKLTREEGTPLTYSHWRKLRDREIQ LEISGKERLEDLNFPEIKRRKMADRKDE DRKQFKDLFDLNSSEEDDTGFSERGIL RPLSTRHGVEDDEEEDDEEDSSNSD GDPDAEAGLAPGELQQLAQGPEDLEDL QLSEDD |

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| 1113 | 9164 | A | 2061 | 203 | 1383 | MSSFGYRTLTVLFTLACCPSGDEKVF EVHVVRPKEAGRLSPKGSLEVNCSTTC NQP*SGVGLGDLSD*GFCWDEQVQLGN NYLGLKHFFIDTVLQCHFTLQSGQESM NSNVSVIYQPPRQVILTLQPTLAVVGKS FTIECRVPTVAEPLDSLTLFLFRGNEILA LWRTFRGRAAPAPQGGPQPHSNSTADR RGLAHRKLSPSLAVLADLMSIRGGWIFHK VHSAPKMLEVYETCVRTSPDWSSSLVTGG VGVACPLFVTSVLLCFIFGQHLRPASG MGTYGVRAAWRRLPQAFRPIATHGVA WPHTTVVTGTQCDSSGLRYQPWLKDCD RQORLGTLPFLARIQTPGLSPVPTVSPGI TMAREGSHHGGLSLDASLPTLSFTGWH EA |
| 1114 | 9165 | A | 2062 | 503 | 1808 | TTVQEESTVDSQPVPNIDHLLTNIGRTGV SPGDVSDSATSDSTKSKGSWGSKQDYS RELLVSSIFAAASRKRKKPKKAQPSSE DELDNVFFKKENVEQCHNDTKEESKES ETLGRKQKIIAKENSTRKDPSTTKDEKIS LGKESTPSEEPSPPHNSKHNSPTLSCR AILKESPRSLAQKSSHLEETGSDSGTLL STSSQASLARFSMKKSTSPETKHSEFLAN VSTITSDYSTTSSATYLA*PGLQSTEP*GA VSAESKGDEADDERSELISEGRPVETDS ESEFPVFTSLDFREAFPRKTARSTKSSR RNSEGESELSCTEGSLTSSLDSSRQLFSSH KLIECDTLRKKRSARFKSDSGSLGDAKN EKEAPSLTKVFDVMKKGKSTGSLTPTR GESEKQEPWTKIADRLKLRPRAPADD MYE |
| 1115 | 9166 | A | 2063 | 2 | 527 | DPEADSIRAEMSRVALAVLALLSLGLE AIQRTPKIQVYSRHPAENGKSNFLNCYV SGFHPSDIEVCLLKNGKRIEKVHSDLS FSKDWFSFYLLPYTEFHPQLKKDEYALP V*THVTLSPAQR*FKWDRGHVKQHHGG LKMPLHGWNDKFLACFFNIDMLITLT LLCTKM |
| 1116 | 9167 | A | 2064 | 3 | 163 | |
| 1117 | 9168 | A | 2065 | 611 | 1432 | TPHLAVITNQPEIAEALLGAGCDPELRD FRGNTPLHLACEQGCLASVGVLTQSCCT PHLHSILKATNYN/GYVCLPALPHPLGGQ VTWRRGRWANLRSPGKSLNS*HLEG*E NMCAKCLDAFIKFQNPDCGFLKFRR* DYLFHKRIGERSEG*NRWVYFFPVLP HTCLHLASIHGYLGIVELLVSLGADVNA/ QGWCFLPPTH*VRLVLML*AEIPNAIS ISNSFWFQEPNCNGRTALYLAVDLPNPD VSLLLKCGADVNRVTYQGYSP |
| 1118 | 9169 | A | 2066 | 1 | 1332 | MVQLSPHYRGDSEDGRKRMVRQRTKPV LFFWSDWLGNSPSLTPPQRNPQAFIGRR GGAAEPTAVRAAVPPASAPARKQRAAR GPAHPQQRPLVRAMFQAAERPQEWA MEGPRDGLKKERLLDDRHDSGLDSMKD EEYEQMVKELQEIRLEPQEVPRGSEPWK QQLTEDGDSFLHLAIHHEEKALTMVIRQ VKGADLAFLNFKTNLQQTPLHLAVITNQ PEIVEALLGAGCDLELRDFRGNTPL*SL ACEQGCLASVGVLDSSLAPPPQLHSILK GYPTTMGHTCLHLAFYPMGYWGHRGSF LVFLGVLDVKCSRSPCKWGPLPIHLAVD LQNPPEPGCSLLFESVGADVQQSLPTQGY SPPTQPHPGPPQAPRIQQQLGQLTLENL QMLPRE/SPDEESYDTRVQSSTGVSPED LAPMDDCGVFGGPRSDVMSAKGLKET |
| 1119 | 9170 | B | 2067 | 169 | 251 | XPQKEPYVIPFTGCVTQKGQVAGDAGW Q* |
| 1120 | 9171 | A | 2068 | 33 | 445 | |
| 1121 | 9172 | A | 2069 | 1 | 1428 | |

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| 1122 | 9173 | A | 207 | 263 | 525 | IKKVRNLGPKHPRFSVLLHVSCSTNGG VLL*RSSVPKKNEEAAEYAKLLAKRM KEAKEKRQEIQAKRRRLSSLRSTFKSES SQK |
| 1123 | 9174 | A | 2070 | 1268 | 2807 | LPLESLAVQVKQHIDAVARFTGIKNCYF GFGGMSTQKPARGC*TRRPEIVVATPGR LWELIKEKHYHLGNLRQQLRCLVVDIA DRMVVEKGPFWLELLHSCFRDASNDSIQ YNPKRTKRLFFLATLTLVHQAPARNPFH KKHTKKMDYTAQLDLLMQKIGHEGAS PKVIDLTRE*GPRWETLTETKIPL*DLIEK DFLLVTTFLMQYSRAAA*CFANSISCIKR LASGLLKV/LLDIMALGPWHGLVWHQEG RGLRNLGSILPRLAEDCVLLAATDVGSSGV WDIPKVVQHVHPFTRVPRTSEIYVHRWS SNLLRSYQLTGLKS*LLIWGLKDVNFKK IYKTLKKDEDIPLFPADINTWDVVKERI RLARQIEESEYRNQVACLHNSWIEQA AAALAEIELAEDMY*GEGKADQOEERR RQKQMKVLKKELRHLLSQPLFTESQKTK YPTQSGKPPLLVLAPSKERVCLSLCSQ GRKEEGRTKEARGGPQPGTATAKLQVQ FNCPGQVCQ |
| 1124 | 9175 | A | 2074 | 1 | 408 | SNPRVRGGGTHRSQGAFANMCRGGR MFAPT/KTWRRWHRRVNTTQKRYAICS ALAASALPALVMSKGHRIEVEPELPLV EDKVEGYKKTKEAVLLKLLKAWNDIK KVYASQRMRAKGKK/RCGR*ERKEGC CWC |
| 1125 | 9176 | A | 2075 | 3 | 1434 | FPVAAAGLRGAWLSPLSAMACARPLUS VYSEKGESSGKNVTLPAVFKAPIRDPDV NFBHTNLKNNRQPYAVSELVAGHTKI AESWGTGRAGGSKFPEVRGGGTHRSIG QGAFGNMCRGGRMFAPTQNLGRRWN RRVDITQNRVAVCSALAAASALTSNW VMSKGHRIEVEPELPLVVEDKVEGLQE EPRKLFLLKLLKAWNDIKKVYASRR MRGGQRQNGETVRRIPGAGGPCIYNED NGINPKFRNIPGNYS*A*AKLNILEALL PGHGGTFLAFGT*KLPRKLDELYGT WR*S/RASPQRSNYHSFPLHKMINTDLS RNLEKQRSQRAPPGRGKREDPIRRVL KKNPVLKNLRIMLKNPICKGPCCR/RHPF FAQAQESQSSGVDKGKLLHQHLOAKS DEKAAVAGKQPVGKTKGKGLLVFK NQKKPLVGKKAATKKPAERSLQRR NATTEKKPAA |
| 1126 | 9177 | A | 2076 | 275 | 652 | TVNLCFSTFLWTVLYFTFFFAKCFQIHL RIYLR**LKTNSWFMLYAVMHVLLVQG QN*NKIFSVMQIYLLCTFIYTGIFW*YHT KG*NKTFTM*NSMYIFGYLHTLKPCKGI KRKHLFATTIC |
| 1127 | 9178 | A | 2077 | 63 | 290 | GGILLSISRPYKTKPTHGIGKYKHLIAEE PKKKKGKQVAVRAINLGTQYNYGVNLNIH LTAYDMTLAESYAQYVHN |
| 1128 | 9179 | A | 2078 | 315 | 1092 | RPRSSKRMSGTSEKVLCLRNNTIFKQAFS LLRFTSGEKPISVGGILLSISRPYKSKP THGIGKYKHLIAEEPKKKKGKVEVRAI NLGTDYEGVLNNHLTA YDMTLAESYA PLFSTTFCNLSH*KSEESYAMPTQNHKK WLPVCRDQGPCKLLGLKCLPHERVA VQISGLSATFARKFSWKIIPKPLP*RESG LFS*REHTERKTSRGRFQRFDPGLGRTFW AKFEVATVDPFHCQQWSYLSAKEKSL GS |
| 1129 | 9180 | A | 208 | 68 | 280 | |
| 1130 | 9181 | A | 2080 | 61 | 346 | LSLFFETEFCSYCPGLECSGVILAHCNFR LPGFK*FSCLSLPSSWVYRYPDPANFL VLVETGFHHVGPGLVLNDPLIFNLDTCY |

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| | | | | | | SAKRQFLE |
| 1131 | 9182 | A | 2081 | 88 | 386 | PHRFGKRRNKTHTLCRRCGSKAYHLQ KSTCGKCGYPAKRKRKYNWSAKAKRP KYHPEPGRMRHLKIVYRRIQGMGFREG TTP*TOEGQAVASIQVHL |
| 1132 | 9183 | A | 2082 | 187 | 913 | STNKRSTRPPLGFEMASPHQEPKPGDLIE IFRLGYEHWALYIGDGYVIHLAAPPSEYP GAGSSGVFSVLSNSAEVKRGVRLIEDVV GGCCYRGQQTAWDHGVPSPRALEG*SF SSAKEMVWFRRLKIVSIVSRNCEALCSP SLRYGQVPAVKQVKGPRFEVG/VLATA LGILVVAGCSFAIRRYQKSDSLKQPQN PVLEAAVGVPVEMSLPRCLQQPDPRALS QAFSRSFPLFPSLAGKSMI |
| 1133 | 9184 | A | 2083 | 1 | 423 | |
| 1134 | 9185 | A | 2084 | 2 | 390 | PRVRYRGVITDPQPLMEQPLGDSRYWL SSRLRVSATFWQNPNRNHFRCQVQFYGLS ENDEWTHDRAKPVTVQIVSAEAWSKADC GFTSGN*QQGVLSATILYEILLGKATLYA VLVSALVLMGMVKKRDF |
| 1135 | 9186 | A | 2085 | 2 | 1027 | HLPDAAMGPQLLGYVVLCLLGAGPLEA QVTQNPRLITVTDKGDVPEGYKVSKE KRNFLILESPSPNQTSLYFCARSFEQGY EQYFGPGTRLTVTEKRNFLILESPSPNQ TSLYFCASSSQRLSPGFNYGYTFGSGT RLTVVEDLNKLFPEVAVFEPSEAEISHT QKATLVCLATGVDPDHVELSWVNGKE AHSGVSTDPQLKEQPALNDSRYCLSSR LRVSATFWQNPNRNHFRCQVQFYGLSEN DEWTQDRAKPVTVQIVSAEAWGRADCGF TSVKSYYQQGVLSATILYEILARGRTLY CLCW*APLVLMAMVKEKGFLKAALEV ELGAY |
| 1136 | 9187 | A | 2086 | 1921 | 1991 | SFVIFDANIFFQFIG*SLLSLWM*ALLCLL VTEHLYLVSIHGLWCVCVCVCVCVCVY DFLIPSHFSIDCFAKAIYILRILIFVIFDAN IFFQFIGCLLILCFR |
| 1137 | 9188 | C | 2087 | 105 | 392 | |
| 1138 | 9189 | A | 2088 | 38 | 230 | LYWQKRKGKLLNNLTQGIVADPVR*KK FHFKCPSPNCPKIHNTESAYAVSFMKYSA HVLGSLYEM |
| 1139 | 9190 | A | 2089 | 487 | 747 | |
| 1140 | 9191 | A | 209 | 465 | 1444 | KKGEKDYSWTDLILTVSPPPGPQKELARI VGQTFPISLKKMMSASML*ESPLNKG*E T*GPKAPKIQRLVTPCSPNGGRIALK KQRT/TRKIKKRLQNMLNFWPRE*RRLR RSARNKLRRDADFPLCELLLWPCPPAT E |
| 1141 | 9192 | A | 2090 | 1 | 1350 | |
| 1142 | 9193 | C | 2091 | 179 | 649 | MFLLVGAPKANTTQPGIVEGGQVLKCD WSSTRRCQPIEFDATELHRELKENQNH YSLKSSASFNVIEFPYKNLPIDITNSTLV TTNVTWGIQAPMPVPVWVILAVLAGL LLAVLVFVVMYRMGFFKRVFPQEEQE REQLQPHENGEGNSET* |
| 1143 | 9194 | A | 2092 | 274 | 423 | |
| 1144 | 9195 | A | 2093 | 1 | 3849 | MCGGVFATEELAVSAGLKRKMCSVVEK RHGDFQVELLLDKLKQKGAIRRALFLYS RSPSHSKNMTISRGLMQCEELIAYLRD ESEFRDKLTPITIFMEYRLDYRTAADTTG LQPILNQFTPANISRQSGFVLLTCSDQKKI YIGDDNPLTLIVKAQNOGEGAYEALIVS IPLQADFIGVVRNNEALARLSCAFKTEN QTRQVYCDLGNPMKAGTQHLLSPCTQF SMQVFLFHYTASSSVVALDSHRSKPYCV N |

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| 1145 | 9196 | A | 2094 | 1126 | 2034 | RCWRPRTLGFASPPTRPCSPHAPGCEM TPRDWHRVLSFASPLRIEIEFQGYDKTFG LKNKKGAKQQKFIKAVTHQVKFGQ/SKS TSGSTE*SWKRKLKDDKKKELQELNEL FKPVVAAQKI/RVKGADPKSVVCAFFKQ GQCTKGDKCKFSDTLTGEKMEKRSVY IDARDEELEKETKSSLIQADTMDNWDEK KLEEVVNKKHGEAEKKPKTQIVCKHFL EAIJENNKYGWFWVCPGGGDCMYRHAL PPGFVLKKDKKKEEKEDEISLEDLIERER SALGPNVTKITLESFLAWKKRKRQV |
| 1146 | 9197 | A | 2095 | 1 | 213 | |
| 1147 | 9198 | A | 2096 | 2 | 170 | |
| 1148 | 9199 | A | 2097 | 3 | 764 | PAVVCGRRLISVLEQIRHFVMMPEINTN HLDKQQVQLLAEMCILIDENDNKIGAET KKNCHLNENIEKGLLHRAFSVFLFNTEN KLLQQRSDAKVTFPG/LVLRNTCCSHP LRQSSRALRESDALGS*/GARQHRGRLES LSLGIPLEEVPEELII*HRIHYKAQSDGI WGGHEIDYILWWRKNVTLNPDNPNEIKS YCYVSKEELKELLKKAASGEKITPWFKI IAATFLFKWWDNLNHLNQFVDHEKIYR M |
| 1149 | 9200 | A | 2098 | 1 | 299 | GIPDQEVIGTGYGILDQKASGVKYTKS/D FRSPRPDDLSSFQ*VTSHWDLRLIEVTE TICKRLLNIACTRRGPAAIDLPRACQRPL RHYTTWYTKGSRW |
| 1150 | 9201 | A | 2099 | 1 | 631 | MDSMPEPASRCLLLPLLLLLLLLLLPAPE LGPSQAGAEENDWVRLPSKCEVCKYVA VELKSAFEETGKTKEVIGTGYGILDQKAS GVKYTKSDRLIEVTETICKRLLNIACTR RGPAADLPRLDGSLFIRSGVRPACILVC LLVHRQKCSVAAPVGT*RH*NGENSAR STMCRKVG*ARCQRTPRACQRPLRHY TTWYTKGSRW |
| 1151 | 9202 | A | 21 | 918 | 1872 | AEKGPPSPGPVSTCLANSPPPSAGSAAV PHSAPPGAAPRRSSRQRPCSPRRCWQEG AGVRAGQDGLGGSATRSAAQQSHQRQT GP/EGSTGKAKARGSTGRKR*AMGGSAA GDGA/PHVLGTGQPRAPPSTGDGARAG NWLAAQGSAPTHRRWSTCWEPASPLPA SSNCCTHTWTRNCPGTAPSGTALPGLPG RPAPHPEPPPPMPPPP/PPRGL/PLGSCVF L*VERPIWREVLSVPAPPRACVDTSGHEA ASGPSVPVAGTEPSRPWLKQPLCPPQQP RSWLTRRPE/AELHMPPTPLPAYLPGS/G VPQSHS*PPATLLR |
| 1152 | 9203 | A | 210 | 87 | 904 | GGWVAPETPSDPWFPVQRGVGDASVPG IGKNVVEKAATSVDAPFRMVTASRYYP QLMSLVGNVLRFLPAFVRMKQLISEHYV GAVMICDARIYSGSLLSPSYGWFCDEL MGGGGLHTMGTYILDLLTHLTGRRAEK VHGLLKTFRQNAAIRGIRHVTSDDFCF FQMLMGGGVCSTVTNFMNMPGAFVHEV MVDVPLLYLKGMVYMVQALRQSFQGG GDRRTWDRTPVSMAASFEDGLYMQSVV DAIKRSSRSGEWEAVEVLTEEPDTNQNL |
| 1153 | 9204 | A | 2100 | 171 | 825 | RANPTKPIGCAVRGPWSALKAGCGCQR RAGGR LAVVVVARRHVCSPGSGEGKLL RAPREEPPGPLGSGPGRAMDSMPEPA SRCLLLPLLLLLLLLLLPAELGPSQAGA EENDWVRLPSKCEVCKYVAVELKSAFE ETGKTKEVIGTGYGILDQKASGVKYTKS DLRLIEVTETICKRLLNIACTRRGPAAIDL PRACQRPLRHYTTWYTKGSRW |

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| 1154 | 9205 | A | 2101 | 2 | 527 | PGRAMDSMPEPASRCLLLPLLLVMLVL LPAPELGPSQAGTDENDWVRLPSKCEVC KYVAVELKSAFEETGKTKEVIGTGYGIL DQKASGVKYTKSISDPPDQDDLSSFQL* VTSHWDLRLIEVTETICKRLLMIACRRG PAAIDLAKVGFIVLHPLWGPGLQCNLS VSAGL |
| 1155 | 9206 | A | 2102 | 3 | 1203 | SSAAEAMRVLVRRCWGPPLAHGARRGR PSPQWRALARLGWEDCRDSRVREKPPW RVLFPGTDQFAREALRALHAARENKEEE LIDKLEVVTMPSPSPKGLPVKQYAVQSQ LPVYEWPDVGSGEYDVGVVASFGRLLN EALILKFPYGILNVHPSCLPRIWRGPAPVI HTVLHGDVTGTWVTIMQIRPKRFDVGPIL KQETVPVPPKSTAKGIGKAVLFKDWGA NMLNSVLEKFGLESLSNGRQQPMEGAT YAPKISAGTSCIKWEEQTFEQKFRLYRAI GNIIPQLTLMANTIKLLDLVEVNSSVLA DPKN*REQALIPGSVIYHKQSQILLVYCK DGWIGVRSVMLKKSALTATDFYNGYLHP WYQKNSQAQPSQCRFQTLRLPTKKKQK KNCCYATMH |
| 1156 | 9207 | A | 2103 | 3 | 215 | |
| 1157 | 9208 | A | 2104 | 2 | 341 | SKPFSLQETYEAKRNEFLGELQKKEEEM RQMFVQRVKEKEA/ELKEAEKELHEKFD RFKKLHQDEKKKLEDKKKSLDDEVNPF KQRKTAELLQSQGSQAGGSQTLKRDK EKKN |
| 1158 | 9209 | A | 2105 | 1 | 130 | |
| 1159 | 9210 | A | 2106 | 2 | 3449 | |
| 1160 | 9211 | A | 2107 | 2 | 1609 | FVPPPFVEAYGWGCRKNWNWAGHRGK RRVKSAPSPYPTFKGWAVEGRLGLEQRR GGPSLAPPPTGLGRARSVTLSCRRSSSV SCAVAPVAAAPVAALADAGAMAATDIS RQVGEGCRTVPLAGHVGFDSLDPQLVN KSVSQGFCFNILCVGETGLGKSTLMDT LFQHQISKGEPAHTHTQPGVQLQSNYDL QESNVRLKLTIVSTVGFGDQINKEDSYKP UVEFIDAQFEALLQEDPKVRRVLQTYH DSRIHVCLYFIAPTGHCLKSLDLVTMKK LDSKVNIPIAKADAISKSELTKFKIKITS ELVSNVQIYQFP/TDDSVAEIQLNP*TP HLPFAVIGSTEELKIGNKMMRARQYPW GTVQVENEAHCDFVKLREMLIRVNMED LREQTHTRHYELYYRCKLEEMGFKDTP DSKPFSLQETYEAKRNEFLGELQKKEEE MRQMFVQRVKEKEAELKEAEKELHEKF DRLKKLHQDEKKKLEDKKKSLDDEVNA FKQRKTAELLQSQGSQAGGSQTLKRDK KEKKN |
| 1161 | 9212 | A | 2108 | 1 | 618 | |
| 1162 | 9213 | A | 2109 | 1 | 427 | HPVRFVHRGPH/VDFSLEVVSQWYELV VFTASMEIYGSADKLDNSRSILKRKY YRQHCTLELGSYIKDLSVVHSDLSSIVIL DNSPGAYRSHPDNAIPIKSWFSDPSDTAL LNLLPMLDALRFTADVRSVLSRNLHQHR L |
| 1163 | 9214 | A | 211 | 217 | 624 | GDELVKREAGMKMLPGVGVFGTG/ELPP EVLVPLLRAEGFTVEALWGKT*GGRRK ALLKEMNIAFHTSRTYDILLHQDVLDVC ISIPPLTRQISVKALGIGKNVCEKAATS VDAFRMVTASRYYPQLMSLVGNV |

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| 1164 | 9215 | A | 2110 | 2 | 835 | WNSAELGRGGPGAGGAGVIGMMRTQC LLGLRTFVAFAAKLWSFFIYLLRRQVRT VIQYQTVRYDILPLSPVSRNRLAQVKRKI LVLDLDETLIHSDDGVLRTVRPGTPPD FILKVVIDKHPVRFFVHKRPHVDFFLAEV VSQWYELVVFATASMEIYGSAVGRLNW DNSRSIL*GGRYVYRQHCTLELGSYIKDP LLWFHRDLSIGVILADNSPGAYRSHPGY GGRIDNAIPIKSWVSVTPSDTALLNLLP MLDALRFTADVRSVLSRNLHQHRLW |
| 1165 | 9216 | A | 2112 | 2 | 846 | RFPLGCFPAQEPQGPVGPMPGAPAGNG HGS*SPHFHQGTGKRAALATWFNQFAP ERSPDVKAPAKPRARRIAPRPRVGVPIRP IVRCPTVARYHTKVVRPGRGFSLEELRVA GIHKKIVARTIGISVDPRRRNKSVTESLQA KRAAG*REYRSKLILFPQSPRAPKKGDS SAEELKLAHPG*PGPGHAPSGTVYKKE KARVITEEKNFKAFASLARMARANAPA LSAYRAKKSPRKPKQTDVEKPTIKPCLG TWNQSGSHAGSPRGVFRGNNWAWDGA SLL |
| 1166 | 9217 | C | 2113 | 714 | 1010 | MKSLNPHLDKIFPHKPLSSLASPSKTLVP GHLCDSTPFKFSFNLYLFPQNHPTSPH LPSPPKDKGISPIYTPHCLGGVITLILCMH FYRFVCHLSY* |
| 1167 | 9218 | A | 2114 | 2 | 227 | ERFRPPIARVIDVSNKGKVVHVAE/SCLEET GGLGVDIVLDAGLDPPDSHCLFLKGATL AFLNDEVWNLNSNVQQGYL |
| 1168 | 9219 | A | 2115 | 3 | 487 | |
| 1169 | 9220 | A | 2116 | 1 | 489 | |
| 1170 | 9221 | A | 2117 | 2 | 221 | |
| 1171 | 9222 | A | 2118 | 353 | 512 | |
| 1172 | 9223 | A | 2119 | 1 | 1706 | MPRAAIAQTPAPTAPAAAAARGPGRRLA ALSSPHLRAAEHDGRCSSETGCHGVLDSD LASPTPPFRSDERPDQWEQGAGSLTKDW KVAVVKVQAVGAAQRQVSPGKRVLC GKRAFKRKVERCPTPCSPGEDGGSRR LTWDLFGPRPSLAEEAEGHFFLPHHFAV FGKQLVVIRCMWLLSQIGPLHYAKRRN HLERDVTMGLYFQQSSTDEEITFVFQE KEDLPVTEDNFVKLVKACALSQINTKL LAEMKMKDLFPVGREIAIGVLDVGSK VSFFQPDDEVVGILPLDS*KTPGLACESL LRVHEPLLGFINPEKVTWTEAAGSISGM GVRAYYSFLHLSFFIFSPGGNQCLIMDGA KCHLRTIAIQLAHHRGAKVISTACSLDK QCLERFRPPIARVIDVSNKGKVVHVAESCLE ETGGLGVDIVLDAGVRLYSKDDEPAVKL QLLPHKHDIITLLGVGGHWVTTEENLQL DPPDSHCLFLKGATLAFNLDEVWNLNS VQQGKYL*QSFQLRLKDVMEKLSTGV FRPQLDEPIPLYEAKVSMEAVQKNQGR KKPSWFQF |
| 1173 | 9224 | A | 212 | 858 | 992 | LKSPQRPGMVAHACNHSTLGARGGWIT/ R*GQEFKTSANMAKFHL |
| 1174 | 9225 | A | 2120 | 230 | 535 | |

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| 1175 | 9226 | A | 2121 | 344 | 2631 | GDREGTGRAHTEEGAGAGMHFYDVEG VDWDRVQGPMMRGLSSSVQVGRFPAPK VSGPLSICVVRQLGLASSRFARSVPFGV WKKDLPCLSLLSQSEDELTPFDMSIQVR LPFNLRQI*KQYWLGMVAAHAGTEKDK NSVNFKNYVLQELDNPGQ*YFKISFSLI YENISTLIKEDMGHGSYSLSEVLWVCA NLFSDVQFKMSHKRIMLFTNEDNPHGN DSAKASRARTKAGDLRDTGGHISPF*IG T*LLFFYFLFF*HISIAEDEDLRVHFEESK LEDLLRKVRAKETRKRALSRCALSPGQL PTLPLNQKQAGRGGFKPPPIKLYRETNEP VKTKTRTFNTSTGGLLLPSTDKRSQVGR DAFCCCCF*DRVSLCRPGWRGLMLMGF KPLVLLKKHHYLRPSLFVYPEESLVIGASS VDHG*VTLTHSAVYGAALC/RYTPRRNIP PYFVALVPQEEELDDQKIQVTPGMWQ RYFQGF*TLPLWNHPWTPQGGGTURLA LDVSKKLETGTNCRQVKGLCWGNTGRN SKYRRAATTVLLSAVSVTHSATPEQ/VW GKMKAIVEKPRFTYR/SDSFEN/VLQQH FRNLRAALDLMEPEQAVDLTLAQCS Q*IKRLGSLVDESKGASLPQPDYNPEGK SYPKRKNTNK*KGLGKKRKPWK*FK KEGA*RPHIKKGVWGWKVCAPC*KEA CRGLRG*KSGLKVKQELLEALT/KHFPGL DQRPAPAAALPAVLPGCPGLVLSQLKCV SPELGRVYPT |
| 1176 | 9227 | A | 2122 | 599 | 1063 | SCSEGLNAVNNLKASRKPKCLSLKWLFL FYFP**IDSQAFYPLISKIVKRKKMTHFW TLFYMYLFLRQSLALLRPGWSAVAQSQL TVALGGL/VLRQSSYVSPPGTWNHRYMP PCPAF*NYFCRDGGLPILFRLVLNSWV*A VLSRPLKMLRLQA |
| 1177 | 9228 | A | 2124 | 142 | 461 | |
| 1178 | 9229 | A | 2125 | 145 | 904 | VINLVYLISPRPELKPVDKESEVVMKFP DGFEKFSPPILQLDEVDFYDPKHVIFSR LSVSADLESRICVVGENGAGKSTMLKLL LGD LAPVRGIRHAHRNLKIGYFSQHHV GAAGT*TFSACGNLLGTQVFLGRPEEEY RHQLGFGMGISGELGHASSLPACLGQK EAEVAFCSDDLPCPNFLADEPTNHLG HGRAIEALGPCLQTISGVGVILVSHE*SA LSRLVCRELWVC*GRRRHPCGKEG |
| 1179 | 9230 | A | 2126 | 39 | 2220 | GASFGVPEWNMATCAELRSEFPEIDGQ VFDYVTGVLHSGSADFESVDDLVEAVG ELLQEVSGDSKDDAGIRAVCORMYNTL RLAEPQSQGNSQVLLDAPIQLSKITENYD CGTKLPGLLKREQSSTVNAKKLEKAEAR LKAKLRKRSEKDTLKTSNPLVLEEASAS QAGSRKESRLESSGKNKSYDVRIENFDV SFGDRVLLAGADVNLAWGRRYGLVGR NGLGKTTLLKMLATRLRVPAHISLLHV EQEVAGDDTPALQSVLESDSVREDLLR RERELTSQIAAGRAEGSEAAELAKIYAK LEEIEADKAPARASVILAGLGFPMQ QPNPGVSQVAWRMLALAGALFARPD LLLLDEPTNMLDVRAILWLENYLQWPS TILVVSHDRNFLNAIATDIIHLHSQRIDGY RIGDFETFIKSKQERRAQOQREYEAQQQ YRQHIQVFIDRFRYNANRASQVQSKLKM LEKLSELKPVDKES*VVMKFP*WV*EAL RRPFCSLDEVDFYDPKHVIFKRLSVSA DLESRICVVGENGAGKSTMLKLLGLDL APVRGLRHAHRNLKIGYFSQHHVEAA WT*TSVLVELLARKFPGRPEEEYRHQLG RYGISGELAMRPLASLGGQKSRVAFQA MTMPCPNFYILDEPTNHLDMETIEALGR ALNNFRGGVILVSHDERFIRLVCRELWG |

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| | | | | | | MRRRRIVTRVEGGFDQYRALLQEQRRE GFL |
| 1180 | 9231 | A | 2127 | 45 | 339 | PPRTPSVFAG*LRAS/STPPRSSSSSSSSSP RKGLSLRPQEALPPPCPSCRSSAPSAPR GGRGETPNKGTGGLCQSCHHPPVDVQ AVLNKCFEAD |
| 1181 | 9232 | A | 2128 | 484 | 1879 | FQQRMAKELKPCNLLEQSILLAKGTS GSSLTALISQVLKAP*VYVFGELLELCNV HELAE*ANAYLQLLNLFAYGTYPDYIA NKESLP*LSTAQONKLLKHLTIVSLARM KCIPYSVLLKDLEMRNLRELEDLIEAVY TDIIQKGLDQRNQLLEVDFCIGRDIRKDD INNIVKTLHEWCDGCEAALLGIEQQVLR ANQYKENHNR/TLQQQVEADVILPQS GNDCRGLRFVSSLIGGVRCVHLKHGD AVVWEAIEEGEALPGKYRLKGRSVWA AAVRVCMQDVITNIKTATASSAQ EMEQQLAERECPPHAEQROPTKKMSKV KGLVSSSPLGPAGAAGTHQAWVRWGG DTKGPFPLSTCSEFQTCPSPHQLPTLL VLFQKNCYSPSPTPSFPSLQTLHQC HPKTGSDTAQLPSRRFLSLCKGLVSLPVF LLPRHFVRLVISRRQL |
| 1182 | 9233 | A | 2129 | 225 | 413 | |
| 1183 | 9234 | A | 213 | 1 | 126 | FRAWTRSRSERRRRRRKRSSSGSEKFDK K*KKNSSRKKQHEE |
| 1184 | 9235 | A | 2130 | 356 | 1024 | GRAEPEDLENGEESAEALDYQDPDATSL KYVSG*CHPPSGWG/HEDALIVHCVDD GHWGRGGLFTALGKA/SPLKPRKIYELA GENEKTLSLGGVLLFPV***KIQDTKGKI CWT*LWLSIVNRSNVLSGI*DGSPIRRA* RRY/CLAAKKAGKSSVQPPHVDMPRK GFKRVGVPEPTLFGKHPGLQRGHPQPYH ILFPLEGKSACPFHSQFFILPSLKDSWCP |
| 1185 | 9236 | A | 2131 | 3 | 205 | |
| 1186 | 9237 | A | 2132 | 3 | 205 | |
| 1187 | 9238 | A | 2133 | 1 | 428 | |
| 1188 | 9239 | A | 2134 | 36 | 417 | QAFKFLPLFDRVLVERSAETVTKGGI MLPEKSQGVVLQATVVAVGSGSKGKG EIQPVSVKVGDKVLLPEYGGTKVVLDDK VCKP**F*KEVRYLQLVVLNNGFFHLQD YFLFRDGDILGKYVD |
| 1189 | 9240 | A | 2135 | 496 | 751 | ISLLNKHPSFFKGGIEQPVSVKVGDKVL LPEYGGTKVVLDDK/DV**F*KEVRYL QLVVSTKGFFHLQDYFLFRDGDILGKYV D |

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| 1190 | 9241 | C | 2136 | 92 | 265 | MSLVIRFIKGEIWEIIMTERISGTSSGM GRHHVDAISNSDLFQSTVLSKNCNNL* |
| 1191 | 9242 | A | 2137 | 330 | 875 | AYAAGFGDSCLIAMSGRGKQ*GKVFAK AKSRSSRAGLQFPGRVHRLLRKGNYA ERVAGAGAPVYLAADVLEYLTAEILAE GNAARDWKKTRIIPRHLQLGHPATTEEL NKLA*GRVTICFRGGVPS*TSRAVLPLK KTESSPQGGQSDFDRLYLPRKRYSNP KGSFSEAPLPFORKS |
| 1192 | 9243 | A | 2138 | 25 | 414 | |
| 1193 | 9244 | A | 2139 | 1 | 65 | RTRGRTRGNLSFI*NHM*QIA |
| 1194 | 9245 | A | 214 | 90 | 943 | SPLADTFLSSGLGRTASPRPKAEARGTGR VRGLRRAVRASPGRMGRSRSSSRSKH TKSSKHNNKRSRSDKERVRKRSK SREK*RNRRRESRSRST/RHWPCPGAS GTGSAPRPRPTASTSSGARRASAGSLDE KQKARGGGEESGVPSEKFDKSK*KKN SSRKKQHEE*KNW*QKRVEELEKRD IEREVLRRVEEAKRIMEKQLEELERQRO AELAAQKAREEEERAKREELERILEENN RKIAEAQAKLAEEQLRIVEEQRKIHEER MK |
| 1195 | 9246 | A | 2140 | 293 | 444 | SPSGYGR*SEASRRPTWCSQFQLRQPPHP EPPKSATWNQTPNIGNLSLPL |
| 1196 | 9247 | A | 2141 | 544 | 1553 | CQMRSCDRTECSFTTARICLSPLPTAFRT HTYGPKSCRSPACDVLGKGRSCRGWL RLASAWCSARVSAGSALRFPMESEM ETQSAGAEFGTQVTRKGRRAKKRQA EQLSAGEGGDAGRMDTEEARPAKRPV FPPLCGDGLSGKEETRKIPVPANRYTPL KENWMKIFTPIVEHLGLQIRFNLSRNV EIRTCKETKDVSDDKRQTDVFKAFILG LSGWKE*HLTLRLDDLFLEISFEITDVKP LKGDLHLSRAIGRIA/GAKEGKTKFTIEN VTRTTIVLADVKVHILGSFQNIKMARTA ICNLILGNPPSKVYGNIRAVASRSADRF |
| 1197 | 9248 | A | 2142 | 1055 | 1223 | SSPGNLNVQEGFRITGLICY*KQYQY*MC FLFLL/SLYVCVVFDFLLLLFCGHPLH |
| 1198 | 9249 | A | 2143 | 2 | 256 | SPGRTAMRSWSCRP CGGGGLG/SSQGRS EPGSSRLGPAPS/CGLTHPCRRGPSCPHPC PAGCRTCGGICPGPHPTSRCPPSRNCQT |
| 1199 | 9250 | B | 2144 | 1 | 2848 | MARRPRNSRAWHFVLSAARRDADARA VALAGSTNWGYDSGQLLQVTCLSLTG SWLWDAGVPAGSAVFDCAACPVS PNG PAVCCGQEHSDSDPEYSTLPSPISAV PVTGESFCDCAGQSEASFCSLSHAHRG RDCRCGEDEYFDVWVWDDLKSSATLL SCDNRKVSFHEYSCGTAIRGTKEGELGE GQHFWEIKMTSPVYGTDMMVIGTSDV DLDKYRHTFCSLLGRDEDSWGLSYTGLL HHKGDKTS |
| 1200 | 9251 | A | 2145 | 3 | 630 | RSGGSASSGRAEARDCWGGRSLPGDR TLEPCGCNCSGSPACCVAPA*GPAA AADPPACLPSLAAAGAGGGSTGTGGKAC AGTG/GG*PSCCSGPPWSTPSGRISC/CCS LVAATPGREGPSLYTSCS*KR*VCRARCP GARQ*WSPGRTATRSWSCRP CGGGGPC RRGPSCPHPCPAGCRTCGGICPGPHPTSR CPPSCRCRRRERS |
| 1201 | 9252 | A | 2146 | 16 | 716 | SVLESKGQRNKGQRKGPVPAQEGSSTG KSVRSGGSASLWQGGSRTAGVGGGRC PGDRTLEPCGCNCSGSPACCVAPA* GPAAAADPPACLPSLGRSICAGGGSTGT GGKWRWHRS*PSCCSGPPWSTPSGRIS C/CCSLV/CCHTY/ITSCS*KR*VCRARCPG ARQ*WSPGRTATRSWSCRP CGGGGPCR RGPSCPHPCPAGCRTCGGICPGPHPTSR PPSCRCRRRERS |

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| 1202 | 9253 | A | 2148 | 123 | 488 | LKCNFRLDKYCGGTAMSGGEQKPERYY VGVDVGTGSVRAALVDQSGVLLAFADQ PIKNWEPQFNHHEQSSEDIWAACC/VCH KGDShrNVIMWLDHRAVSQVNRINETK HSVLQYVGGVMSVE |
| 1203 | 9254 | A | 2149 | 2 | 321 | |
| 1204 | 9255 | A | 215 | 739 | 857 | IIPSPNSNQLNPP***FPGNYY*YFNITQI NKDNYKTE |
| 1205 | 9256 | A | 2150 | 257 | 565 | INKDPIFVPGVWGPYFSAMVPGFWLNE GGQSVTGKLDILSTNTPHPITILGNTNSIL KTQLQHQQPFLITSPHIPKTPQTSRTDQA SFLCSPSSDSLQILSL |
| 1206 | 9257 | A | 2151 | 1 | 291 | VADLTCLKGMVTGLKLFQDLEYLAILEYLA TVQAIALGTRFIEAMEAAGHSISTLFLCG GLSKNPLFVQMHADITGSNGKNEQSWE SCVPETTG*KIL |
| 1207 | 9258 | A | 2152 | 1 | 1690 | FRDDPRVRARLRAESVYLKFNRLDKYC GGTALSGGEQKPERYYYVGVDVGTGSVR AALVDIQSGVLLAFADQPIKNWEPQFNH HEQSSEDIWAACCVTKKVQGDILNQI RGLGFDATCSLVVLDKQFHPLPVNQEGD SHRNVIMWLDHRAVSQVNRINETKHSV LQYVGGVMSVEMQAPKLLWLKENLREI CWDKAGHFFDLPDFLSWKATGVTARSL CSLVCKWTYSAEKGWDDSFWMIGLED FVADNYSKIGNQVLPAGSLGNGLTPEA ARDLGLLPPIAASLIDAHAGGLGVIG AHVRGHGLHL*GAASDVTLAVICGTSS CHMGISKDPIFVPGVWGPYFSAMVPGF WLNEGGQSVTGKLDHMQGHAAFPPEL QVKATARMPEYILHI*TVTWDL*GRVQ PVGFSFTV*FYMFGPDFHGNRSPLADTL KGMVTGLKLSQDLDDLAILYLATVQAIA LGTRFIEAMEAAGPL/ESSTLFLCGGLSQ E/YPLFVQMHADITGMPVVPVARGGSPF LCGA AVLGCASGDFASVTEAMAKMS KVGVVFPRLPE |
| 1208 | 9259 | A | 2153 | 1 | 479 | AATSWGAAQTISSPILDKSLPADISIEDQQ CLVFRDVAPQAPVHFLVIPKKPIPRISQA EEDQQLLGHLLLVAKQAKAEGLDG YRLGE*LLALGPSMPNHSYFSI*SSFFDL CHDPDSLTPSSISVINDGKLGAQSVYHLH IHVLGGRQLQWPPG |
| 1209 | 9260 | A | 2154 | 284 | 604 | RERRDIGGCWSSSAWGNPREWGFLGN DQGRCTGSLRGPTSREHKTLAGPHKRIV SWGGSCPRIRGEDGWGCSRSLAGAL ATFIP*KAPFPRITPG*RRRPAATYVPLS L*LLGHLPMLSRQQLRGLGDGYRL VINDGKLGAQSVYHLHIHVLGGRQLQW PPG |
| 1210 | 9261 | A | 2155 | 496 | 1579 | NCLNSFSCSMNQMYLLIALMTIEYNLAY DSYYICHFIFKIVYKLTDFLQMR*ILM QIFW*GSLFLL**FQLIRDLPFAFSR*KL CPHLLKYKILWKQIILVLC*R*ILILMC DLFALSGIIVFLSFIMRKFSHL*VTVKFIY MSIPRRPVQIL*EHLGLQDIIGI*ILISCY** ENRYSIVPLF/CF/VILITHFGFFSLF*I*LL VFV**F*FNNPNQYI*FI/CFLSNLTTFFL CFLVGG*/CFVKGIV*DHCFHTCFTLHV *STFIY*AFGLE*FHQMNTFW*FVMSSSN CYTLLGT*Q*ICKGKRNNFLYSANLNFJ** IIHFFLKIVWIDCF*NTNLWLWFFSSAFP ASK |
| 1211 | 9262 | B | 2156 | 302 | 451 | XEFLFKHPKRTATLSMRNTSVMKKGIF SAEFLKVFLPSLLSHLLAIGL* |

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| 1212 | 9263 | A | 2157 | 1 | 765 | PPLSPGAHVGRGAPTSAPPPAAEAHPA ARRGLRSPQLPSGAMSQNGAPGMQEEES LQGSWVELHFSNNGNGGSVPASVSIYNG DMEKILLDAQHESGRSSSKSSHCDSPPRS QTPQDTNRASETDTHSIGEKNSSQSEED DIERRKEVESILKKNSDWIWDWSSSAGKI FPPKEFLFKHPEAARPTLQA*GNRAVMK KGGIFSA/ENFLKVFLPSLULLSHFAGPSG LGVIYIGKGVLTSTSTFWMKELGVLTIV R |
| 1213 | 9264 | A | 2158 | 1 | 381 | |
| 1214 | 9265 | A | 2159 | 2 | 312 | |
| 1215 | 9266 | A | 216 | 263 | 425 | FAFQKFYIYTYF*KHTL/WLGAVAHGCN PSTLGGQGGQIT*DEEFETTLDKMVKS |
| 1216 | 9267 | A | 2160 | 1 | 576 | |
| 1217 | 9268 | A | 2161 | 2 | 313 | VSYYHFHRMEKAHPEPGTWDSFLEKFM AGE/VWA*LEEGGCEAEGWWL*RTATL CRCPLPASLVSYGSWYQHVQEWELSR THPVLVLYFYEDMKVVRPTVMLPPM |
| 1218 | 9269 | A | 2162 | 901 | 1848 | RRNMELIQDTSRPPLEYVVKGVPLIKYF AEALGPLQSFQARPDLLINTYPKSGTT WVSQLADMIVYQGGDLEKCNRAPIYVRV PFLEFKAPGIPLRMETLKDTPAPRLIKS HLPLAALLPQTLDDQVKVYVVAQRKR SVAVSYHYFYHMAKVHPEPGTWDSF LGESSVLV*KVVLADSWYQHVQEWEL NRTHPVLVLYFYEDMKENPEKGRFQKDP WSLGGRLQEKTGDFQVQVHTSFKEMK KNPMTNLHPTVPPGSSMDHSISPL*GK GMAGDWKTITFTVAQNERFDADYAEK MAGCSLSFRSEL |
| 1219 | 9270 | A | 2163 | 3 | 287 | |
| 1220 | 9271 | A | 2164 | 75 | 301 | AHKKLRAAPLAPMTGTH*KIVFVKAGD KVKAGNPSWVMFPMKMEHTIKSPKDG TVKKVFYREGAQANRHHSFSRV |
| 1221 | 9272 | B | 2165 | 63 | 368 | MKGGRSPASPAKADGSHCDPKTAPKAK EAPAPPKAEAKAKALKAKKAVLKGVRS HTQKRRSACHSPSGGPRHCDSGGSPDIL GRAPPGETSVATMLSSKFR* |
| 1222 | 9273 | A | 2166 | 153 | 370 | LIAGAFRKASGGNNIFRRPKTL*LRRQPR *PQKSTPRRNKLGHYAIKFPLTTESAVK KIEETNTLVFTVLV |
| 1223 | 9274 | A | 2167 | 842 | 1770 | CTPEKCLPAVHRRNWLRNAEPPVWKRH LSPICRKRQGRATKPKRRPWYTPPTRR VRDVALRPYSRH/GRQPHAKKKIRMSLT FRRPKTLRLRRQPRYPRKSTPRRNKLGH YAIKFPLTTESAVKKIEENNTLVFTVDV KANKHQIRQAVKKLYDSVAKHTEERR HDEQNILTREAKNRNDNTRNARTETN TETQKNSGYQALISFHSYSDSDNKAH LVSYQSGQCTYDRLGWNLLIRMTCSL QHTYDIQSTQIASCFHPVSVRVNRLYC ANYGGISAVFMPLRKELLILTRSSNSKVS QLRI |
| 1224 | 9275 | A | 2168 | 3 | 281 | |
| 1225 | 9276 | A | 2169 | 353 | 605 | EMAPKAKEAPAHKAEAKAKALKAKK AVLKGVRSHT/RKKKIRMSLTFRPKTLR LRRQPRYPRKSTPRRNKLGHYAIKFPLT T |
| 1226 | 9277 | A | 217 | 2 | 660 | FVTRPDAGVMRLPLVLLAVLLAVLCK VYLGLFSGSSPNPFSEDKRPPAPLVTDK EARKKVLKQAFSANQVPEKLDVVVIGS GFGGLAAAILAKAGKRVLVLEQHTKA GGCCHTFGKNGLEFDTGIHYIGRMEEGSI GRFILDQITEGQLDWAPLSSPFCIMVLEG P/KWPKGVPHVQWRESLHSGPQG/GSFH RRKLSLTSI*SWLRWYPVEPLMPSC |

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| 1227 | 9278 | A | 2170 | 301 | 946 | PGSYLKPLSWTVALSRLPGFMSRWPCQR LTWQRRSVTQASGASGASLCASRLPRDK TAPKAKEAPAPPKAEAKAKALKPKKAV VERCPHTHAKKRIRMSPTFRPKTLRLR RQPRYPKSTPRRNKLGHYAIKVFPLTE SAGKKNKNNNTPLVHCGC*RPTRHQIR QAVKKLYDSDVAKVTTLICPDKEKKA YVRLAPDYDALDVANKIGII |
| 1228 | 9279 | A | 2171 | 1 | 1602 | |
| 1229 | 9280 | A | 2172 | 243 | 620 | LLTSSKVMNLSLLEVFS/VSSSRSPSPGP NHTSNSSNASNATVVPQNSSARSTCSLTP ALAAHFSENLIKHVQGW PADHA EKQAS RLREEAHNMGTIHMSEICTELKNLRS LV RVCEIQATLREQR |
| 1230 | 9281 | A | 2173 | 3 | 688 | QRSFLRVPQSPPIPLLQDPNLLRQLLPAL QATLQLNNSNVDISKINEVLTA AVTQAS LQSIHKFLT AGPSAFNITSLISQAAQLST QAQPSNQSPMSLTSDASSPRSYVSPRIST PQTNTVPIKPLISTPPVSSQPKVSTPVVKQ GPVQSATQQPV TAG/PGPRS/SEPVSRR SSALK*PEKSITWVPIHTSNSSNGIQMAT VVPQEFLARSTCSLTAGTSSTLQ |
| 1231 | 9282 | C | 2174 | 1 | 1038 | MEDFTTPLSTLASSMRQKVNKDIDLDS ALQQADVIDIYRTLHPKSTEYTFFSALHC TYSKSDHVGSKALLSKCKRTEITNCVS DHS AIKLEFRIKKLTQNR TTTWKLNNLL LNDYWVDNEMKAEIKVFFETTQHDQNF TKARCIQEHRTYPYSQSFKLKAETRDPSF TKNVQKMKRVRDADLAVAALSRLRGK VWVKAWPPLRGRCV LGCCFLAFCIRSL MDVKHSCPVCQRELFYHRLRPRSPRSA YLAVRDIGPKMARDTVNLWPQARDPSE NASPALLQTHAEKVLVRRVGSGLGTTLP RRGDDPTPERQISFLKCLLKL SHGFGSE GAMPEEISH* |
| 1232 | 9283 | A | 2175 | 1 | 1312 | MGRNQSRKAENSKHESTYSPPKDHSSQ AMEQSWTENGFEKLGFRKEALYYLDL TASCQSQELFQLYAGMSVVGTSMPVQA VCPYCGNRIITVTFVPGALTWLLCTTLF LFGYVLGCCFLAFCIRSLMDVKHSCPVC QRELFYHRLRQME LASSARTVVAPSRP CAGREGRGDANGKNSSPTAGSAMSSEPP PPPQPTHQAIGVGLLDTPRSRRSPSP/L RGNVVPSP/LPTRRTRTFSATVRIASQGP VYKGVCCKCFCSQRAIGFNYPAGWAG PDIF/LWHIS*LWKGGVIVPSGKGDEGHP NKMCSHPHPKE*R/IAARPVKV VVHHLTL APQAPKHETWSIGHVISSLGGVLESTPLS LCFVGDFAGRRQQTLEDDILPHETGLQR GNGPSQVSPGGKGYGGAGVCGGVFPAIS TAYGPLQQPLHHLKSIKSI |
| 1233 | 9284 | A | 2176 | 75 | 411 | PIITKEHLFYVILVPSSGLDGIQG*SQKEG RGLAVPTPVSAAGLPAASMAEEAADQ VGRAALAWLCPAGRRRGFGGEVMRAL VASRPDLLTSASSGWALGSEGRVKASA D |
| 1234 | 9285 | A | 2177 | 1 | 361 | GIKRRSGREATRALITSPNPFRFPAGQS QARAARPTWSAASSAMEAAGSPAATET GKYIASTQRPDGTWRKQRRVKEGYVPQ RRSQYMKTSM*SFSRVNQSCPQG*ALRP LLSPHPGPEGGEPLQGQPNVNLEGE REKEAAAGKRKERAEGLSKDS*LRCPW EETAQLPSAPQGSRAAPTAASDQPSAA TTEKAKKIKNLKKLRQVEELQQRIQAG EVSQSKEQLEKLARRALEEELEDLEL GL*GLSPEATAPVTPSRA |
| 1235 | 9286 | A | 218 | 151 | 414 | ERERESVCVCMCVRV CVCLRERERQ RQRDKRLCGEMRKIQYVNKLHYI/SKYL YIYKYVILQT*TFIHIYIYLYK*ICIHTQMY |

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| | | | | | AVY |
| 1236 | 9287 | A | 2182 | 3 | 140 |
| 1237 | 9288 | A | 2183 | 365 | 2078 |
| | | | | | NLVHCHCLDIFINQAFDMQORDLOITPKR LEYTRKKENELYESLMNIANRKQEEMK DMIVETLNTMKEELLDDATNMEFKDVIV PESGEPVGTREIKCCIRQIQELIISRLNQA VANKLISSVDYLRESFVGTLECLQSLEK SQDVSVHITSNYLKQILNAAHYHVEVTFH SGSSVTRMLWEQIKQIIQRITWVSPPAITL EWKRKVAQEAIESLSASKLAKSICSQFRT RLNSSHEAFAASLRQLEAGHSGRLKTE DLWLRVRKDHAPRLARLSLESCSFTGC LCLHRKP/KLGQELGRGQYGVVYLCDN WGGHFPCALKSVPPDEKHWNDLALF HYMRSLPKHERLVDLHGSVIDYNYGGG SSIIVLLIMERLHRDLTYGLKAGLTLETR LQIALDVVEGIRFLHSQGLVHRDIKLNK LLDKQNRKITDLGFCCKPEAMMSGIVG TPIHMAPELFTGKYDNSVDVYAFGILFW YICSGSVKLPEAFERCASKDHLWNNVRR GARPERLPVFDEECWQLMEACWDGDPL KRPLLIVQPMQLQGI/L*NRLCKSNSEQP NRGLDDST |
| 1238 | 9289 | A | 2184 | 2 | 468 |
| | | | | | GPEAVPHRACSLWLPTPSGPTCPATRHS EHEFTFQMWPGCASSLLCVGTPGEARA DHRCMRVTPVHLGLPGWVGAGARPH CCESATPGGPRGCTP/DDWVAHIPPSF HK*GNPGCIRGDPGRLLWPLCPMTCVAS DKAPALLGSACCSVWSVR |
| 1239 | 9290 | A | 2185 | 170 | 1224 |
| | | | | | PVWRGPAGPTPGIPSTTEKHTRLPSANM MVLKVEELVTGKKNGNAGEAGEFLPED FRDGEY*AAVTLERQEDLKTLLAHPVTL GEPQLRKRETHERAELKKKLEQRSKLE NLEDLEIHIQL*EK/RKKSRETKVPVLKDP EP*IHGTCWECPTFLKA/SLWENNLPPV EKFLSDKNNPDVCEYKRTALHRACLE GHLAIVEKLMEAGAQIEFRDMLESTAIH WASRGGNLDVLKLLLNKGAKISARDKL LSTALHVAVRTGHL*GCAEHLIACEADL NAKDREGDTPHDAVRLNRYKMIRLLI MYGADLNIKNCAGKTPMDLVLHWQNG TKAIFDSLRENSYKTSRIATF |
| 1240 | 9291 | A | 219 | 4 | 328 |
| | | | | | HGVSLFFPRLECNGTISAHNLRLLS*SD SPASASQVAGITGMHHHARLIL/YFLVEM GFLHVGQAGLELPTSGDPTLPWPSPKCW DYRREPTSPGPQTYIHTQSKSSP |
| 1241 | 9292 | A | 2190 | 93 | 458 |
| | | | | | LLLWTMSVIFACVVRVRDGLPLSASTD FYHTQDFLEWRRRLKSLALRLAQYPGR GSAEGCDFSIHSHQKVKWHFNYVSSSQ MECSLEKIQEELKLQPPAVLTLEDTDVA NGVMNGHTPM |
| 1242 | 9293 | A | 2191 | 1077 | 1818 |
| | | | | | LLLWTMSVIFACVVRVRDGLPLSASTD FYHTQDFLEWRRRLKSLALRLAQYPGR GSAEGCDFSIHFS/SFGDVACMAICSCQC PAAMAFICFLAETLWWEFTASYDTTCIGL ASRPYAFLEFDSIIQKVKWHFNYVSSSQ MECSLEKIQEELKLQPPAVLTLEDTDVA NGVMNGHTPMHLEPAPNFRMEPV TALG ILSLILNIMCAALNLQPVQHVVYLGQLDLG AH/HRKSFIREKGNILVF*VDMIQ |
| 1243 | 9294 | A | 2192 | 1 | 999 |
| 1244 | 9295 | A | 2193 | 1544 | 1928 |
| | | | | | QKVRGQIREGCLEEVAGSSRPPAHVCL GLPTGQTADGKSYVKYQVIGKNHVAVP THFFKVLILEAAGGQRELRTYVMPNAP VDEAIPLEAFLVPIESIERASGLLFVQNIL ARAGSLKAITAGSK |

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| 1245 | 9296 | A | 2194 | 2 | 1068 | ARGWVPRPKPLAVFVSGREVTLSSAAPA ALCPRWIPRRGSFKSLAGRPPLGRSPAM RALRAGLTLASGAGLGAVVEGWRRRRE DARAALGLLGRLPVLVAAAAELPPVPG GPRGPGLAKYGLPGLAQLKSRESYVLC YDPRTRGALWVVEQLRPERLRGDGDRR ECDFREDDSVHAYHRATNADYRSGGFD RGHLAAAAANHRWSQKAMDDTFYLSKV APQVPHSNQIAWNNLAEKYSRSLTRSYQ NVYCLH*GHFFLPRTEADGKSYVKYQV IGKNHVAVPTHFFKVLILEAAGGQIELRT YVMPNAPVDEAIPLERFLVPIESIERASG LLFVPNILARAGSLKANTAGSK |
| 1246 | 9297 | A | 2195 | 204 | 507 | GSPGTRSETREPGAMSQPPAPPPLPPPPP PPEAPQTPSSLASAAAASGGL*SGETGESF PGAARIRSVRRVYFSRPPVLSASSVPSAA SGTSSNSCWGLRR |
| 1247 | 9298 | A | 2196 | 1 | 460 | EFKQLIHIEHQPNGGASVIHAYSNELSHL SPMEMERFARKSLVGS*CSSENENSGSFP T*WGIVHGAATYLPDFLDYFSNFNPN PVKMEILGKKDIETTTMSNFHAQSLTVL QPGRQSETPSQKKRKKFMIMLSSRWEGE TKNKYRRLTN |
| 1248 | 9299 | A | 2197 | 199 | 769 | |
| 1249 | 9300 | A | 2198 | 182 | 2889 | TEKGAAAGTAGSCSRQHASPSQSYGSPA SWSFAPLSAAPSPPSSSRSSFSAGTAVPS SASASLSQPEPRKLLVPPTLLHAQPHLL LPAAAAAASANAKSRPKEKREKERRR HGLGGAREAGGASREENGEVKPLPRAN DKTRSFDDFSPDQAAAECLSRKRRILKG SCQTGYLRKALFSDTVTLGIKASTYGF GGMIQSIVKGLAETFNFWIHIWELNDLQ YISALFACSEEMP DYHLEKQLADKIKDKI KERDKEKEREKKKKHKVMNEIKKENGEV KILLKSGKEKPKTNIEDLQIKKVKKKKK KKHKEKRRKRPKMYSKSIQTICSGLLT DVEDQAAKGFLNDNIKD YVGKNLDTK NYDSKIPENSEFPVSLKEPRVQNNLKR DTLEFKQLIHIEHQPNGGASVIHAYSNE LSHLSPM/EGWERFAEEFVG/L*VFSENE NSAAFYVMGIVHGAATYLPDFLDYFSN FPNSPVKMEILGKKDIETTTMSNFHAQV KRTYSHGTYRAGPMRQISLVGAVDEEV GDYFPEFLDMLEESPFKCTLPGWTLSSL KLQSRKDSDDGPMWVRPGEQMPVAD MPKSPFKRRTTNEIKNLQYLPRTSEPRE MLFEDRTRAHADHIGQGFERTTAAGV VLKAVHCGEWPDPRTKDVICFHAEDF LEVVRQMLDLHEPPLSQCVQWVDDAK LNQLRREGIRYARIQLYDNDIYFIPRNV HQFKTVSAVCSLAWHIRLKLHSEEDTS QNTATHETGTSSDSTSSVLGPHTDNMIC AVSKASLDSVFSKLSKHYELQKHEPI ASVRIKEEPPVNNIPEKTTALNNMDGKN VKAKLDHVQFAEFKIDMDSKFENSNDK LKEELCPGNLSLVDTRQHSSAHSNQDKK DDDLIC |
| 1250 | 9301 | A | 2199 | 2 | 122 | |
| 1251 | 9302 | A | 22 | 10 | 284 | |
| 1252 | 9303 | A | 220 | 436 | 777 | IYSYGKTGPV*KRKNCQSRIKEQNPIICW LQATHLKCKETYKLK/MRKICQANTNQ EEIGIL*NSRLYSKNYYQG***KGSILQED MTILNMYAPKNRGSYMRQKLIELQGE |
| 1253 | 9304 | A | 2200 | 1130 | 1437 | LSRIMKAWFPLFFKIPFRDKVFFLSPPAW SAVAQSRLHCSLELVGSINSSISAS*LGW EYRCAPQCPG*FLAFFCRDGALPCCPSWS QVICLP*PPKALGLQA |

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| 1254 | 9305 | C | 2201 | 279 | 449 | MHPVSCWVIMSCRPLCTRLILSDSPPGPP SDICVSRKNPSNYPAMVLPQCFTICII* |
| 1255 | 9306 | A | 2202 | 1 | 1173 | |
| 1256 | 9307 | A | 2203 | 1 | 2112 | MGVELFTPASVMGVKRCCCSIPGQLSGN GEPFSEIDSSVSVRGGWQPRWFLLCGGI LSYYDSPEDAWKGCKGSIQMAVCEIQV HSVDNTRMDLIIPGEQYFYLKARSVAER QRWLVALGSAKACLTDSRTQKDKEFAE NTENLKTkMSELRLCCDLLVQQVNKTK EVTTTGVSNSEEGIDVGTLKSTCNTFLK TLEECMQIANA AFTSELLYRTPPGSPQLA MLKSSKKVNQKYITNKEEFTTLQKIVLH EVEADVAQVRNSATEALLWLKRGLKFL KGFLTEVKNGEKDIQTALSFSSN/SCT/CI WRLGPGDVLTL*RKRR*LANAAL*LQ* SQPVSAFSSLSPP/CGTIFNGKEKGGCKFD IFVLMFRLISKKTQTQALRRFFEKCLH NSYSEPVGSLMHSSGIMVPFSHFEPAFI SRDTLFEFREDNAYGKTLRQHGWVWV RGVFALALRAAPSYEDFVAALTVKEGD HQKEAFSIGMORDLSLYLPAMEKQLAIL DTLYEVHGLESEDEVLYPLGCLDCCPEGE QSWFQKKNVFGCLSQLPVGRGVQLPCG HEGPAKENRVWLCMLAITPESAEQNR DNHLWSSVVRVDGELMNDGGLTSALRT QITFGMICCVNALSSNKVVASLLTLVRF TAAPSLPTLHCVRHLQVEDPHLVMSVC ECGTTISLPEPRSQLQCSTAVSQLEDSRR MAEH |
| 1257 | 9308 | A | 2208 | 132 | 509 | NMVQTTCPGLMSTPCTGPAQARR*K/ WLVECLSLTGMGPGEGRGQGAEEAEP N*VLGTPAGGSGPCPPGIQTPPSPHQPH SQVLSLSPTRICPGFLAYLLSLFTPREE LQLTQNDTFLAPRV |
| 1258 | 9309 | A | 221 | 212 | 275 | FLILNCNSF*KIYPKYKSLIR |
| 1259 | 9310 | A | 2218 | 491 | 812 | |
| 1260 | 9311 | A | 2219 | 2 | 948 | IFKIAFAKFGVWAGEWGREGMGSRKWS ARAAAQRAEPRSGRQVRPRALRLPPARQ PRQLESPRPAAAPESPSSSAMAGWN AYIDNLMADGTCVTGAIVRYQDSEPPF WHAVPGK/TRFVNITPAEVGCPWLAKTR SSFLR*MGLTLWGGQKCSVNRGLHCLQ EWGIIACDLRYQEPGPGAPHSIVTCHPR LNKDAKSWLMGQRKVS HGGLTNKKCY VEMASHLSGFPSTDLRLVPFPLSPFPTAFA PLSLPIHTQTNFYFLGPLPHTPYCCQNHM GLGGQGLMGQTPSPTHIPSRVWLEKLLF FGVFFFSE |
| 1261 | 9312 | A | 222 | 770 | 1573 | NHLEIVNLCNVGISQSFPQI*LKAQATKE KINCIPIKLKTFG/TEKYIKNVKROYIE*Q KISANHLSDKRLVFRIYFLKTITVQY*KD KPIIK*VKDLNR/HFSKEDT/YMTNKYMK RC*KSSSTIREM*IKTTMR*TLPHYRWNIK KTDNNNC**GCG*TGILHCWLECKIMY P/IFRTV*QFPEKVQOHYPDAAILLLGIY PRNMK/SKCLPKNYTRMFITELLILKK*K QLKC/PIN**W/K*NDKMW*IHMICYSA IKRHRVLNA |
| 1262 | 9313 | A | 2221 | 259 | 941 | PVSWSLNSCRFFFFF*DQSLPSVV/QAGS GQ*RNLDLAQPLASRFK*FSSSRL/SSW DYRHMATMARLIFLVEGMFTMLARL VLNFLTSSDPPTSAPFKWLGQGVKPN RAVGFN**LGYYSIILYHSNSPGTDLVFI FIYLFYFLRQEQNSAAQARVQ*WHNL GSLQSPPPGVH*FLCLSLPSSWDYRCAPP HQANFCIF*RDGVFPCWPGWSRTDPLR |

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| 1263 | 9314 | A | 2222 | 343 | 600 | MSPLSQFVDGTLKIQCYYGTFEHSVA/ RLECIGMISAHCNLCPLPGSSNSPASAS*IA GHAP/CHHAPLIFVFL*RQGFTRIYFFK |
| 1264 | 9315 | A | 2223 | 142 | 583 | |
| 1265 | 9316 | A | 2224 | 163 | 1603 | IQAGQCGNQIGAKFWEVNSDEHGIDPTG TYVHGSDQLQDRISVYYNEATG/GKY VP/RAILVDLEPGTMDSVRSQPGQIFRP DNFVFGQVWGQVTTWAKIGHYTEGAE LVDSVLDVVRKEAESCDCLQGFQLTH SLGGGTGSGMGTLTYQQGFEKEYPDRI MNTFVSVPSPKCLDTVVEPYNATLSVH QLVENTDETYCIDNEALYDUCFRTLKLT TPTYGDLNHLVSATIE/CVVTTC/LRFP/GQ LNADLRK/LAVNMVFPRLAHFFMPGFA PLATSRG/SQQYRALTVP/ELTPARSDAK NMMAACDPRQGPINFNRGLLSSRSGSC PMKEGRMKQML*RCKNKWSSYFCGNE SPNNVK/TAVCDIPTSWASKMAVTFUGQ *HSPSQELFKW/SEQFTA/MFRRKAF/LH WYTGEGMDEMEFTEAESNMNDLRL*S IKQLPRMPTQEEEDFGEEARKRRPKGR APNQLKASQFP |
| 1266 | 9317 | A | 2225 | 234 | 1374 | KSGGLRRRQRPGRSAAVGEEELPPGMEK FKAAMLLGSVGDALGYRNVCKENSTVG MKIQEELQPVAGGLGHLVLSPEWVPSD NTIMHIATAEALTTDYWCLDDLYREMV RCYVEIVEKLPERRPDATIEGCAQLKPN NYLLAWHTPFNEKSGSGGAATKAMCIG LRYWKPERLETIEVSVECGRMTHNHPT GFLGSLCTALFVSFAAQGKPLVQWGRD MLRAVPLAEKYCRKTIRHTAEYQEHWF YFEAKWQFYLEERKISKDSKNKAI/FPDN YDAEERE*TYRKWSSEGRGRRGHADAP MIAYDALLAAGNSWTELCHRAMFHGGE SAATGTIAACLFGLLYGLDLVPKGLSQD LEDKEKLEDLGAALYRLSTEEK |
| 1267 | 9318 | A | 2226 | 139 | 366 | AMAYQLYRNTTLGNSLQESLDELIOGSL NTYRFCDNVWTFVLNDVEFREVTELIKV DKVKIVACDGKNTG/SNTTE |
| 1268 | 9319 | A | 2227 | 160 | 588 | AMAYQLFRILPLETSFQESLD*LIQSQQI TPPTCPFKFY/LQDRANNAALA/QRVN RVNFRGSPKYGTRFCDNVGDFWYRND/ VEFQRG*PEPIKRG*K*KLVA/CDGKNTG LPIPTEWNRKKYDFFYTHLLFIAFEREA |
| 1269 | 9320 | A | 2228 | 918 | 1085 | QEKLF*VLCFNFFSFFFFFCFL/VD*F*FL FGKGAV*TLFVFSSASHRYRQ GKTR |
| 1270 | 9321 | A | 2229 | 145 | 365 | |
| 1271 | 9322 | A | 223 | 86 | 427 | SPQIRKQEISI/SLTDTGILYIENPKESPPP KLLKVIKFNKATRFKINMQKSVVFLHPR N/QFENEFKKILSFGTEPS/RSEYLGINITK EV*NLNTKNDIVEKMKELLSKWKDSPC |
| 1272 | 9323 | A | 2230 | 2 | 750 | ILGFDLQPPGRRWAAPAVSGLSRKVRRC FSTG*VVRPFAKLVGPSVQVYGIEGRYA TALYSAASKQNKLE/QLEKELLRVAQN PRRNPKVACFLFLNPLCESRSIKSEKALN DITSKKRRFSPPSTTQ/LLNQFCLAGKMG PI*ANNPKGVVSGLFLTMDGVFHSRERV PLHSGPLASSFRKESHTLLNLKTVLKEFP KVKGQVLELGAK/IDPSNLGGMIVRIGE/ KYVDMSVKTKUQKLG/AMREIV |
| 1273 | 9324 | A | 2231 | 100 | 468 | ATEPLAPSERREVSIPLLVPAPLPPPPPP VPSRTRTRPWRRP*ACFPMTLAASCGPT RSPWPSQQPIQPAPVG/PNGIKTLGDAY EFAVDVRDFSPEDIIVTTSNNHIEVRAEK LAADGTVM |

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| 1274 | 9325 | A | 2232 | 228 | 721 | LWQLHAAPLGAPGLPRQVIRALRGGEV HREGTSAPGRHRRRCGCPVGLEQVLHSL QPCVATKTDVATGTDVAMKTGNIKTLG DAYEFAVDVRDFSPEDIIVTTSNNHIEVR AREA/ERP DGTVMNTFAHKCQLPEDVD PTSVTSALREDGSLTIRAWRHPHTEHVQ |
| 1275 | 9326 | A | 2233 | 3 | 605 | KKLTPVVRSRVERDPRVRRGLRHPVLS SLRPPGQGPAPSVDEPQNLFLHLPAGEKIP FLFLLLLFTPPRPPVLSRPRTRPWRRP* ACFPMTLAICGPTSPWSPAPV/VAG NIKTL*DAYEFVVDVRDFSPEDIIVTTSN NHIEVRPEKLAADGTVMNTFAHKCQLPE DVDPTSETALGEDGRLTIRARGHPHTE H |
| 1276 | 9327 | A | 2234 | 229 | 510 | KGIIWYINMEEQFVI*IHFL*TRSQFYFVNI TFKYIYTHIYVQLYIHVH/MICKFIFYNIFI *IDICRQVIDYRDPRKQLNNCSKFSSSLTA GV |
| 1277 | 9328 | A | 2235 | 203 | 334 | SRRDHSFIL*ILHLSIYIHTYMYNYIYMC YMYQRKQYGKTNP |
| 1278 | 9329 | A | 2236 | 1023 | 1470 | TPKTKHNSNPFSVPHAHKFACSYFFFLC VFMGSKNLNLLAIYKVNNSKLYLLRNVI F*FIFTQLFILIYFFYTVLNTQTYFLFMIFL SCSHGICFPIFLSLISITGWDLTNNNVRGR KYFATVDYYTLKFYIMKIYNSLYASKKK KKA |
| 1279 | 9330 | C | 2237 | 226 | 450 | |
| 1280 | 9331 | A | 2238 | 3 | 449 | LLRRVSVTAVAALSGRPLGTRLGFGGFL TRGFP/KAAAPVRHSGDHGKRLFVIRPSR FYDRRFLKLLRFYIALTGIPVAIFITLVNV FIGQAELAEIPEGYVPEHWEYYRVKELE VRKLMHVRGDGPWYYYETIDKELIDHS PKATPDN |
| 1281 | 9332 | A | 2239 | 3 | 635 | HASAHASAMSLRRVSVTAVAALSGRP LGTRLGFGGFLTRGFPKAAAPVRHSGD HGKRLFVIRPSRFYDRRFLKLLRIHLAL TGLPVTIFIALVNVFIGQAELAEFPEGYV PEHWGILLRHPISKMGFAR*FLMIGPEK DIMERNNGPSFQIGSLKKAGIYGVKGSW EVRKI*WHVEEGDGAPWVLLWRPFDQGT LLDHSSRKPTPWTN |
| 1282 | 9333 | A | 224 | 35 | 397 | FLTGTQWGK/DSPFNTWC*DH/WNIHRN LDLYLIPYIKINLKQLTGPNLRAKTIKLPE QNIGENLCDL*LSRERYSTKSITIRIKL/D TLGFIKIKNKCISKDTIRKR*ATDWEKIFA NHVLKG |
| 1283 | 9334 | A | 2240 | 811 | 1005 | SNFTGKIHK*LTSFKIVNLFYIY/FFETGFH SLTRLECSGMILAHCNLRFPESRKLFFFG AIDSF |
| 1284 | 9335 | C | 2241 | 256 | 540 | MSPAKATEMLIFGKKLTAGEACAQGLV TEVFPDSTFQKEVWTRLKAFCKLSPNCL EIFKEVXRKRERXKLXAVNAEECNVLQG RWLSDECTNAV* |

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| 1285 | 9336 | A | 2242 | 602 | 2067 | SSSSGLALGMQRPLLARLRGTPGRALSA PAATGFAELRAAQGMAMAYLAWRLAR RSCPSSLQVTSFPVVLHNMRTAMRASQ KDFENSMNQVKLLKKDPGNEVKLKLY ALYKQATEGTCKMPKPGVFDLINKAKI WDAWNALGSLPQSGCPG*NYVDLVSSL SPSIGNPPSIQVEPGTERDNQLGFETLVVT SVEDGITKIMFNRPKKKNAINTEMYHEIM RALKAASKDDSIITVLTGNGDYSSGND LTNFTDIPP/GVGVEEKANTNA/VLLR/EF VG/CFIDFPKPLDCSGSMGSPCGASPVTL LGAYSMPLVLLHLDRTGFHTPF*SP*AQS PEG/CSSYTFFKIMSPA/KATEMPFIFGKE VNQREEACASRD/LTEGFPWIALFRKKV WDQG*RAFCKSFPPQMALEEFKEVIRK REREKLHAVKAEECQCPFGKWLSD CTNA/VVNFLSQKIKNCDDHLQQHQSM SQGRMCCSLCLSSTGTK |
| 1286 | 9337 | C | 2243 | 2163 | 2402 | MSQAAASHKSKLTPKNQRAPFTLLRKSQ CQDP SRGESEEGWWPIQRACRSMETFLP QMFQSWHQIYKNVSRDQFFTLK* |
| 1287 | 9338 | A | 2249 | 761 | 1178 | LSTPLTSWCWMRRTPGSPTTRCSCSSA/ PGTQPLGGGHQ*RGCHQCVASSPR*AWP ASGPAKLQ*LQPKTQQRAPATGEHVPP VQPSAQ*PHSRFQSSETSRPADGSEQQPA RASGPGARRPPHQPRQVINCWLRR |
| 1288 | 9339 | A | 225 | 832 | 1043 | LLWWFRLRSSPCGTQQGPWHLVCVYGY AGGWAGPPWHTCPWDP SHCPGTE*CP WCVWCFCCNTYLLVPN |
| 1289 | 9340 | A | 2250 | 135 | 408 | PHSRFQSSETSRPADGSEQQPARASGPGA RRPPHQPRFHPPPSA/RAISIECPA*AVMR SGSEPRARQEYSLGLWTPSQFLQILYLA RSPT |
| 1290 | 9341 | A | 2251 | 123 | 578 | TTNNIFKWAKYFKRHFSRDI*MANEHM KRCLTSLTIMEMQIKTTIRCHLT/PRMPII KKIHKC**GWRETGTLI/YAWWECKIVQ/P AFR/TWVQFLKRLSQHPTIPFP/GMCPRET KTHIHSKTY/TQMFMAALFIEARKWKQF KCLSTNEWNTNVVRP |
| 1291 | 9342 | A | 2255 | 209 | 531 | |
| 1292 | 9343 | A | 2256 | 1 | 308 | AKRAQSYAERLRLGLAVIHGEAQCTELD MDDGRHSPPMVK NATVHPGLELPLMM AKEKPPITVVG DVGGRIAHVWLYVIHV QRWHSWLLVSRLSTLGLYF |
| 1293 | 9344 | A | 2257 | 2 | 1161 | VRKGTDLGALPVPPPAMNAARTGYRVF LVANSTAVICSELAKRITERLGAE LGKSV VYQETNGETRVEIKESVRGQDIFIQTIPR DVNTAVMELLIMAYALKTACARNIIGVI PYIPYSKQSKMRKRGSI VCKLLASMLAT AGLTHIITMDLHQKEIQGFFSFVPADNLR SLHLFLAFSIIQGRKFPNLQEMQVIVG*V FLDAGKGAQSYAERLRLGFWAVHSR GEGFSCTKLDMDDGRHSPPMVK NATV HPGLELPLMMAKEKPPITVVG DVGRI AIIVDDIHDVSEFVAAAEILKERGAYKI YVMATHGILSAEALRLIESSVDEVVVT NTVPHEVQKLQCPKIKTVDISLILSEANR RIHNGESMAYLFRNITVDD |
| 1294 | 9345 | B | 2258 | 80 | 402 | XVPTVD TYDGRGDSVVYGLRSKSKKFR RPDIQYPDATDE DITSHMESEELNGAYK AIPVAQDLNAPS DWSRGKDSYETSQLD DQSAETHSHKQSRLYKRKAYDESH* |
| 1295 | 9346 | C | 2259 | 272 | 409 | |
| 1296 | 9347 | A | 226 | 764 | 1016 | LLQAGAHACNPSGFGEAKAGGSTDLRS GDQPGQHGETPSLLKVQKVA*RGGA PL* SQL/LRGGGGCSEPRSHD*IPAWMTEGDS V |

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| 1297 | 9348 | A | 2260 | 2 | 628 | EHSIVGTRLVSGQLQPSQPNADQGKLT MRIA VICFCLL GITCAIPVKQADSGSSEE KQLYNKYPDAVATWLNPDPSQKQNL PQTLPSKSNESHDMDDMDDDDDDG PCGDSQDSIDSNDSDDDVDDTDDSHQSDE SHHSDSEDELVTDFPTDLPATEVFTPVVP TVDTYDGRGDSVVYGLRSKSKKFRRPDI QVNPLTDTDPGSD |
| 1298 | 9349 | A | 2261 | 67 | 1276 | SHASGRRQSTASSGPDVSVSGQLQPSQPN ADQGKLT TMRIA VICFCLL GITCAIPVKQ ADSGSSEKHFY NKYPDAVATWLNPD SHKQNL LAPQMAVSSEETNDFKQETLPS KSNESHDMDDMDDDDDDHVDSDSI DSNDSDDVDDTDDSHQSDESHHSDS DELVTDFPTALPATEVFTPVVPTVDTY DGRGDSVVYGLRSKSKKFRRPDIKYP ATDEDITLHMESEELNGAYKAIPVAQDL NAPSDWDSRGKDSYETSQDDQSAET HRVHQQSRLYKRKANDESNEHSDCW* ARTFPKVSREFHSHEFSSPWRFCFVAP KSREEDNTPLEFRYSQELDSASSGGQLK GGKNTISPLCHLVQKKNFGIAKMKENHE MLLSPVYWLKCVSI |
| 1299 | 9350 | A | 2262 | 1 | 651 | MTAFNSGKVDIVAINDPFIDLNYMVYMF LYDSTHGKFHGTVKAENGLVINGNPIT IFQDQDPSKIKWAP/LAKVIHDNFGIIEGF MTTVHTITATQTINGPSGNCHVMAAGL SRTSSLLA/LAKPVGKVIPELNGKLTG MAFHVPTANVSVADLTCRLEKPA/KYDD IKKWNTHSSTFDAGAAIVLKDHSVKLISW YDNEFGYSNRVVHLMAHNASKE |
| 1300 | 9351 | A | 2263 | 2 | 5264 | |
| 1301 | 9352 | A | 2264 | 56 | 1357 | IRLSVCSSCSTVSRIFFCVASRATSLRTPM GKVKVG VNGFGRIGRLVTRAAFN SGKV DIVAINDPFIDLNYMVYMFQYDSTHGKF HGTVKAENGLVINGNPITIFQERDPSKI KWGDAGAEYVVESTGVFNQPWKKA GAHLQGGAKRVIISAPCLMPPMFVGM VNHKEYVNSLKIISNAFLQPPTCLAPL AKG*FHDNFG*SWEGLIDHSSMAITGNP RKTVDGPSRGWNCGRGWAAGLARSSTL GLYWALPKAVGKGHP*G*TGKLTGMA FPVVPNCQNVSVVDLTCRSRKTLPQYD *HQGRVVKQAISEGPPQGAILGYTEAPR WVSSDCNSGPPVFPFDAGAGIALNDH FVKLISWYDNEFGYSNRVVLDLHGPHGL QGSKTPGTTEPQARGTRGRDELTAGES LPHSDPHHTESPLLTVM |
| 1302 | 9353 | A | 2265 | 34 | 476 | LSGCPRAASCASSAGLLVLLPFMPMFI VNTKLHRASLPEGFLSKLTQQLAQAN RQAPPN*FAFNVPDQVVSFGGSSEPCA LCSLHSIGKIGGAPDPAPYSKLLACGPAG RSRLPIQARTRVYINYYDMNRGQMWA GNNFHLSP |
| 1303 | 9354 | A | 2266 | 63 | 470 | QQPPPERPAHQFARPPAPFTMQPASAKW YDRRDYVFIEFCVEDSKDVNVNFEKSKL TFSKLSFLSNDVK*SFTQLNNFDWL VFS LKLLLFVSLKRLNSFFIILYSLGGSDNF KHLNEIDLFCIDPNVSSLYA |
| 1304 | 9355 | A | 2267 | 2 | 854 | RAFCCVTSRRPASPLVCTHARSFSLAP LFLHFP LLPDRRSRFRVHFWGPRSSPP HAAVRLREARRGRDRREKAESPTGEKST SPSSRRQRGPPTKVRPPAPFTMQPASA KWYDRRDYVLKWEFVFLNLTLDVNV NFAEKSKTYNFSCLREGSDNF*GI*MEHD LFHCIDPNDFQGLKGTDRSIFMFVLRKR RIWASSWPGLTKERGKGLIWWVSDFN VWVKDWEDEDEMSNDFRSEMMNN MGGDIEVVDYPEVDGADDDSDSDDE |

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| | | | | | KMPYLE |
| 1305 | 9356 | A | 2268 | 117 | 388 |
| 1306 | 9357 | A | 2269 | 66 | 354 |
| 1307 | 9358 | A | 227 | 748 | 1488 |
| | | | | | RLTKRPETFPRRHPKLP TLKTPVAGATPL SPSHPDWPFVFNPIPLTNRT*PPLQLQLRQ PSRSCPETTQGAISSEAE L PVRSPPPFR LFPTPE/PGLSRQWP*EVEGTSRTPFFKAE GQK/EGKVKEGKTEGPCSPSRTRILPPY SRLESGPVHWGEQGP NRKSWPPNLPDQ GF*QEREEAMGHIPSPPGIRQRHRTSVQE *GSEIKPK*CPEPGKAFNPRPWGLGLT/TR PLPLHSQKSRQDS*NTG |
| 1308 | 9359 | A | 2270 | 148 | 398 |
| | | | | | RPAKRGAAAMDGRVQLIKALLALPIRPAT RRWRNPIFPETFDGDTDRLPEFIVQTAS YPWARTRSSARPISSPPPETSCVLA |
| 1309 | 9360 | A | 2271 | 356 | 1241 |
| | | | | | KVTFLITRLTGPALQVGDPLHQEGEP PPQ LITGAFWPEMKRVFGWGGRGLALGRET LGWPGIGGCSGEGPLCYWPPGSPAPSF RASPPLEPPRCPLRSCSLPRSACLCSRNS APGSCCRPWASLWSEPPSPSSQPAPPM YIWTLSCAPVAQS*APVTHWTDHPLPPL PSPLLPTRLPDDLHHFGPQLRCQSHRH PSHPRQDCWLL/M*IWTHLGGWAGH SPWTVIQTAGRPRLDPSARPISPIPE TFCAPATWLPGLSCAWQAKFESLIFSLW TKLVFAHKRSIS |
| 1310 | 9361 | A | 2272 | 2 | 178 |
| 1311 | 9362 | C | 2273 | 88 | 228 |
| | | | | | MKVDKDRQMXVLEEEFQNISPEELKME LPERQRLQRXTTDDVCRE* |
| 1312 | 9363 | A | 2274 | 3 | 382 |
| | | | | | VDRTIMSDSLVCEVDPELTELKRLKFRF RKETDNAAIIMKVDRQMVVLEEEFQ FVVYSYKYVHDDGRVSYPLCFIFSSPVG CKPEQQMMYAGSKTRLVQTAELTKVQT GMWLQSVRERWCGSWV |
| 1313 | 9364 | A | 2275 | 89 | 636 |
| | | | | | KTAELRKEEACGQNNHALPGSLRQSDSL VVCEVDPELTELKRLKFRFRKETDNAAI MKVDKDPARWWCLEGKNFKNISPQREL KMGFPRRDKPRFVVYSYKYVHDGGR VSYPLCFIFPRPVGCKPEQQMMYAGS KNRLVQTAELTKGVPKSRTT*LTSLRP WLAQEKLSFLSLISGAGD |
| 1314 | 9365 | A | 2276 | 2 | 2453 |
| 1315 | 9366 | A | 2277 | 1 | 1008 |
| 1316 | 9367 | A | 2278 | 1 | 884 |
| | | | | | MVDKCRYHQSLHKVSNSESKISSGLLL SRLQRRPRGRGDAELRRAGSVKRRQRG KMAAAVPQRAWTVELRSEQLPKDDII KFLQEHGSDSLAEHKLGNIKNVGKT ANKDHLVTAYNHLFETKPF*GYLKV*S KVSEQVKKCERLMKINPKETKSERDPW NEGPPKIYTKSCS*KRGDKTQLFPKRGD VVHACWYTGNTTKMGTVF*YLIFQ TSA KKKEKCPSL*GFKVRSRPKLSRGWDEA LLTMSKGEKARLEIEPWEAFGKKGLPD AKIPAPNAKLTFEVELVDID |

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| 1317 | 9368 | A | 2279 | 3 | 510 | AIRAVAYCADMAQSMNHTTLHQSRWH RIGIKKPRSQTDQSLTGVDPMFLKNMRF AKKHNNMGLKRMQANNAKAMSARAE AIKALVKPKEAYL*IPNGVSRKLDPLAYI AHPKLAKRALARIAKGLKCRPEALAEA RAKDQTKVQGVAPA*APAHAPKRTQAP TKASE |
| 1318 | 9369 | A | 228 | 34 | 478 | LSPRLECSGAI*AHCNLRPPGFKQFSCLSL SSSWDYRHAPPTQLIWFWYFK*RPGF QLVLVQAGLELTL*IPPASASQKCWD YQV*APH/WPALYKVS*EKWFPIMFFA PFSWLSLGTEKFVRKVAVAGLTPTG WALCSLWKY |
| 1319 | 9370 | A | 2280 | 9 | 674 | IERLQVRIACSCRDAIPGSSHASAHASEA LREPRNGADMAKSKNHTTNNQSRKW PWRNGIKKPRSQRYEFS*RGWPPQVSLR NMRFAQRSTNKKGP*RLQANKLPRAM SATCPRLIKAPPLKAPRRFKPDPPKGVS RKLDRLAVIAQPPQLGSVARCP*LPRGP RLVCPPKAKGQGGQAKAKDQTKGFKP RPRVQAPVSVVQAPKRTQAPTKASE |
| 1320 | 9371 | A | 2281 | 417 | 822 | RENCILLSTRAQSVFNAQGTALWSFQDP ATGEGGAGHGGRLMRPSLLPSQGASAC* /PRFGESKLAPVGKFKMCLLELPFLSHH LSRGCSGASEGQLCLEVPATARVGVHK PSQSRGLEFSWVMSDLCSPPL |
| 1321 | 9372 | A | 2284 | 85 | 409 | TCGLPMCQKQTVSWGKTPSLRRFPQR PRPPRGQPPSGARWEH/PPGTTAPRRSR RPSPPARLAGPEP*AKSPLHAANSRGQTK GHLWKTLLVLFKKPNFFFNHFN |
| 1322 | 9373 | A | 2285 | 193 | 609 | NQINFCLNGKYTYICIDTPLYMFIHTL KHINTSVIISLEFAI*HKGQVELHIKITYRS N*MWLGHNRN/LCPQEGEEIPNEA*IF SIKRQSWPGTVAHACNLITLGG*DGRIS* DQVFKTSLINIVETPSLLKK |
| 1323 | 9374 | A | 2286 | 117 | 433 | |
| 1324 | 9375 | A | 2287 | 2 | 1923 | VETPPQGSVHSGHLGSVVGDPHTGTGN AGERGPRGKGARVLALDSSGMDSSPSLP LIRTPESLHEALDQCM TALDLFLTNQFS EALSULKPRTKESMYHSLTYATILEMQA MMTFDPQDILLAGNMMKEAQMLCQRH RRKSSVTDSFSSLVNRPTLGQFTEEEIHA EVCYAECLLQRAALTFLQGSSHGGAVRP RALHDP SHACSCPPGPRQHLFLQDEN MVSFIKGGIKVRNSYQTYKELDSLQSS QYCKGENHPHFEGGVKLVGAFNLTL MLPTRILRLLEFVGFSGNKDYGLLQLEE GASGHSFRSVLCVMLLLCYHTLTFVLG TGNVNIEEAELKLPYLNRYPKGAIFLFF AGRIEVIKGNIDAVSDGGPGRGWGSLGV SQTSRKSGTCDILDRIDWGRGGGPREN QPESRGRGPSGRAAWEDKGGGICGA WDFDWEI*DCSIAVEGGGGRCLREAEVR KAHLFRA*RLGWSLVPLHYSSLLLFHF VTKNQSPRRGLYLSPTSCKT*EVKPGLE ARSPGSWGPT*A*HRAGPLCPGGVPVCC GVGRFGGCRGVGAGWAPVRLTRCLQ AIRFECCCEAQHWKQFHHMCYWEL MWCFTYKGQWKMSYFYADLLSKENCW SKVG |

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| 1325 | 9376 | A | 2288 | 1 | 1818 | LGEGGGKKGLWDLVAGLHPLGGQQSP MCQKGHKDSLPCGGTPESSLHEALDQ CMTALDFLTNQFSEALSULKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGN MMKEAQMCLCQRHRRKSSVTNSFSSLVN RPTLGQFTEEEIHAEVCYAKCLLQRAA LTFQLQDENMVVSFIKGGIKVRNSYQTYKE LDSLVSQSSQYCKGENHPHFEGGVKLG GAFNLTLTMLPTRLRLLEFVGFSGNKDY GLLQLEEGASGHSFRSVLCVMMLLCYHT FLTFLVLTGNVNIEEAELKLPYLNRY KGAIFLFFAGRIEVIKGNIDAAIRRFEECC EAQQHWWKQFHHMCYWELMWCFYTKG QWKMSYFYADLLSKENCWSKATYIYM KAAVLSMFGKEDHKPFQDDEVELFRAV PGLKLIAGKSLPTEKFAIRKSRRYFSSN PISLPVPALEMMYIWNQYAVIGKQPKLT DGILEIITKAEEMLEKGPENEYSVDDECL VKLLKGLCLKYLGRVQEAENFRSISAN EKKIKYDHYLIPNALLELALLMEQDRN EEAIKLLLESAQNYKNYSMESRTHF*IQ AATLQAKSSIENSSRSMVSSVSL |
| 1326 | 9377 | A | 2289 | 486 | 713 | SKFYLFYLFYFFVYTYVINIVYIKI*QQID LNFYLFYLFYFWRQSRFLSKL*CSGA NMTHLSLNLPGSRNTPAPALQAAGTTG M*HHTWLFVVFVTEFHHVGLKFLSLD IHPPWPSKVLG*QGGWIV |
| 1327 | 9378 | A | 229 | 28 | 359 | KGKIPWLCGI*PQNEKLM*HSKSLATVFC IYR/TN*KNKRIISNAEKAIHQHTFMNF LKNF/MKTVRKLMGDSILNIIKEICERP TNM*DGELLDDFPKIGDEAQRPP |
| 1328 | 9379 | A | 2291 | 1 | 774 | |
| 1329 | 9380 | C | 2292 | 214 | 483 | |
| 1330 | 9381 | A | 2293 | 701 | 1033 | |
| 1331 | 9382 | A | 2294 | 440 | 1383 | SSSWNRAFSRKKDKTWMHTPEALSKHFI PYNALFLGSTVEQPKGTEVVRDAVRK LKFARHIKSGGQKIPKVELQISIYGSK NS*DPKTKREVQHNCQLHRISFCADDKT DKRNFTFICKDSESNKHLCYVDFSEKCA EEITLTIGQAFDLAYRKFLSEGGKDVETR KQIAGLQKRIQDLETENMELKNKVQDLE NQLRITQVSAPPAGSMTPKSPSTDIFDMI PFSPISHQSSMPTRNGTOPPPVPSRSTEIK RDLFGAEPFDPFNCGAADFPDIQSKLDE M/QAPEMEGFKMGLTLEGTVFCLDPLDS RC |
| 1332 | 9383 | A | 2295 | 412 | 842 | GKVSPPGL*GP*GEQGPLGPSGAATGLP HSLCPEAFASPRSVEYR*DQAQLALWAV PL*EGPL/PDLVRGVVPGSPVKVPGDEV T/CHSCGRFPRALGQSKTLPPNLPLTTRR GVNSEDLPSPVYRAADRGNRFPAGVGG SCHR |
| 1333 | 9384 | A | 2296 | 1036 | 1429 | GRAWRTCPRAHQPRRSHLRPSSCSTLQ RG*SPPPGRSSSPVQP*CA*ARGWGSQPG *HWTCLFLAWQSPQCTGPIQCYPRPLR SPRPAGPPGTSGHSPPDARAPRRRPAP CGRECSSSSGRNAAPLG |
| 1334 | 9385 | A | 2297 | 44 | 396 | |
| 1335 | 9386 | A | 2298 | 298 | 409 | |

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| 1336 | 9387 | A | 2299 | 123 | 1221 | KRQLFPLSWAMAASGSRMAQKTWEALA NNMQEAQSIDEIYKYDKKQQQEILGGEA LD*GVRSHHYFKYCKISALALLKMMVM HARS/GEKNLEVMGLMLGK/VWDGETM IIMGKFFFCLEGTETRVN/SLQAAAYEY MAAYIENANQV/GSPENAIGWYHSHPGI YGCWLSGNDVSTQML/NQQQFQEPFVAV VIDPTRTISAGKVNFGAFWAHPK/GGYN PPDÆGP/SGVPGLFPLNKIEDLGVHCKQY YALEVSYFKSLLGSQNCLELLWNKIWG GIRWSS/SLAGLLNADYPTGQVL*FVLKK LEQSRSPSLGRGEFPCWGLETHDARKSED KLAKATRSS/CKLPIEA/HGLMSQVIKD KLFNQINIS |
| 1337 | 9388 | A | 23 | 3 | 438 | LFISLLSISEKIIENCWV*LSAARS*ALRKL AFF*ATRSFF*ARDILGRFHLLFF/CNFFLG LLFIDWILSYSSMSFLIHLHPAGQQQAS TICCSIICQANLHTFVWQFVCIRCADYHIP LYTGISNLTNDISVCHTNYHPVIGVW |
| 1338 | 9389 | A | 230 | 1216 | 2017 | HPRGAKYPETNPGFVTL SYVGPPDSRQL THSRPSRSENACGHRPGELNWLNCSCGL LVPRGKRVWTETCNLVWKEASGPPPG DPLPSLSPITHQTQARPT/DTQAHCPAPCP PH*PLALNPQQNFCPEESAAQVGQGEED RTSRGWWHGSQPQVGAGK*PLSTGSKA QGARTGGGVPSRPLR*EQALVRCRCRL CRLGSCVRSHSLKFIDEAGEAPSAAGLD GGGTGRAPGAPEARCPRAESGEGPGSG QAPAEQDPQPRALRA |
| 1339 | 9390 | A | 2300 | 2 | 433 | |
| 1340 | 9391 | A | 2301 | 1 | 2423 | MAGALAGLAAGLQVPRVAPSPDSDDT DSEDPSLRRSAGLLRSQVIHSGHFMVSS PHSDSLPRRRDQEGSVGPSDFGPRSIDPT LTRLFECLSLAYSGKLVSPKWKNFKGLK LLCRDKIRLNNAIWRAWYIYVKRRKSP VCGFVTLQGPEDAHKRPAAVVLGN YWKRRIEVVMREYHKWRIYYKKRVSGG GPGRPQSFPAAAGYRPPRKIPGKILTP ELAPLGPSIQSRADSATVWPORLLAASLP RGRLRKPSREDDLLAPKQAEGRWPPEQ WCKQLFSSVVPVLLGDPEEPGGRQLLD LNCFLSDISDTLFTMTQSGPSPLQLPPED AYVGNADMIQPDLTPLQPSLDDFMDISD FFTNSRLPQPPMPSNFPEPPSFSPVVDLSF SSGTLGPEVPPASSAMTHLSGHSRLQAR NSCPGLDSSAFLSSDFLLPEDPKRLPPP PVPPPLLHYPPPAKQETVPEFPCTFLPPTP APTPPRPPPGPATLAPSRPLLVPKAERLSP PAPSGSERRLSGDLSSMPGPGTLSVRVSP PQPILSRGRPDSNKALLGSFLGSPNSLLPE TENRRITHISAEQKRRFNILGFDLHGL VSTLSAQPSLKVSKATTLOKTAEYILMLA QGERAGLQEEAQQLRDEIEELNAAINL CQQQLPATGVPIHQRFDMQMRDMFDAD YVRTRLHNWKFVWVSSLKPMAGGLQ GLWQGSSLTWAQFSILIRPLFESFNGMVS TASVHTLRQTSALWLDQYCSLPALRPTV LNSLRQLGTSVTSILVTDPGRIPI/EQATRA VTEGTLGKPL |
| 1341 | 9392 | A | 2302 | 1 | 535 | |
| 1342 | 9393 | A | 2303 | 155 | 276 | |
| 1343 | 9394 | A | 2304 | 1 | 477 | |

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| 1344 | 9395 | A | 2305 | 221 | 2323 | LGLQMHTTSGRHQAMVTSLNEDNESVT VEWIENGDTKGKNEIDLESIFSLNPDLVLP DGEIEPSPETPPPPASSAKVNKIVKNRRT VAASIKNDPPSRDNRVVGASARARPSQFP EQSSSAQQNGSVSDISPVQAAKKEFGPP SRRRSNCVKEVDKLQDKREMKRLQQQE LREIRAQDV DATHPNYEIMCMIRGFTGS LDYRPLASADPIDEHRIYVCVRKRPLNK KETQMKDLDVITIPSKDVVMVHEPKQK VDLTRYLENQTFRFDYAFDDSDAPNEMV YRFTARPLVVTFIFERGMATCLAYGGTGS GKTHTMGGDFSGKNQDCSKGIYALAAR DVFLMLKKPNYKKLEQVYATFFEIYSG KVFDLLNRKTKLRVLEDGKQQVQVVGL QEREVKCVEDVLKLDIGNSCRTSGQTS ANAHSSRSHAVFQIILRRKGKLGKFSLI DLAGNERGADTSSADRQTRLEGAENKS LLALKECIRALGRNKPHTPFRASKLTQV LRDSFIGENSRTCUMIATISPG/MWASCEN TLNTRYANRVKELTVDPAAAGDVRPIM HHPPNQJDDLETQWGVGSSPQRDDLKL LCEQNEEEVSPQLFTFHEAVSQMVEEMEE QVVEDHRAVFQESIRWLEDEKALLGD*L EEVDYVDVSYATQLEAILEQKIDILTEL DKVKSFRAALQEEEQASKQINPKRPRA L |
| 1345 | 9396 | A | 2306 | 264 | 451 | VLPNLTVHASPTTIKIWAGKVTHAYNPS TLGGQGRGRIA*AQEFKTSLSNIMGLRLSK KKKKK |
| 1346 | 9397 | B | 2307 | 1 | 642 | MLEEQLVRMLTREVMDLITVCCVSKKG ADHSSAPPADGGDEEMMATEVTPSAMA ELTDLGKCLMKHEVLSGTLADAVTWL FTSVLKGLQMHGQHDGCMASLVHLAFQ IYEALRPRYLEIRAVMEQIPEIQKDSLDQF DCKLLNPSLQKVADKRRKDQFKRLIAGC IGKPLGEQFRKEVHIKNLPSLFKKTTPML ETEVLDNDGGGLATIFEP* |
| 1347 | 9398 | A | 2308 | 3 | 101 | STHASESNFICSILCFCLEAPISLMLSLSA SLEDQPWAWALCGGGRAPSTT*PPLSL* HL |
| 1348 | 9399 | A | 2309 | 360 | 483 | SMCLTVSMLVTACPADPCVT*A*NRSSF EVPPPWTSDLRFF |
| 1349 | 9400 | A | 231 | 5 | 399 | DGVSLV/SPRLEYSGAISAHCKLRLPRFK *FSCLSISSWDYRHHVPPPPANSVFLVKT GFHHVGGAGLELLTSGDLPTSAPFKCW DYRCDHCAWAKD*KFKCVSVGRRGGP GEAVHQNSNRLSYWWEDGGKGTG |
| 1350 | 9401 | A | 2310 | 100 | 190 | |
| 1351 | 9402 | A | 2311 | 2 | 193 | WRRRRRRFCPPQPSLIWSGMRSPKKLTP PR*NYLRQALRRNLSTLRRPFAQETAWY QWCFLGL |
| 1352 | 9403 | A | 2312 | 103 | 237 | |
| 1353 | 9404 | A | 2313 | 3 | 1361 | VETQEGKTTIEGRITATPKESPNNPPNSG QCPICRWNLKHKYNYDDVLLLSQFIRPH GGMLPRKITGLCQEEHRKIEECVKMAHR AELQRELQRLSPLPATQVYYQITGLGFLK ELFRRANPNSTGPLAKAQGGYLTRWAP GSVKPIYKKGPRWNRGEANRKAHFTV QWPAPSAIAHAKDDVSPLQPTQCLLDNI KKKVVPLSGRPGNTDSTCQESRSIYLS QALAVTFTHTLTATAEQAEPSSLSPPPG LGEKPPADLVQW/SEAPRAKQHYCTSP SHPAQRVVSSSDSIEHPAAASHPRRPPRP GTNGWSRRGSCRASWSRDCSGVRSRRV ALGMAMDQVNALCEQLVKAVTVMMDP NSTORYRLEALKFCEEFEKCPICVPCGL RLAEKTQVAIVRHFGQLILEHVVKFRWN GMSRLEKVYFEEQWSWNLIAKGPFEHF GRGEPY |

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| 1354 | 9405 | A | 2314 | 138 | 397 | SHCPLSMHVGGTRPSWWGGTGV*LWPR AC/RVGLLLPSTGAGGTLEALLSVSDTAS KVFEELARHCPSEGVNPTGHAHPVPSRG PFL |
| 1355 | 9406 | A | 2315 | 16 | 546 | QLNGRSIRHEVMSHRKFSAPRHGSLGFL PRKRSSRHRGKVKSFPPKDDPSKPVHLTA FLGYKAGMTHIVREVDRPGSKVNNKEV VEAVTIVETPPMVVVGVGVVETPRGLR TFKTVFAEHISDE/CRLLPLRQKKAHLME JHVNGGTVAEKLDWARERLEQQVPVNP VFGQDEMIDVI |
| 1356 | 9407 | A | 2316 | 2 | 451 | PRAKAQKQSPVLWAQKSCPPKTTTRALA KVACIGAWHPARVAFSVARVGQKGYH PRTEITKKIYKIGQGYLIK/DGKLIKNNNA STDYDLSDKSINPLSLLVQTKRRALEKID LKFDITTSKFGHGRFQTMEEKKAFMGPL KKDRIAKEEGA |
| 1357 | 9408 | A | 2317 | 1 | 625 | CKFIRVMAHTRLRLPLRRKKAHLMEIQ VNEGTVAEKLDWARERLEQQVPVNPVQV GQDEMIDVIGVTKGKGYKGVTSRWHK KLPRKTHRGLRKVACKDGLIKNNAST DYDLSDKSINPLGGFVHYGEVTNDFVML KGCVVGTKKRVLTLRKSLLVQTKRRAL EKIDLKFDITTSKFGHGRFQTMEEKKAF MGPLKKDRIAKEEGA |
| 1358 | 9409 | A | 2318 | 1 | 1251 | |
| 1359 | 9410 | A | 2319 | 1 | 903 | |
| 1360 | 9411 | A | 232 | 481 | 525 | AAGTYSL*IGKE*VKLSLSDSMILYIDN LKTLPKTLTDDKFSKISEYNISVF*CIND EKAKEIRKTIPFTIHKR*NTSDLTKKVKG LYKGNKTLMEINKWKDIPCA*IRRINI IKIVYPK*T*FKAISIKILLSFVTEIEKKIPK FI*NQKRIRIAKATLSCWNLFPMNSWHN RC |
| 1361 | 9412 | A | 2320 | 1 | 1341 | |
| 1362 | 9413 | A | 2321 | 1 | 1131 | |
| 1363 | 9414 | A | 2322 | 10 | 1304 | ESDGVTSRHRKFSAPRHGTLGFLPRKRSSR HRGKAKSFPTDDPPKPGHLTGFLAYTAG MTHIVREVDRPGSKANTKEAGEAATIVE TPPMVSVGVGVGVVETPRGLRTFKTVFAE HISDECKRRFYKNWHKSKKKAFTKYCK K/WQDEDGKKQLEKDFSSMKKYCQV RVIAHTQWRLPLARQKKAHLMEIQV NGGPCGPRSWDWAREKLEQQVPVNPV FVGQDEMIDVIGGDPGAKGYKRGSPVR WHTKKAAPARPHPRACAKVGLVLGAW HPGRVAFSVASRWGRKGLPFHRTEINQ GRIFKDWPRATLIKDGKLIKQCLHLNY DLS*PRASNPLGGFVHYW*SDRNDFVM L/KGCVVGTKKRGAHPFRKSLLVQTKAR RALEKIDLKFDITTSKFGHGRFQTMEEK KAFMGVPLKKDRIAKEEGA |
| 1364 | 9415 | A | 2323 | 138 | 737 | TTTMSSKKAKTITTKRPPQATSNVFA MFVHSQIQGVQRGPFNMIDQWRDGFHS DK/EKVLHDM LAFSREESPLDAYLDAM MNEAPGPHQVSPWFLTMFW*ESLNRTD PLKIVIQKPPFA/CFD*KKATRHPFREDYL /REELLTNPWGDRVYQIEEVG*TCTGEAP I*QKKGNFQITSEFHHGILTGRPPKHKDD LKELLA |
| 1365 | 9416 | A | 2324 | 2 | 307 | |
| 1366 | 9417 | A | 2325 | 2 | 215 | |
| 1367 | 9418 | A | 2326 | 1 | 213 | |

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| 1368 | 9419 | A | 2327 | 2 | 935 | FRPRYEGRGRGCCGRVRLRRGLHVDC GKLGKLTSSCGKPSNRMSLQWTA TFLYAEVFFVLLLCIPFISPKRWQKIFKSR LVGVVSVPMGNTFF/VLVILVLLVIE CRAAKFREVMWDVDGKRVNLPGTIPGG HGEALSHMEAFSVAPGGNLLHWLGFSL LLSFLRLRLVTLSQQATLLASNEAFK KQAEKC*VKAARKYMEENDQLKKGAP FDEGKLNFEAELKLEEKINRELKIANLQ KLKDELGQALSCKLEK*KTSFWPMRK QFMRGLTQ/ERYDRLLLEQPKAAGLQV DGPMDKKEE |
| 1369 | 9420 | A | 2328 | 2 | 1217 | QARGASLRPSLLRIPSEYAFTMQLRLFR LLLAALLLVIVWTLFGPSGLGEELLTSL AFLLPAPALPGPPLALPRLLIPTQEACCGP GAPPFLILGGTAPENLNQRNAIRASRGG LREARGLRVQTLFLLGEPNAQHPVWGS QGE*TPSESAAQGDILQAAFQDSYRNL TLKTLGSLNWAKEHCPMARYVLRDDED GIANVPELVSELVLRGGRWGQWERSTEP QREAEQEGGQVLHSEEVPLLYLGRVHW RVNPSRTPGGRHRVSEEQWPHTWGPFPP YASGTGYVLSASAVQLILKVASRAPLLP LEDVFGVSARRGGLAPTQCVKLA\GA\I THYPLDRCCYGFLLTSHKLDPWKMQE AWKLVGGS\DGKDCAPFAPWFGKSL GILRCR\A\A\WLQS |
| 1370 | 9421 | A | 2329 | 1 | 395 | AINYNEKIYELRMETKPDKAVSHIED MNVDFAF/LGYKEPERQVQHEESTEGE ADHSGYAGE/LGFRAFSGSGNRDLGKKK GVEPSPSPIKPGDIKRGIPNYEFKLGAEAG GRFVAFSGEGQSLRKKGRKP |
| 1371 | 9422 | A | 233 | 20 | 129 | |
| 1372 | 9423 | A | 2330 | 1 | 1494 | |
| 1373 | 9424 | A | 2331 | 2 | 1062 | GRAVGGVSSLHCPERSGVCQVVSIMFSF NMFDHPIPRVFQNRFTQYRCFSLSML AGPNDR/SSIGEKEGKIIMPPASALDQLSR L*HYRIPMLFKLTNRNSDRMTALLOCLE FVADEGICYFPTL/WMMQNLLLEEGGLV QVKS\NLSSATLLPNFQPS\DFLADITN PKAVFENALRNFACLTTGDVIAINNYE KILRNCVVMETQTPTRPVSHH*SVNH*T V\DFDCFLGLPKNPGKTKSHHEESEQKV KADPTVAYAWKSLGFPRFSRSGSNRLD GKKKGVEPSPSPIKPGDIKRGIPNYEFK LGKITF/VSRSRPLVKKVEEDEAGGRF VAFSGEGQSLRKKGRKP |
| 1374 | 9425 | A | 2332 | 1 | 214 | APARSALCSGAPRTSGQPWGTAPAPPS FHQRNTPCPWSAPPSGAAPWGSTKGQR LDGPCCAPFPPRGLSM*SKVPWWPA*TA PAPPSFHQRNTPCPWSAPPSGAAPWGST KGQRLDGPCCAPFPPRGLSM |
| 1375 | 9426 | A | 2333 | 1 | 1515 | MAPLQQHIAVLPTTADQVTTEDDGYT WTALQHVATAKEKRKSSQTMEESQDFP LHIPRAQGTQRAVARPSGPKAWTEAG PAKDAARSEKPGGRKAPGGRGQLTCRR SLSPVRQPPVSVVSDSLRRRSPCSPADW REAGATSLDRIPILVLMVDKKLVVVF STGAQGGSVARILLEDGTFKVRVVTNRP RKKA AKELRLQGA EVVQGDQDDQVIME LALEWAYATFIGTNYWESCSQEVEVTP A/GSLDRIPILVLMVDKKLGLHYVVYS GL\GTSRS*RQGDWPRTLTAKGRWRNI SGTLAFP*PVWGFLANLENLLQLFFPR KTPEGKELLCGACQVTFPWMACPLT WGPVVL\SLFEDARKIRPEHRG*LAGT RPRSTLPCSPSTPARSCTMPR*LPEDYEK LGFGARDLGQHVFLCPETPTRDI/PSLT LRLNPKALTLDQWLGTARGLQPAVTL |

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| | | | | | | PASRPLVGIRGHQRGKKAPTSEIKPICSPK KKKK |
| 1376 | 9427 | A | 2334 | 3 | 1037 | ILRSVARAQRGRRSLRFHWSPGGHGGRS EAGAAGP/VEMRRCTAAPQGRVPGL/PS KLGIPDALPTVAAPRPVCQRCGQPLAAL VVQVYCPLEGSPFHRLHLHVACACPGCS TGGARSWKVFRSQCLQVPEREAQDAQK QGNSLAAEDWCEGADD/CGK*Y*GGAFT TVYLGFE*CCQC/HKT*TGLLGSKTS/C LQDAVLGAAHPVPPGLPLFLPYVICVAD EDDYRDFVNLDHAHSLRDYQQREGIA MDQLLSQSLPNDGDEK/S*EDHN*KVGG SRPF*QIP*KRNWLLVREQLRVFPGVES HSF*PAPTSEVTELPQLQPVWEAKRIFEF QLMPALGQHASRVLI |
| 1377 | 9428 | B | 2337 | 240 | 387 | NGKERGTGDVKLLKHKEKGAIKLLMRR DKTLKICANHYITPMELKPNAX* |
| 1378 | 9429 | A | 2338 | 1 | 152 | |
| 1379 | 9430 | A | 2339 | 1 | 830 | MRRPRRRLCWLRLVECGPLQSRSAVG NSEEQRKAYVFFSSLSLVDTHEDHDTST ENTDESNHDPQFEPVSLPEQENKLEED EEELFKMRAKLFRFAENDLPWKEKRG TGDVVKLLKHKEKGAIKLLMRRDKDP *KICANPLPSRPLMGAESPTAGRSPVW VLETPHADFRPNECPPSPPLGPPRFLN A*RMPQKFQNSFEELQKRSSEEEEEKE SRFQKNDL/HRKKCAEKPSSLR*REE TKEDAEAEAINRLILLSFSSLSLS |
| 1380 | 9431 | A | 234 | 16 | 370 | |
| 1381 | 9432 | C | 2340 | 392 | 631 | MRTAESCRRLSWAALLGSHWRCCSHPC AAGQGPYPRAAVNGPRTPLAYLRKEM FSSGLINVEFPQFLYLSHFHSLLR* |
| 1382 | 9433 | A | 2341 | 3 | 121 | |
| 1383 | 9434 | A | 2342 | 1 | 2970 | |
| 1384 | 9435 | A | 2343 | 48 | 1493 | DGQYRIWWLIEWHVDGGCGDTETWKD RWNHVKKVFLERSGPFTHPDFEPSTESL QFLDTCIVLVIGAGGLGCELLKNLAL SGFRQIHVIDMDTNDVSNS*IRQFLFRPK DIGRPKAEVAAEFLNDRVPNCNVVPHF NKUQDFNDTFYRQFHINVCGTGLSCA RRWINGMLISLALNYERMVS*DPSSIVPLI DGGTEGFKENARVILPGMTACIECTLE LYPPQVNFPMCTIASMPRLPEHCNEYVG MLQWPKEQPFGEVPLDGGDDPEHIQWI FOKSLERASQYNIRGVYRLTQGVVKRII PAVASTNAVIAAVCAT*/EVFKIATSAYIP L*IITWVFNVDGLYTYTFEGRKGVEN CPACSQLPQNISVFLHQAKLQEVLGILT NSASLQNEILPAITATLGGEKIGTLYLQS VTSIEERTRPNLSKTIGRIGLLDGPKTG RLLDVTTPTQTVLFQTSILLKKGKSP |
| 1385 | 9436 | C | 2344 | 166 | 312 | |

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| 1386 | 9437 | B | 2345 | 355 | 487 | MLGLRSGIPAPVRLQLAVVLGNSLGNFG TEGPGLKGRTMTVTGDPX* |
| 1387 | 9438 | A | 2346 | 754 | 1035 | GKVRTVKIKYWMLARSSGSSL*SQHFGR LRQADHEVQEIKHHPGKHSANP*SLKI QKVS*LVSQAWWWVPVPAIREVEAGE WCEPGRQSLQ |
| 1388 | 9439 | B | 2347 | 80 | 432 | MANGPRAXFCENFQAALALSRVGLHKN PEKEPYKSKYSARALLEEVKALLGPAPE DEDERPEAEDGPGAGDHALGLPVAQRA VRLAVIEFHLGVNHIDTEELSAGEEHLVK CLRLRS* |
| 1389 | 9440 | A | 2348 | 2 | 1060 | HWLSTANVISDYDDKSSPTQDTAETV*D TPELYHQGKGEIARCWKYCLTLMQNA QLSMQDNI*ELDLKQSELIALRKKELDE EESIRKKA VQFGTGELCDAISAJEEKVSY LRPLDFEEARELFLGQHYVFEAKEFFQI DGYVTDHIEVVQDHSALFKVLAFFETDM ERRCKMHKRRIAMLEPLTVDLNPQYYL LVNRQIQFEIAHAYYDMMDLKVAIADRL RDPDSHIVKKINNLNKSALKYYQLFLDS LRDPNKVPFEHIGEDVLRPAMLAKFRVA RLYGKIITADPKKELENLATSLEHYKFIV DYCEKHPEAAQAEIEVELELSKEMVSLFP TKMERFRTKMALS |
| 1390 | 9441 | A | 2349 | 11 | 2571 | VKCRKAEGRRRESRLQTFEESQAVEAAM ANVPWAEVCEKFQAALALSRVELHKNP EKEPYKSKYSARANMEEVKALLGPAPE DEDERPEAEDGPGAGDHALGLPAEVVE PEGPVAQANRLRLAVIEFHLGVNHIDTE ELSAGEEHLVKCLRLRRYRLSHDCISLC IQAQNNLGIVWSEREEIETAQAYLESSEA LYNQYMKEVGSPLDPTERFLPEEKL VEQERSTRFSKVYTHILYYLAQVYQHLE CFETAHYCHSTLKRQLEHNAYHPIEW AINAATLSQFYINKLCFMEARHCLSAAN VIFGQTGKISATEDTPESEGEVPELYHQR KGEIARCWKYLF*LLMQNAQLSMQDNI GELDLKQSELRALRKKELDEEESIRKK AVQFGTGELCDAISAVEEKVSYLRPLG FEEARELFLGQHYVFEAKEFFQIDGY VTDHIEVVQDHSALFKVLAFFETDMER RCCKMHKRGGLAMLEPLTVDLNPQYYL VNRQIQFEIAHAYYDMMDLKVAIADRL RDPDSHIVKKINNLNKSALKYYQLFLDS LRDPNKVPFEHIGEDVLRPAMLAKFRVA VARLYGKIITADPKERAGKIWATSLAEH YKFIVDYC/EKRHPEAAQAEIEVELELSKE MPGRRSETPSLKERNKKDKIQTAKTTSA PPAQLALATPQPVRMCRQLTRVISLGSS KGKASFAGPDRPPYEDPHIVRLQLYHPQ RERSCVTSSRRSCAKSPWTLSSRWPHGS SWEKSYELSDGQVITSSNKRFFHCPEALF QPSFLGMESCGIYKTTFKSIVKCDVDIHK DLYANTVLSGSTTMYPGIALQDAEGDHC PGSQHEEDQDHCSF |
| 1391 | 9442 | A | 235 | 1 | 1125 | |
| 1392 | 9443 | A | 2350 | 1 | 421 | GTVVMGLPKYFISLSTKFPLSFSLSADEL HIASLFLWPRSKPFGVIQRSCASQLNALP EVLKNPGDPDKMLRFAESPRNLPAAGVL GDIWTDGKGSVSLQEQQVYHFPLIRTPGS *ARASFLSCG*EEFRRHGLTFSSTRE |

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| 1393 | 9444 | B | 2351 | 211 | 1632 | MSTELFSSTREEGSSGSGPSFRSNQRKML NLLLERDTSFTVCPDVPRTPVGKFLGDS ANLSILSGGTPKCCLDLSNLSSGEITATQ LTTSADLDETHGLDSSGLQEVHLAGMN HDQHLMKCSPAQLLCSTPNGLDRGHRK RDAMCSSSANKENDNGNLVDSEMKYLG SPITTVPKLDKNPNLGEDQAEISDELME FSLKDQEAQVSRGLYRSPSPENLNRP RLKQVEKFKDNTIPDKVKKKYFSGQGK LRKGLCLKKTVSLCDITITQMLEEDSNQ GHLIGDFSKVCALPTVSGKHQDLKYVNP ETVAALLSGKFQGLIEKFYVIDCRYPY LGHHIQGALNLYSQEELFNFLKKPIVPL DTQKRHIVFHCFSSSERGPRMCRCLREE DRSLNQYPALYPPELYILKGGYRDFPFE YMELCEPQSYCPMHQDHKTELLRCRS QSKVQEGERQLEQIALLVKDMSP* |
| 1394 | 9445 | A | 2352 | 200 | 1525 | IMASAHLATSAFCTRSSSSGRSGCKRGS WDSEQALIRAWTTLPSLHAADGSFAGG RGIPSKRWSWRAGQQSSLCLIMQTSNC GNSFQLVSEGASWRGLPHCSCAELQDSL NFSYHPSGLSLSVRPSSPGNSPKQPFSSQ VLRPEPPDPEKLPVPPAPPSKRHCRLSV PVDLSRWQPVWRPAPSKLWPIKHRGS GGGGGPQVPHQSPPKRVSSLRFLTSSQC LFSMCPSSQTLQPSFLQPGGPASSSRPCA ASPQSGSWESDAESLSPCPPQRRFSLSPS LGPQASRFLPSARSSPASSPELPLAT*G/L SATFPESRSQPCDLARKTGKRRHEED PRRLRPSLDFDKMNQKPYSGGLCLQETA REGSSISPPWFMACSPPLSASCPTGGSS QVLSESEKEEGAVRWGRQALSRTLC QRDFGDLNLNIEEN |
| 1395 | 9446 | A | 2353 | 2 | 280 | |
| 1396 | 9447 | A | 2354 | 2 | 971 | |
| 1397 | 9448 | A | 2355 | 604 | 876 | SLHHKDFTGMLLLQFAHHLGEIGFSLIS PKSRQPRFLPSVRQCGAAAA/RRCYRL APRPVCSGKRRTAPGAGD*GGERARPPR ARVFCPR |
| 1398 | 9449 | A | 2356 | 1 | 1042 | DLFRRHFKSSSIQRSAAAAAATRTARQH PPADSSVTMEDMNEYSNIEEFAEGSKIN ASKNQDDGKMFIGLSWDTSKKDLTE YLSRFGEVVDCTIKTDPVTGRSRGFGFV LFKDAASVDKVLKEHKLDGKLDIPKR AKALKGKEPPKKVFGGLSPDTSEEQIK EYFGAFGERENIEFSMDTKTNERRIGFCFI TYTDEEPVKKLESTYHQIGSGKCEIKV AQPKEVYRQQQQQKGGRGAAAGGRG GTRGRGRGQGNWNQGFNNYYDQGY GNYNSAYGGDQNYSGYGYDYTGYN YGNPMEYGRGYQTYQWPQSTLMG KIASRGGGQSTQNNYPAHT |
| 1399 | 9450 | A | 2357 | 586 | 1970 | PQEFTPLRFSLLILLFSQARVPSRVASLLA GRAAMEVPPRLSHVPPPLFPSAPATLASR SLSHWRPRPPRQLAPLLPSLAPSSARQG ARRAQRHVTAQQPSRLAGGAAIKGRR RRPDLFRRHFKSSSIQRSAAAAAATRTA RQHPPADSSVTMEDMNEYSNIEEFAEGS KINASKNQDDGKMFIGLSWDTSKKDL LTEYLSRFGEVVDCTIKTDPVTGRSRGF GFVLFKDAASVDKVLGT*KGHKLDGKL IDPKRAKALKGKEPSPKRFLWSGLSPDTS VEEQIKEYFGAFGEIENIELPMDTKTNER RGFCFITYTDEEPVKKLESRYHQIGSGV KCEIKGCTTPKRYLGQQQQPPKGCK/RG AAAGGRVGRGRGRSQGNWTOGFNN YYDQGYGNYNSAYGGDQNYSGYGGYD YTGYNYGNYGYGQGYADYSQQSTYG KASRGGGNHQNYPY |

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| 1400 | 9451 | A | 2358 | 592 | 608 | WLRWATYKAGQPQLEAQNPFYFREGQ PFLRLDHLRTAGAEQNCAAAVWVRRL* RNMGFVLLTGAVSFIMVAHLSHQCSQG PAKKVPKWEYPYPCTATEPLNNGHHPST CIQAKPHPRNTVGKV*PSPSLFFPSLLGG VYHPAV*ASWPWAWPWICWTEFLYAY GLLHGENPSKRSPRSPWGSTALLAFGWG TTVCSGFPSILVWVKISGLGQVEPKACH LKKL |
| 1401 | 9452 | A | 2359 | 857 | 1343 | SFRISFSGIITFKIVSFGIMAQTHAMGQFF ERNVSP*LTQGEIENLNRPIPVKL/ESITNN LL**KAPGLDGFTDD*SNIEINL*PRNISL KFFFLRKKSQFSTIASKKIEAKGTHPN* L*ETSITLILSKDKDMTRKGLQSLINIDA KILNKILANQMQ |
| 1402 | 9453 | A | 236 | 426 | 2173 | MRAQTHNRAVDIALGTAGAHLEDPGAQ QGQDRCSWQVCRSARRRRRREAAGGRR AARRAQHPCCREPSGNQSLSAHLHTGAT KGPASSLLHEHLWKPIARSARLPGNSSPL FSAPCSMGAGPSLLAALLLLSGDGAV RCDTPANCTYLDLLGTWVFQVGSSGSQ RDVNCVSMGPQEKVVVYLQKLDTAY DDLGNFGHFTIYNQGFIVLNDYK\WF AFFKYKEEGSKVTTYCNETMTGWVHD VLGRNWVFFTGKKVGTASENVYVNTA HLKNSQEKYSNRLKYDHNFKAINAIQ KSWTATTYMEYETLTLDGMIRSGGHS RKIPRPKPAPLTAEIQQKILHLPTSWDWR NVHGINFVSPVRNQASGSCYSFASMG MLEARIRILTNNSTPILSPQEVVSCSQY AQGCEGGFPYLIAGKYAQDFGLVEEACF PYTGTDSPCKMKEDCFRYYSSEYHYVG GFYGGCNEALMKLELVHHGPMVAFAFEV YDDFLHYKKGIYHHTGLRDPFNPFLT HAVLLVGYGTDSASGMDYWIVKNSWG TGWGENGYFRIRRGTDCAIESIAVAATP IPKL |
| 1403 | 9454 | A | 2360 | 84 | 326 | DKAYQCSDDCK/ELHSVTLVSR*SVLSM HQSIHWKKKCLICFLK/CHKAFSQ*SAII KQRIHVAQII*ICCIWESLQPEVVL |
| 1404 | 9455 | A | 2361 | 635 | 1170 | RLFKCILGLLTFPPDSSHPQLPGESPGSFE KSRCPCGWPHPAQPHQSRWAIGPACSSY SGVLQG*EPQI*SLQHGRGGGGRTGGLE KETRTGSRISDTALGG/EAGPCPCGQLPH LPGPPAAHDAGPYIP/PKGPGGSGYLHP HGSAKLGSNQGAMKQAGRTGSAGSQG SAEFHKAALWT |
| 1405 | 9456 | A | 2365 | 2 | 333 | EPVCATWKNRTPEPTRQCRPAEKQRASA TQHQEGRQPGWKPRRSSDPPHRPRGFSS THDVSD*PKVTNCREAKGEEAGSLPTGT GIGGSKPSNRLRSTHTTTPGTVFNT |
| 1406 | 9457 | A | 2366 | 208 | 491 | KQSQVWCVLWSEGLLGLDPPNPASCG GDRLS/RTSAVPPVP*S*NSSAHGPGGRP GKPQGWG*TVTSGRSVAGKPGVPSNRR CFLPPHPWLLDN |
| 1407 | 9458 | A | 2367 | 2 | 1010 | PQPAQPCPGKELRTVNGSQMLLVLLVL SWLPHWGALSLAEASRAISFPGPSELQ LRRTSKIPKSLRKRIYEDLLNPGCGPNQS WEDSNTDLVPAPAVRILTPAEVRLGSGG HLHLRISRAALPEGLPEASRLHRLFRLS PTASRSWDVTRPLRRQLSLARPHGPAH LRLSPPSSQSDQLLAESSARPQLEHL RPQAARGRRRARASNGDHCPLGPGGCC RLHTVRASLEDLGWADWVLSPREVQ VT/LCAIGACPSQFGRQKMHQESKTN PAPALKAPNTVPKRPCLVPRQLQIPWVL HSKRPTDGVCFQDL/SD*LVKPKTCHLH Y |

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| 1408 | 9459 | A | 2368 | 68 | 430 | HVLT AHPPHRLGPGPQGRSGMGREL V GPTVCLSSLPRLAASFPRPP/VGLGPQQV QVVNGGCWPCRGY GEGTQAPQPPS*VG DPGEPNPQAPGAQSSTPKPAHIPPTQEA GRRWEGKWFF |
| 1409 | 9460 | A | 2369 | 694 | 872 | VCPGTGGE*GLWGQLGGLPKETPLKPM DAFTGSGGLKRKFDDVDVGSSVSNSDDEI SSSDSADSCDSLNPPTTASFPTTSILKRQK QLRRKNVRFDQVTVYYFARRQGFTSVPS QGGSSLGMAQRHNSVRSYTLCEFAQEQ EVNHREILREHLKEELHAKMKMLTKN GTVESVEADGLTDDVSDDEDIDVENVEV DDYFFLQPSAIPKRRRALLRASGVHRIDA EEKQELRAIRLSREECGDCRLYCDPEA CACSQAGIKCQVSDRMSFPCGCSRDCG GNMAGRIEFNPIRVTHYLHAIMKLELES KRQGAQQPQ*GALPDCQLQPDRTSGP *DPLTWHLIPAWLQAHASGSQYSRQSOP HSSRRDRMARSSCFSSASIRCTPEALSRA RLRLVGRWLQEEVIIHLHIFHINIFI |
| 1410 | 9461 | A | 237 | 3 | 463 | GTRFLHSFLSSLKHGCGPSLLAALLLS PGDGAIVRCDTPANCTYLDLLGTWVFQ VGSSIGSQRDVNCVVMGPQRKKK*VVY LQKLDTAIYDDLGNWGHFTIYNQGFEL VLNDYKWF AFFKDVTFISHLFMQLGT VGIYDLPHLRNKAGY |
| 1411 | 9462 | A | 2370 | 2 | 295 | |
| 1412 | 9463 | A | 2371 | 2 | 345 | |
| 1413 | 9464 | A | 2372 | 156 | 1437 | GIETRRPWGRPYVAWLLVVM DALVEDD ICILNHEKAHKRDTVTPVSHLPGDESVA SHFALVTPYEDIKKRLKDSRKRTSFLKK RIRFLEELI/GSDLKKKQVT*GREQVVK AYHAYREVCIDRDNLKS KLDKMNKDN SESLKVLNEQLQSKEVELLQLRTEVETQ QVMRNLPNPSIQTGEVGVGAGDLKIH GFGNQELELMRKECSDLKIELQKAKQTD PYQEDNLKSRDLQKLSISSDNMQHAYWA ELKERKCLNLHLVTSSYKLELLRKT*KT STAIKKIACAPVGCVEDLGRDSTKLHL DGFLLATYARHPPLPNGKALCHTTSSP LPGDVKVLSEKAILQSWTDNERSIPNDG Y/DAFREHSSYGQNSLEDNSWGIFQSPPK /SQSETAFGETKTKTLPLNPLPHYLDQ HNQNC LYKN |
| 1414 | 9465 | A | 2373 | 28 | 405 | FLYDPAPPFLSIYPKELKVES*IDTCTLFI AALF/LIGKRWK*PKYPLTDEWINK/VWY INTIEYY/SHLKRKDILTHYTTWVNREDLI LSEISQSQKINTVESTYMRYKYISNS*ISIG TSYKSHRV |
| 1415 | 9466 | A | 2374 | 1414 | 1607 | DRVSLWLPRLECSGAISAHCNLCFSGLS NSPTSASRVAGTTGACHHTLLI*FLFV FV VVVFETES/HLWLPRLECSGAISAHCNLC FSGLSNSPTSASRVAGTTGACHHTLLIFV FLVEMGFHHVGK |
| 1416 | 9467 | A | 2375 | 558 | 985 | KKDPRWALYSLYVYKFLHFSYSSAKNP DGCFFQKVLNGFTKFFCKEQYCKLLKLY FYRLFALLWILCLSGFLKFFFYSEIMELV LAAAGALLFC/GNFIIYDTHSLMHKLSPE EYVLA AISLYLDIINLFLHLLRFLEAVNK K |
| 1417 | 9468 | A | 2376 | 664 | 937 | VLLILFSNINIFL*SLPY SFFFIGEDNGSWV LAAAGALLFCGDSSMDTHSLDGINWS PEEYVLA AISLYLDIINLFLHLLRFLEAVN KK |

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| 1418 | 9469 | A | 2377 | 1 | 739 | DPTPVTPRSSLKNDSTNGSSVASATVHIE WAFRLRKVYSILSLQVLLTTVTSPVFLYF ESVRTFVHESPALILLFALGSLGLNFALT LNRHKYPLNLYLLFGFTLLEALTVAVV VTFYDVYIILQAFILTTTVFFWDCVYS YQSKKDFSCKFGAGLFALLVG*LCLS\GF LKVFFFYSEIMELVALAAAGAPFPVDFII YDTHSLMHKLSPEEYVLAASLYLADII NLFLAHLRLFPQSQNLKK |
| 1419 | 9470 | A | 2378 | 272 | 1668 | AMSQGSVTFRDVAIDFSQEEWKWLQPA QRDVYRCV\MLENYGHVLSLAGLSISKPI DVVSLLEQGKEPW/VWGKREVKRDLS VSESSGENQGLFHQKNVIYDGLHPSI*IM ERNISKVKAPVYSSFKGGWKCKDHTEML QENQGCIRKVTVSHQEALAQHMNISTVE RPYGCHECGKTFGRRFSLVLHQRTHTGE KPYACRACGKTFSQISNLVKHQMIHTG KKPHECKDCNKTFSYLSFLIEHQRTHTG EKPYEECTECGKAFSRASNLTRHQRIHIGK KQYICRCKCGKAFSSGSELIRHQIHTGK PYECIECGKAFRRFSPLTRHQSIHTKTP YECNECRKAFRCHSFLIKHQRIHAGEKL YECDECGKVFTWHASLIQHTKSHTGEKP YACAE*NKAFSRSFSLILHQRTHTGEEP YVCKVCNKSFSSWSSNLAKHQRTHTLDN PYEYENSFNYSFLTEHQ |
| 1420 | 9471 | A | 2379 | 1322 | 1644 | HLELFLGIRGIKMFVGWNTNE*EEKAGLN GSRL*SQHFGKPRWVDH/LRSGVRDQSV GQHCKTSSLQKNTKTSWAWWRAPVVP AT*EAEVGGWLEPRGGGCSEAVSGAF |
| 1421 | 9472 | A | 238 | 12 | 362 | DRVSLSPRLECNSAIPAHNCNCLP/GFK QFSCSLSPSSWG*RCLPPRLANFLY/SLVE IGFHHVGQAGLKLLTSCDPPTSA/FPKCW DYRHEPQ/WPDL*LTSE*GYRYEDSFDFL PKVPI |
| 1422 | 9473 | A | 2380 | 319 | 724 | EASLDLAPNISPPKTSCLPTGSCCSFTQT WMPQSKVFIHGPEQGPWDWALGTDLTA LPFKARNMPNLDTAGLPSIALRLTVNHR RSPGSQELSCLPDSCLSQ/PPQPC*GSLLP LEYKCTPKEALRK*KRLSFLV |
| 1423 | 9474 | A | 2381 | 38 | 704 | SSEEEQSFSSWHQGDPAVTWKWLPK VPPRWRFSHFLDSPWHFLQTAVTPLP QISAAPPKPLLPPTSPLAFFSLLTDLPYL HPQGFSAGATAINKASHNRTRALQSHS SPEGKEEP*TPYPELEYIPARKRGKNPHG KLVGTGLGHSFAFCGYSFLFHPSPKRG GTRDRVEGRLKARQNRVCSNN/AGEYE EARRFKGLSSQ/SGPVPPDVAGSGVQT |
| 1424 | 9475 | A | 2382 | 107 | 449 | |
| 1425 | 9476 | A | 2383 | 68 | 422 | |
| 1426 | 9477 | A | 2384 | 54 | 859 | LRRGRSRETNEEPPPTVQVQGGPGQREE KQKTKMAKFVIRPATAADCSILRLIKEL AKYEYMEEQVILTEKDLEDGFGEHPFY HCLVAEVPKEHWTPEGYS*LRHVHGPS VYMDGRGGN*KILYTIK*MIMINEDTAL VGFAHVLIYPMNPWDWQSYLYLEDFSIV MSGYKGLGIGSEILRNLSPGCQ*RCR\CS SKHFLVAE\WQ*THPITFYKRRGASDLS Q*RRGWETCSKIGQGSTWLKIGQPEGVR ECCLLGWTTSHSYF |
| 1427 | 9478 | A | 2387 | 112 | 861 | NPGAACKMPAYHSSLMDDPTKLIGNM/A HLLPIRSQFKGPAPKRDTRIPDIVDEAIFL PSGPNVFFKNYEIKNEADRTLIIYITLYISE CLKKLQK\COFPKAQGEK\EMYTLGIPLN FPI\GEPGFSHFNANLCPNPANKIQEDEA VMRAIYLP\SLRPTLGLKTL*EKFFGPS RMDKPQSGWTWLC*RDSFMNKSLSG PWTIEREFGAAHRLPRGPGAAFFQDVT QSFCLYFSKVFIQRRRACLYLKNS |

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| 1428 | 9479 | A | 2389 | 1 | 395 | AKAKMADVLDLHEAGGEDFAMDEDGD ESIHKLKEKAKKRKGRGFG/SR*VWGKW GRVA**GRSYGFWSPPHRRNNGRKEEF SVISCMSLIEGSRARMREDYDSVEHDG DEPGQRSVEGWILFVTGVHEEA |
| 1429 | 9480 | A | 239 | 3 | 153 | |
| 1430 | 9481 | A | 2390 | 146 | 831 | CLSGTDEISIEGEMADVLDLHEAGGEDF AMDEDGDSEIHKLKEKAKKRKGRGFGS EEGSRARML*DYDSVEQDGDVPGPQRS VEGWILFVTGSP*RKPEEDIHDKFARIM GEIKNISSTFDRRTG/YILKGYYTLNLIET YKEAQAAMEGLNGQDLMGQPISVDWC FVRGPPKIGKRRGGRRRSRSPDRRPSLT GPLLSRCSLQDSIWTMAALGQIGLGWEL CCVYI |
| 1431 | 9482 | A | 2391 | 2 | 442 | FYVILISVRELYLCHHLPFLCAGVYMTNS AMKVFLIWLIVVITVLEFKKLSWPGAV VWF*GLILYTHI*TL/NTHI*VQNVCYIIL QRNK*FHRFCINIKSWLGAEPHACNPSTL GG*HS*VT*AQKFETSLGNIVRPCLYKKY KN |
| 1432 | 9483 | A | 2392 | 2 | 425 | RRANPPSISPSAQDSRVTPGEGPGSP/G* PSRPVS/GPA/PGSGGLRGSSAPATPLGE APSPSA/GPTPALQPCDPGAGP/GTARPG QTASAAPAPLPFRRGAGAPPQAGREGG PCGEEERPPSGREKVSC*KRQTGPGQRR ADK |
| 1433 | 9484 | A | 2393 | 2 | 662 | ACTAADLIAGTTISEAGPHMENQP/GEVA GPAGPPTPSWAPRIPLAPPWRAAAGRDP AT/GQEDSQ*PTPGCPSWPPWPTQLSPSA AGSPIHTPPIQGFHSQLLS*RSPGTEEP*E ANKLPPWTGHREPEPHPLPGHPCAAGS IGHWHLLLLCLATLHGERQRHLHPGQR SGCGVQGRTPPGSAQIQDLPAAPSSILQN LSTQLCSAARPRSMPSRMRM |
| 1434 | 9485 | A | 2394 | 115 | 187 | |
| 1435 | 9486 | A | 2395 | 93 | 584 | KHSASAAQALPGTLGACTGSGGLRGSS APATPLGEAPSPSA/GPTPALQPCDPGAG PVLPGQVKLPQ/PPAPLPFRRGAGAPP PEIPSGSSFGYWEQGAQTPGLLPAQRPL PPFPALGSGCSALEEG*ATGTRGHKGG CS*GLWGEPGRACKHPPHLL |
| 1436 | 9487 | A | 2396 | 46 | 438 | LQKRVGDWLGEAPPWGWVSHRCRAR TARPGQTASAAPAPLPFRRGAGAPPLAR VPAPPCAQRAPPSSSQGRNQ**AASGP WRPFR/PGREVTGCGEEERPASGREKDS C*ERQTGPGQRRRAVKMTQIR |
| 1437 | 9488 | A | 2397 | 455 | 1241 | ARELRAGGFYVPHRGLEMPETALEAG VSGVGLQHLP/HLGEAPSPSAWPDTR CSRVPVQGPVLPQVKLPQ/PPAPLPP RRGAGAPPLDLARVPAPPCAQRAPPS SSQPGRNQ**AASGPWRPFRQAEKESNC GEEERPASGREKDS*ERQNGARSAAGR QAKESPQTSRPPDGEPAGEVAGPAGPPTP SWAPRSPLAPPWRAAAARDPATGRRTV SDPHRPAHHGLPGQHSYLLQLQDHLSIH SPIQGFHSQLLS |
| 1438 | 9489 | A | 2398 | 2 | 328 | PLFSDNGKKRGLALDGKLGKLEDNLASS TIVKEGANKEVLGILVSYRVKVLVSR GGAPETDVPVDTNLIEFDNTYATDDDIV FEDFARLRLKGMKDDDYDDQSTRP |
| 1439 | 9490 | A | 2399 | 2 | 417 | EIRAFCAKSLE*KSHKRNSVRLVIRKVQF APEKPGQPASAEITRHLMSDRSLHLEAS LDK/EVRQYADICLFSTAQYKCPVAQLE QDDQVSPSSTFCKVYITITLLSDNREKRG LALDGKLGKLEDNLAFSTIGKEGGH |

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| 1440 | 9491 | A | 24 | 497 | 752 | DGVLLLLPRLECNSAILAHRNLRP/GFK RFSCLTLLSPWDYRHLPPRLAIFVFLVY VGFHHVGYAGLEVLLTSR*SARPRPKIA |
| 1441 | 9492 | A | 240 | 3 | 423 | GSTHASARMAMVAPRTLLLLSGALAL TQTWAGSHSMRYFYTSGSRPGRGEPRFI AVGYVDDTQFVRFDSDAASQRMERAP WIEQEGPEYWDQETRNVKAQSQTDRVD LGTLRGYYNQSEDGSHTIQIMYGCDVGP DGR |
| 1442 | 9493 | A | 2400 | 188 | 340 | GGALLKDPLGGPNLPGGGKDKFFSFWG AF*NPPGDFWEGTFFLGGGILGP |
| 1443 | 9494 | A | 2401 | 117 | 457 | |
| 1444 | 9495 | A | 2402 | 39 | 447 | |
| 1445 | 9496 | A | 2403 | 3 | 1359 | FPGRFRGGAGILAAGEEAASEPRTERA AGARTMGEKPGTRVFKKSSPNCKLTVY LGKRDFVDHLDKVDVVDGVVLVDPD/Y TMKDRKVFTV/LSPCAFRYAGREDLDV/L GLSFRKDLFIATYQAFPPVPNPPRPPTL QDRLLRKLGGHAHPFFFTIPQNLPCSVTL QPGPEDTGKACGVDFEIRAFCAKSLEEK GHKGTSVRLVIRKVQFAPEKPGQPQSAE TTRHFLMSDRSLHLEASLDKELYHGEF LNVKCSFTNNSTKTVQGRFKVSC*GQ YADIWPLSGTAQYKCPVAQLEQDDQVS PSSTFCVYTITPLSDNREKPCIALADG KLKHEDTNLVSSSTIVKEGANKEVLGILV SYRVKVKLVVSRGGDVSVLPFVLMHP KPHDHISLPRPQSAAPETDVPVDTNLIEI DTNYATDDDIVFEDFARLRKGMKDDDD YDDQLC |
| 1446 | 9497 | C | 2406 | 933 | 1070 | MKRKNILYYGTNKLNTNNLLNNFINI LVSSLGLSERSFYRYIL* |
| 1447 | 9498 | A | 2407 | 138 | 1166 | VVAMAQVLRGTVTDFPGFDERADAETL RKAMKGLGTDEESNLTLLTSRNASQVRQ EISCS/AFKTLFGRDLDDLKSELTGKF EKLIVAMKPSRVL*MLIELKHALKGVA GTNEKVLTEIIASRTPEELRAIKQVYEE EYGSSLAED*RWLGDPGSGYYPAGCWLVA LLQANRDPDAGIDEAQVEQDAQALFQ AGELKVGTDDEKFITIFGTRSWSSF*GK VFDKYMITSRISKRETIIDRETSQGFRSQ LLGCCGILFRRYTSPTLQETFIYAMKEA GTDDHTLIRVMVSRSEIDLVIYIPGREFR KNFCHPPPYSMIKGRYIWGTIKKALLLAL CGEDD |
| 1448 | 9499 | A | 2408 | 1 | 498 | |
| 1449 | 9500 | C | 2409 | 14 | 394 | |
| 1450 | 9501 | B | 241 | 1 | 540 | MPVNXHKRHDITAESLITPNVTSDSVKD CIKELGNRLFLWTQGCSSHVATVAPPTA PRGLRVRS AVRPLPLGGWAAAMEGEP PVEERRRLQEELNEFVESGCRTLEEVAS LGWDLSDLPGEAAAELHQIRCQESWE FASSPFCALKLDTSDWDSTNSRIKGCCHQ EVVTGNSCGH* |
| 1451 | 9502 | A | 2410 | 2 | 353 | |
| 1452 | 9503 | A | 2411 | 1 | 349 | |
| 1453 | 9504 | A | 2412 | 123 | 195 | SWKPSFSAN*HSNRKPNTACSHS |
| 1454 | 9505 | A | 2413 | 240 | 743 | |
| 1455 | 9506 | A | 2414 | 284 | 672 | GGWEGLTDTSYRRAPAGIRPVLQRKEQT VIFAVLQPLLVIPTASGVDLQQT/GRP AEERPVRKTKKQNAATTSKSTKGTPTQK PHSNVIRFKDERDMDEAGNHHSQQTNT GTENQTTTCSHSYVGVEQ |

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| 1456 | 9507 | A | 2415 | 579 | 1383 | VGSCAFYLAVSVFLAPRPFLLHLLQLGAD EARSWDFLRSPEEFNTNMDIRPNHTIHI NNMNDKIKKEELKRSLYALFSQFGHV DIVALKTMKMRGQAFVIFKELGSSSTNA LRQLQGFPFYGKPMRUQYAKTGSDIIS KMRGTFADKEKKKEKKKARTVVDQTAT TTNKKPQGQTPNSAIPQGNSTTQIPQVP DYP SKLNFYSLNKLQRETNEMMLSHA V*ISSTWPSSEVPSGYPRHDAFVFEFEN VDGQAGAAARDALQGF |
| 1457 | 9508 | A | 2416 | 1186 | 1451 | DLLKVLHEKPKLARRSGSHL*PR/HFGR RLWKDCIKPGVQDHSGQYRESPSLQNIKK KIIWAWWCMPIVPTTQAVKVGGSLK RLRLQ |
| 1458 | 9509 | A | 2417 | 1 | 412 | |
| 1459 | 9510 | A | 2418 | 298 | 532 | MGSWSLPGRTLWKEKVRFLKSKERTNP GSNFFSFPQSQHTREERSQECLSLPVLPS YLATRLSLPDSCPLKGRKAH*QRHSEI*L MGFEPGWPGKL*GWIELAFLGCLHLTL PLPCPTPLPPKSTKSGCFSLSIALCFNKQF AVTK |
| 1460 | 9511 | A | 2419 | 5 | 977 | VRGGLAAGRGRGSAGAAPVVVAAMLG AWAVEGTAVALRLRLLLLPPIRGPL GVAGVAGAAGAGLPESVIWAVNAGGEA HVDVHGIHFRKCIPL*GRVGRASDYGMK LPILRSNPEDQSCYQTERSNREETFGYESP IQREGGLTCWSLKFAE\YFAQSQQKVF DVRLNGHVVKDLDIFDRVGHSTAHEI IPMSIRKGLSVQGEVSTLYTGNSNME/F VKGYL*PIPKVCALYIMAGTVDDVPKL QPHPG*ERKKGEEEEEEYDEGSIPKKNR PIKNGGQSGPRHNPT*ASDNSSLMFPIL VAFGVFIPTLFLCLRL |
| 1461 | 9512 | B | 242 | 232 | 387 | MEGEPPPVEERRRLQEELNEFVESGCRT LEEVTASLGWDLDSLDPGEEAAE* |
| 1462 | 9513 | A | 2420 | 1 | 453 | RNSEKEVEKRKVALQEAKLKAKGLNPD GTPALSTLGGFSPASKPSSPREVKAEES PISINAKTVKKEPEDRQQASKSPYNGYN NRRSRSGTYSR SR SR SHSESRRHHN HSSPHLKAKHTRDDLQSSNRHGHKRKK SR SR SQSKSR |
| 1463 | 9514 | A | 2421 | 19 | 434 | QRGNYSFEIVAMACINLASKIEEAPRRIR DVINVFHHLRQLRGKRTSYIYQSLGDVE WYIEMKLSSWQQTPSPLILDQNYINTKN QVIKAERRVLKELGFCVHVHHPHKIIVM YLQVLECERNQTLVQTAWVVHDGIT |
| 1464 | 9515 | A | 2422 | 171 | 437 | TSNFYYSYNRRSRSGTYSR SR SR SR HSESPRRHHNHGSPHLKAKHTRDDLKSS NRHGHIRKKSRSRSQSKSRDHSDAG*KH RLE |

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| 1465 | 9516 | A | 2423 | 21 | 1855 | FPGRFRFLRWACVRLAKTMASGPHSTA TAAAAASSAAPSAGGSSSGTTTTTTTT GGILIGDRLYSEVSLTIDHSLIPEERLSP SMQDGLDLPSETDLRILGCELIQAAGILL RLPQVAMATGQVLFHRFFYSKSFVKHS FEIVAMACINLASKIEEAPRRIRDVINVF HHLRQLRGKRTPSPLILDQNYINTKHQVI KAERRVLKELGFCVHVKHPHKIIVMYLQ VLECERNQTLVQTAWNYMNDSLRTNVF VRFQPETIACACIYLAARALQIPLTRPH WFLFGTTEEEIQEICIETLRLYTRKKPM YELLEKEVEKKRVALQEAKLKAKGLNP DGTPALST/LGVGFSPASKPFIHQENVKA GRRKSPIFHLMWKDSSKKEPGG*D/RQA FPKALYNGVKEKDS/RRSRNSRSASRS RSRTRSRSRSHTPRRHYNNRNRSRSGTYS SSPRSRSPSHSESPRRHHNHGSPHLKAK HTRDDLKSSNRHGHKRKKSRSRQSKSR DHSDAAKKHRHERGHHRDRRERSRSF EEVP*KARHHGWVPSGTWARAQGADL SSSLWSPAIOFLGFGPIYQCDGMGLNPKT IKRKTGLGDFLETPPRSS |
| 1466 | 9517 | A | 2424 | 1 | 1566 | |
| 1467 | 9518 | A | 2425 | 328 | 889 | GLRTPAAVLYCGTVRTAGVAAASRYQG DNIYVKNLDDSIDDERLQKEFSPFGTI*S AKGMMEGGHSHK\GFGR/ICFSSPEEASK AGTELNGRTVATKPSYVALAQKEECQ AHLNQHMQRMASVRAPNHVMNPYK PAPPSGYLMTGIPETQNRPPRGAVGHPC NPSTLGGQEGKNTGSGDRDHPG |
| 1468 | 9519 | A | 2426 | 1 | 2262 | |
| 1469 | 9520 | A | 2427 | 365 | 2419 | FSIPVDFCPSALAPRSPPPGSGPQPRHLS SSHGKVAACGPAGSRAEMNPSAPSYPM ASLYVGDLPDVTEAMLYEKFSPAGPIL SIRVCRDMITRSLGYAYVNFQQPADAE RALDTMNFVDVKGKPVRIJWSQRDPSLR KSGVGNIFIKNLKSIDNKALYDTFSAFG NILSCKVVCDENGSKGYGVHVFETQAAA ERAIEKMNGMLLNDRKVFVGRFKSRKE REAELEGARAKEFTNVYIKNFGEDMDDE RLKDLFGKFGPALSVMVTDESGKSKGF GFVSFERHEDAQKAVDEMNGKELNGKQ IYVGRAQKKVERQTELKRKFEQMKQDRI TRYQGVNLYVKNLDDGIDDERLKEFSP FGTITSAKVMEGGRSGKGFVCFSSPE EATKAVTEMNGRIVATKPLYVALAQRK EERQAHLTNQYMQRMASVRAPNPVIN PYQPAPPSGYFMAAIPQD*DRIAAYPPS QIAQLRPSRWTAQAGARTHPFQNMPGA IRPAAPRPPFSTMRPASSQVPRVMSTQR VANTSTQTMGPRPAAAAAATPAVRTV PQYKYAAGVRNPQQHLNAQPQVTMQQ PAVHVQGGQEPLTASMLASAPPQEQQM LGERLFPLIQAMHPTLAGKITGMLEIDN SELLHMLESPESLRKVDAAVAVLQAHQ AKEAAQKAVNSATGVPTV |
| 1470 | 9521 | A | 2428 | 2 | 237 | |
| 1471 | 9522 | A | 2429 | 68 | 866 | GSTGAVTAATATAATAAGASAPLGLPV YLPAPRSTAPAPSPAASALLFLVTPPSRP ERLPSHQPPSATMATAPYNYSYIFKYIII GDMGVGKSCALLHQFTEKKFMG*FVPH TIGCWNLGTRINESLVGQKIKLQIWGLR QGQERLRAVYT/RAYYRGAAGALMVY DITRRSTYNHLSSWLTRCQGISPNPKYW **FSIGN*SQIWRPQRDVTYEEAKQFAEE NGLLFLEASAKTGRRIVEDAFPLRACPR KIYQNIQDGKLG |

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| 1472 | 9523 | A | 243 | 1124 | 1394 | ACDDWNRMDKSHLHPPPPFFRDPDYV GPSGTRSPPTSGSRSPNRNSAPPAPAA PPQVQARPP*HSPPDKRKRPNCRTRGSP PWFRS |
| 1473 | 9524 | A | 2430 | 229 | 593 | SLICFVGVGDCAEFWVTRLAPRAEKRR LAPAVPPHHQDERGGTSTPHFHNLSHGF WVTFPALLPQYDILPLNSFLHEIQEPSLGI SGLGPFSCNTYLISFSSTCHLAPVINLWA LPGASIM |
| 1474 | 9525 | A | 2431 | 594 | 829 | PCALVLPLRPYATK*GMLPWLLGLHLS RAFAVALDHILF*VL/CHV*IPSILTKIFEN GYFVISVLLMRNILSSALL |
| 1475 | 9526 | A | 2432 | 1479 | 1734 | LKVNISLGMVGHACNPSTLGSQE*ATVP LILYFLNKLAFTSHCGITLNSFLHKIQEPS LG SRLGPLSCNYHATALQPGQQSKALS |
| 1476 | 9527 | A | 2433 | 30 | 508 | |
| 1477 | 9528 | A | 2434 | 338 | 853 | EGRGFGRAGLPPLCIAALFQKMNYPG TAVTLIEDNDKKHLVLLRDGRTHIGFLRS IDQFANLVLHQTVERIHVGQK/YTGDIPR GIFVVRIGENVVLLGAEIDLEKESDTPALQ QVSH*RKFLIEQKGNQQTKLAEAKL KVQALKDRGLSIPRADTFDKDLFFCPEA VGS |
| 1478 | 9529 | A | 2435 | 357 | 893 | TVFQIWANHGPQRPARQLCPVHLLGGQS HQEPRHITSNSEPSRASASLRRLTPLKPTG IGPGSQILED RDFRAFT*WGDYFWGKGA PACLIQDGVKGQWAGPHSGVGGVWGP APRACPPVFSPPQSSACGCQYYLSRP KAYPQGWGRGGDPGQNVRSVCDLRC CMWTLNCTCSF |
| 1479 | 9530 | A | 2436 | 233 | 566 | RLFLVRKRMISFSAPPLMLPFSFYFFVC PAARTARKRKPSPEPEGEVGPCKINGEA QPWLSTSTGLKIPMTPTSSFSVSPPTA* PHSNRTTPPEAAQNGQSPMAALIL |
| 1480 | 9531 | A | 2437 | 219 | 702 | ARKVRARAAGLESRTGSTGPRPCATRC WRCTSTATRGPSRASFKKEPALTA VART ARKRKPSPEPEGEVRAPLRSTEKAPGC PHSTGLKIPMTPTSSFSVSPPTASPHSN PGPHRLES GPRMGQFFIGSPDLSSRQFRG QSCSKDANQVHSTTRRNSN |
| 1481 | 9532 | A | 2438 | 173 | 1136 | ALEGAGKSRGFWRAGLGQQAQDRARH AAGRCTSTATSGPFESKFKEPALTAGR LFGVFEGQRGQPLKAVCKNSKGKGP LPEPRKVKSGPLKIQRGSPSRRL/SPHPQR GSRSP*LLHPLLCLRHPLPHLIPTGPHRL KRPRMASPPWQP*S**QTMQGASHASKD ANPGSLPTTRKE*PTVGPSSVLL*TKERL GPKRGGGPREQATQEDWEPVHPASLPDF LFGQPVAPLCCTLCHERLEDTHFVQ/CPS VPSHKFCFPICSSQGIKQGSISGEVYCP SGDKCPCGLPMSPWAFMQGEIATILA GDVKVKKERDS |
| 1482 | 9533 | A | 2439 | 1 | 206 | PTRPRTSYEKQGYLLPVPFSIVLEVLR AISQETEIKSVQMGKEEVKLSLAFVCVYI YA*ENPVESTK |
| 1483 | 9534 | A | 244 | 171 | 512 | CTVGVRCVFPTEHKLP AVESHIVSRSE SVINKI*ANQIWEH/TKKIIHHEEVGFI LGM QGWL NIRKAPTEIYHNR/SKDKNHMIILT /D*EKAFDKI*HYFILKTLDKLGI*GNF |

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| 1484 | 9535 | A | 2440 | 611 | 1203 | ERLLRVCLALGSAGTADDVKLHPVSCA DTARSTPGTSAPSTSGTSAPFTPGTSAPST PGTSAPSTPGTSAPSTPGTSAPSKPGTSAP STPGTSAPSKPGTSASSTPGTSAPSKPGTS APSTPGTSAPSKPGTSAPSTPGTSAPSKPG TSAPSTPGTSAPSTPGVQHPPHRRGPQHPP SRGPQHPPHRRGPQHPPSRGPQHPPHLLGP QHPPSRGPQHPPHQQGPQHPPSRGPQHPP/ PPGTSAPSKPGTSAPSTPGTSAPSKPGTSA PSTPGTSAPSKPGTSASSTPGTSAPSKPGT SAPSTPGTSAPSKPGTSAPSTPGTSAPSKP GTSAPSTPGTSAPSKPGTSAPSKPGTSAPS KPGTSAPSKPGTSAPADPGVL |
| 1485 | 9536 | A | 2441 | 447 | 920 | GWHWFLASQKSLLKPPLSRNPCVLVSCH MAQSWARTQEFLCPMCPTT/CAQSGTGT ESCFPNPN*VLGAGAPQPDQRCHKAGPF SSVPGFRLPSSRHGGPVLPGLGPPGPPG RPPHKPSNEQRDAGQQLQLPPACPQKG LPQLPFCLKFYSLPELPH |
| 1486 | 9537 | A | 2442 | 1 | 374 | LRKDDTQIREAFHIFVQSWRPALPSLPSL PLARALAETLNQPPFGSLITPSGILLNSQ MLDFSWPNRTANHSAPS/TVVRPAEGLC GTYLALGANGAARGLSGLTQVLLNVLN *NRNLSDSLARGR |
| 1487 | 9538 | A | 2443 | 1 | 315 | |
| 1488 | 9539 | A | 2444 | 3 | 2027 | NSRVDDFVARARMAAENEASQESALGA YSPVDYMSITSPRLPEDEPAPAAPLRGR KDEDAFLGDPDTDPDSFLKSARLQRLPS SSSEMGSDGSPLETRKDPFSAAAEC SCRQDGLTVIVTACLTATGVTVALVMQ IYFGDPQIFQQGA VVTDAARCTSLGIEVL SKQGSVDAAVAAALCLGIVAPHSSGLG GGGVMLVHDIRRNESHLDIFRESAPGAL REETLQRSWETKPGLLVGVPGMVKGHL EAHQLYGRLPWSQVLAFAAAVAQDGFN VTHDLARALAEQLPPNMSERFRETFLPF GRPPLPGSLLHRPDLAEVLDVLGTSGPA AFYAGGNLTLEMVAEAQHAGGVITEED FSNYLSALVEKPVCGVYRGHLVLSPPPH TGPALISALNILEGFNLTSLSREQALHW VAETLKIALALASRLGDPVYDSTITESMD DMLSKVEAAYLRGHINDSQAAPAPLRP VYELDGAPAAAQVLFMGPDFFIVPMVS SLNQPFSGSLITPSGILLNSQMLDFSWPN RTANLSAPSLENSVOQGRPLSFLPTVV RPAEGLCGTYLALGANGAARGLSGLTQ VRFTPWLAFSREPSCLDCRCLS*QSNL LQVDSECAETSWGGHRDR*RKDSQSG CPVWHGSRRTNNFIIVKDPSPDAAGA TIL |
| 1489 | 9540 | A | 2445 | 83 | 310 | IFQCTKFTWDSQITPRLFHPAPPTWCRPL PVSG*RRVRGWATTRQSGGGGRGPAPLS SQAPPKGPVPFQWHLRAEG |
| 1490 | 9541 | A | 2446 | 1 | 1833 | |
| 1491 | 9542 | A | 2447 | 3355 | 3951 | |
| 1492 | 9543 | A | 2448 | 699 | 975 | |
| 1493 | 9544 | A | 2449 | 3 | 132 | GRFSSESPRA\GPPAPHRGHVQRCCVS PTGLLIWKELEPFCC |
| 1494 | 9545 | A | 245 | 1 | 293 | FLRWSLALSPSLECSGAISAHNRL/RLPGS TNLPA\TSRVASTVGMATAPGLNFCIFS REG*VKHVGPGCLELP\TSSDPLPLVSPK LRDYRPEPLCLA |

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| 1495 | 9546 | A | 2450 | 2 | 1734 | TDLKRCTYYETCATYGLNVERVFQDVG IDSAVPCSAQKVVALRKKQQLAIGPASH CPNSPKHWAWSAASIPAVHNTQATNGG GKAFFSDYSSVPSTPSISQRELNIETIAAS STPTPIRKQSKRRSNIFTSRKGADLDREK KAAECKVDSIGSGRAIPKQGILLKRSRK SLNKEWKKKYVTLCDNGLLTYHPSLHD YMQNIHGKEIDLRTTVKVPKRLPRAT PATAPGTSRANGLSVERSNTQLGGGNR GRGVV*ICGWVSLTGADVGTGEGFNGR RERELGFSVQAQILASLQGCQCQGG DFDLGNQNAALAVQAVRTVRGNSFCID CDAPNPDWASNLGALMCIECSGIHRHL GAHLSRVSLDLDWPELLAVMTAMG NALANSVWEGALGGYSKPGPDACREEK ERWIRAKYEQKFLAPLPSDDVPLRQQL LRVVEDDLRLVMLLAHGSKEEVNET YGDGDGRTALHLSSAMANVFTQLLI/W GESRASSLP*PRSS*PCSLKATSSFLPYNQ SLSSHVLPVTNMCFLQYGVDRSRDAR GLTPLAYARRAGSQECA |
| 1496 | 9547 | A | 2451 | 329 | 3294 | ESEILWGEQLAGGPPQFALSNSAAIRA EIQRFSVHPNIYAIYDLIERIEDLALQNOI REHVISIEDSFVNSQIEWTLRSVPKIV GIVGNLSSVGSALVHRYLTGGPIVQGG SPLKGGGLRSEIAADGHSYLLIRDEGGP VGLQYAAWVDAMVF/VWSPCEDGITFS KTVYNYFLRLCSFRNASEVPMVLVGTQ DAISAAANPRVIDDSRARKLSTDLKRCTY YETCATYGLQCGSVSFQDV |
| 1497 | 9548 | A | 2452 | 493 | 955 | TLCTYLISEVISLPGTAFIQRKGLGLRPS QNNAYLSQTSPLIIFLRVQGFDLNLA LVLFSSGGTESRSIAQLECSGMTSAHCN LRFLGSSYSPASAS*VAGTTGACHHAQLI FLVFLVEKGFHRVSRDGLHLLNLVIRPP QPPKALGLQA |
| 1498 | 9549 | A | 2453 | 158 | 720 | PPPCRAKQHQTCTKKRPQKATSNVFM FDQSQIQEFKEAFNMIDPDQDGFVIRE DLHDMLASLGKNPT*WSILDAMMMRA PGPPSNFTPWFPHHGFGE/RLNGHQIPE DVHRKMPFACFE*KKPLGTIRIEDYLARE LLTHGGIGFTDEEVDELYREAPY*PKRG NFNYSEFTRILKHGAIKDKDD |
| 1499 | 9550 | A | 2454 | 2332 | 3329 | VAGATGTHHAWLILSFLRWSLTSPRL ECSGTSAHCNFRLLGSSNSPASAS*VAR ITGAHHHTRLIFVFLVETRFHHGGQVGL KLLTSGDPPASASQSTGITGVSHHAWPY FKLFCRDGVLLCCPG*SQLGLKQSSCQ SFPK*LDYRCEPPRPTNL*RLARDVPYL TTSPVRSRGGTRM/EKEVPEQRLAGSRM GQELTQPPSTETSWSLGRRRTKSPLF*IFF MFLRRSLNSVTQAGVQ*HNLGSLQPPPH GFKRLSCLSLSSWDHRCPTPPCLDNF*IF GRDG/GFTMLARQVNS*PQ/GPPTLASQ SSGNTGLSHCNQPVAPIFAPR |
| 1500 | 9551 | A | 2455 | 566 | 1037 | GSTLSPSLPGFCPENSCKFNLLTAES LKLPODLSFDPSQKPTQVRHL/ESPPGEG PPSRAPQKNSHEIRWCLMKCIFL*LGR MKAQTPTLFSPGLGMSPAARPRSPGG LGEVGAGTISVPSTLTPSTSETTLQPRY GMKLADADVGGKKKK |
| 1501 | 9552 | A | 2456 | 349 | 679 | ELGHWGNRVCLSEALGLAELHPCPGNE VGPQRQG*GLAVLILAILLQGTLAQSIK GNHLVKVYDWQEDGSVLLTCDAEAQN/ ISTWFKDGKMIGFLTEDKKK WESGEVM PRDPRGMYQC*RDHRNKSSTTSQVLFT GMCSGTCL*DLNAATISGFPLWLKTVSL FVLAFGVYFIA/GQGWSSASPRASDKQT LLPNDPAPTQPLKDPKMTQYSHLQGN |

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| | | | | | | QLRRN |
| 1502 | 9553 | A | 2457 | 356 | 505 | WTGGKKKAGWMPKKE/SVKLAQ*CMP VIPATQEAETGKLEPRSSRS AWET |
| 1503 | 9554 | A | 2458 | 35 | 359 | |
| 1504 | 9555 | B | 2459 | 102 | 431 | MIYRDLISHDEMFSDIYKIREIADGLCLE VEGKMVSRTEGNIDDSLIGNASAEGPE GEGTESTVITGVDIVMNHHLQETSFTKE AYKKYIKDYMKSIGKLEEQRPDR* |
| 1505 | 9556 | A | 246 | 466 | 743 | LNHAVQEMIVKIELTQHMYINFHGIKLEI NKGKKFGKLIHLWKLNNVTLSAQ*VKA EIQKGNKEIVLRWNKKEGMMYQNT/W/ DVAKPVLRAAW |
| 1506 | 9557 | A | 2460 | 1 | 581 | |
| 1507 | 9558 | A | 2461 | 88 | 779 | STWAVRSGRWGVGWGGGGGSHDEMFS SDIYKIRGDRGRGLCLEGGRRVWSRT EIGNIDDSLIGGKCPPLKGPEGRRVPERH QLITGVADIVMNHHLPGNKFSQKEASKK VHQRITMKSIGKGL*RTDPEKSKTFL* QGAAEQIAHPLPNFQKLTSTFNGENMN PRWAWVLLLDYREDGWCPP*YDFLLRD GLEMEKMLTNVGNVFGSITLSSITGLLPC HPTQPPGT |
| 1508 | 9559 | A | 2462 | 12 | 159 | WSHLLRMLQL*WS/HPPKNAAAYSSCRV **ERRGLIRTYGLDMCSQSFQYAKDIGF IKLD |
| 1509 | 9560 | A | 2463 | 46 | 371 | FVILGKRCRGALGCLKSQVEEATGGTRE HADWESLVPLQACTVAWESRDAGSSR LSAESCNFYDLQNRCLFSYSRVCSNRHG LVRKYGLNMCRCQCFR\QYAKYIGFI |
| 1510 | 9561 | A | 2464 | 1 | 591 | GLLQAECPWRSSGEAAFREITMEIWLLA WAISPVALSESTDPETWQSRCEDRHFLF KFLVIGSAGTGKSCLLHQFIENKFKQDSN HTIGVEFGSRVNVVGGKTVKLQIWDTA GQERFRSVTRSYRGAAG/ALLVYDITSR ETYNSLAAWLTARTLASPNIVILCGN KKDLDPEREVTFLASRFAQENELMFLE T |
| 1511 | 9562 | A | 2465 | 3 | 495 | GRDRVMAETYDFLKFVIGSAGTGKSC LLHQFIENKFKQDSNHTIGVEFGSRVAN LGGEPPVKLQIWDTAGQQTGFAGKTYT SLAAWLTARTLASPNIVILCGNKKDL DPEREVTFLASRFAQENELMFLETSALT GENVEEAFLKCARTILNKIDSG |
| 1512 | 9563 | A | 2466 | 1 | 2022 | |
| 1513 | 9564 | A | 2467 | 3 | 715 | REQARPRRHIAALSGRDRVMAETYDFLF KFLVIGSAGTGKSCLLHQFIENKFKQDSN HTIGVEFGSRVNVVGGKTVKLQIWDTA GQERFRSVTRSYRGAAGVALLVYDITSR ETYNSLAAWLTALTPVQPKTGAFCLC GNKK*PGPLEREVTFL/APSRFAQENEL LMFLET\SALTGENVKAFLKCARTILNK IDSGELDRERMGSIGYGIASLRKLRQP RSAQAVAPQPCGC |

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| 1514 | 9565 | A | 2468 | 3 | 953 | VKMALVASVRVPARVLLRAGARLPGAA FGRTERAAGGGDGAIRPFGSQRVLVEPD AGAGVAVMKFKNPPVNSLSLEFLTELVI SLEKLENDKSFRDVTSDRPGVFSAGL DLTEMCGRSPAHYAWVLERPVQELWL RLYQSNLVLSAINGAICPAGGCLVALT CDYRILADNPRYCKGIQIRPKVGIICPFW G*KETLGKNLLGPGGGESALQVGLLFP PAGRPKVGIVDQVWSPEKQVQSIGLS AIAQWMAIPKPMMAHKLTAKIMRKGQGP PAWSRKGADVQNFVVSFISKDSIQKSLQ MYLERLKEEG |
| 1515 | 9566 | C | 2469 | 1 | 774 | MKEVVYWSPPKVVADWLLNAMPEYCE PLEHFTGQDLINLTQEDFKKPLCRVSSD NGQRLDMIETLKMEHHLEAHKNHAN GHLNIGVDIPTDGSFSIKIKPNGMNGY RKEMIKIPPELERSQYPMWGWKTFLAF LYALSCFVLTVMISVVHERVPPKEVQP PLPDTFFDHFNRVQWAFSICEINGMILVG LWLIQWLLKYKSIISRRFFCIHTLYLYR GITMYETTLTAPGMLCNCSPKLCGDCEA QLR* |
| 1516 | 9567 | A | 247 | 243 | 935 | IPVGELYPLEDGIAAFIEWNPHEALWE PQEQQETQGPKSKHGEAPVGASWPFR GFGEARPPPPVRPTLIHAWKSS*PICLFS RHCHQALPGGTLDKWPSSPRG/GCSPRT PGVTQQAARLSPHRVAG*QSSSGACPW MSRSSAPFPFLTSPSPRAAL*VRKTKSP GTGEHRLWTGLGAGGV SARPVVKSAG PGGIHGGRAPGAEQRSGLWKAGCWGSV RASAPGP |
| 1517 | 9568 | A | 2470 | 263 | 621 | EVRLLSRPWPHEHEHGPWPLTIKWDFP DYRQWKIEGTPFRKTIQKKLGCKKGLR DWPWGRNEAWRYMGGFAKVSFS*CIL FKGFKWGDLLAFVAVRELEYLPGES* IKDKKHH |
| 1518 | 9569 | A | 2471 | 1 | 225 | |
| 1519 | 9570 | A | 2472 | 99 | 493 | TASPAPPQAFRRSSSLKIRESIIRRGSEKL VSRLRGEAA/RRTSRVSDQVGKEP*HQ QNRQPTPPPPFCSTFHGSHLPDTHRS NPVLESLVEGGHSWIHSFPCCPLCRM KRDMSLNTLNVDA PRAPG |
| 1520 | 9571 | A | 2473 | 70 | 299 | AVGSVHAGVQWVSGGVGPPGSGAGPP GRKPRL*RGPSDPARRNAPAIERLSRRR GRCSARGLRGRDQEEGQPGRT |
| 1521 | 9572 | C | 2474 | 129 | 602 | MFERIVXADEHVIDQDGDGNFYVIERG TYDILVTKDNQTRSVGQYDNRGSFGELA LMYNTPRAAIVATSEGLWGLDRVTFR RIIVKNNAKRKMFEFIESVPLLKALKD GQRFNPHLHFAFEGPFIRPLVKITPTQFLY LWFKTACLSNNLSA* |
| 1522 | 9573 | A | 2475 | 38 | 1523 | RRVARPGNAEPAKERRDVSRGRARRDL AGAERKAGVSEGRDGRRRPNPSIPSAA AGMSHIQIPGLTELLQGYTVEVLRQPP DLVEFAVEYFTRLREARAPASVLPAAATP RQSLGHPPPEPGPDRVADAKGDSESEED EDLEVPVPSRFNRRVSVCAETYNPDEEE EDTDPRVIHPKTDEQRCRLQEACKDILLF KNLDQEQLSQVLDAMFERIVKADEHVI* PKGDVGRQPFYCHRTGGTYDILVTLDN QTRSVGQYDNRGSFWRLALMYNTPRVA ATIVATSEGLWGLDRVTFRRIIVKNN KKRKMFEFIESVPLLKSLEVSRMKIVD VIGEKIIRADGER*ITQGEKADSFYIESGE VSILIRSRTKSNKDGGNQVEIARCHKGQ YFGELALVTNKPRAASAYAVGDVKCLV MDVQAFERLLGPCMDIMKRNISHYEEQL VKMFSSVDLGNLRAVGVPHTSLLSVT PKPSGQPONTYRKQT |

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| 1523 | 9574 | A | 2476 | 1 | 912 | EEFAAVSERIHEQVRDRQLENEYVCRVE GEFPTTEVTCKEPILVVSYKVGVCVRVDP RGKPCETVFQRLSYNGQSSVVRCLRPLTG RTHQIRVHLQFLGHPILNDPIYNSVAWG\ |
| 1524 | 9575 | A | 2477 | 3 | 806 | PSRGRGGYIPKTNEELLFVPG*AEHQAK QSLDVLDLCEGDLSPGT/LTDSTAPSEL GKDDLVEELATAAQKMGGK*AEAAPQE LDTIALASIEKAVETDVMMNQETDPTLCK MPAGATGSLAPRPCDVPTCPNAIKGQAL STFHMPAWAQDDWQKD |
| 1525 | 9576 | A | 2478 | 184 | 793 | DFLLLVLTGLYIYRKSIIHKVLE*IEFINV TSYKVNIQKDIALRTSQKH*KTN*KYKA KYLEIN*TNQDFYNENYKTLRKVKDN LGKWTIIPYSSTGKLDIVKMSIILRLFYKT NAITGIVPK/HSFVKINPEIPKLI/YGNMGN REGKTILKNKKVGRSLPDPFKYYKAT*I KIVWY*CKKRQMNQEAETSARKRPWS L |
| 1526 | 9577 | A | 2479 | 69 | 403 | SALRRGAGAKAGRPLAPATALGGQTQP EKGPAPP*NGWTGLGAGPPAWRARPRPS PPEFSQFSLSYNMS*AKVGG*EHGSTAPG EGG/P*RKGGGPPPPNPQRQGGSPGTSP |
| 1527 | 9578 | A | 248 | 56 | 247 | QEONPQISILTLNRNG/LNATLKRYRLN QIK/SFCKKDQTMCCLETYLTCKDTHR PKVKG*KNI |
| 1528 | 9579 | A | 2480 | 502 | 834 | RRLPTGILAGRVSAAVKPTHRTQNSLLQ QRITPRPWRGGSHL*SQHFGKPRQADHL SPGV/PRVSPG*RGETPSLQRIQTLAQVLC CAPVVPATREVEVGGSPEPGRSRLQ |
| 1529 | 9580 | A | 2482 | 1 | 220 | VNMRDRFGQIMIENLRRRQCELAGVETC KSLESRIESLEFLDEM*/LLEQLM/RHYCL CWATKGGNELGLKEITY |
| 1530 | 9581 | A | 2483 | 98 | 394 | |
| 1531 | 9582 | A | 2484 | 1 | 381 | |
| 1532 | 9583 | A | 2485 | 1 | 645 | |
| 1533 | 9584 | A | 2486 | 10 | 1228 | AAPAEPRALPSSVAFSLWLAPSPAARR PRFHVPGGAQLPGTVHARWPARQRIESSI VSCCSTSSCDADDEGVRGTCEASLCKR FAVSIGYWHDPYIQDLAVRLSKQRKAP EINRGYFARVHGCSVOLIAFLRKTEC HCSNCSNLGGQGMGSPFWRLKDEDLS SQVNIFEVDFFMIVTRKLHSIKWLAFLS SPIELHSEDTLQMASDCICDGHILDSKR YAVIGADLRDLSEEEKLKKCNMNTQL\ |
| 1534 | 9585 | A | 2487 | 3 | 247 | PTP*IAECVLVYMTPEQSANLLKWAAN SFERAMFIYYQQVNMGDLFQIMIENLR GRPV/CDLAGVETCKSLESQKERLLSNG WENKHPVRT*LEFVPPGLPSKLK*SRIE SLEINLDENWELLEQLMRHYCLACWATQ RRK*SLGLKEITY |
| 1535 | 9586 | A | 2488 | 1 | 922 | MQLKPMIENPEVSARCTATRRARGRGR GSRVADRFGFAFFFAFQMLNKVLSR LGVAGQWRFDVLGLEEESLGSVPAPA CALLLLFPLTAQHENFRKKQIEELKGQE VSPKVYFMKQTIGNSLGPLPNSTQGPNI KDQLGFEDGSVLKQFLSETKKNVPLKD RAKCFEKNIAQAAP*MPVGTGKAQCR VDDR/VNFHFYSG*PTVDGPPSMNLDGP NAFSPWTHGPQLQEDTLKWDASKVCRR NSPEREQRRSPASSARGFSCKGSLNALW GGICWIFSPFPKHGKYITPCQSKMLQY L |
| 1536 | 9587 | A | 2489 | 18 | 255 | NWISFLPWHYSHFEVYERYDSVL*IPFSL LQ*PIENVYPKI*KKKSTSSNKIALVLSGT YKNSLEPRSGASSVLWFTPNL |

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| 1537 | 9588 | A | 249 | 1 | 372 | RALAVSMLGAWPGPWALDWGPYSMTA RHGTFSL*APYPDPCPAGPPAPRQGGK APSGCGGRSICSGRLPSVVWPLMPAWQR PS*/GGGLHSAPNARKAQAYPGCLPFYLP LPGLLSGWSAGFLC |
| 1538 | 9589 | A | 2490 | 2 | 568 | ERGRKMAVESRVTQEEIKKEPEKPIDRE KTCPLVLRVFTTNNGRIHHEMDEFSRGW VPSTELQIFPL/WMDATLKELTSLVKRV YPEARKKGTHFNFAIVFTDVKRPGRYR*F SFLQS*GGLASTMSGRKGTDDSHPELQ SQKFQIGDYLDIANYPLPNRGTHPPSG RMRPILNFYLLFVEFIFPSVM |
| 1539 | 9590 | A | 2491 | 3 | 506 | FFFFLKTSTLSFITTHCLQIQREGPGAEG AAVAGGAPRGAEGPAATSTETGGSAGD/ AAPSP/RGLPSK*QEGPGFWGDPNARQ WPGGRGRREAWRGLRAGSGESHQVGP WPAASRSTGGSGQVGGAGERLGEDSGL GQVKATRWWGLSPPPAALEEA VANTGPSP PC |
| 1540 | 9591 | A | 2492 | 3 | 639 | APEFPGRHLLLTQLCSLASLIQTRMVHLT PEEKSAVTALWGKVNVDDEVGGKALGR LLVVLPWDPKRSFEVLWGNLSQLECC *WGKPLKVKGSMAKEKVLGCPLSDGLA HLGQPSKGTFAHTEVSLHCDK\LRGSL KNFRLG\NVGLCLAHFAGKRISTPP VQAA*SRKLVGLVLAKCPWPHKYHLKL AFLAVQFLFKGFLWSLKTNY |
| 1541 | 9592 | C | 2493 | 217 | 396 | MSEETAKEVMRAYLQQLRQETGLRLCE KVFDQNDKPSKWWTCFVKRQFMNKS SXPGQ* |
| 1542 | 9593 | A | 2494 | 79 | 778 | NPAAKMPAYHSSLMDDTKLIGNM/A HLLPIRSQFKGPAPKRDTRIPDIVDEAIFL PSGPNVFFKNYEIKNEADRTL\YITLYIS VECL\KKLQK\QFPKAQGGGKEMFYAGE STNFSHFLGEPGFFPL*PPFYAQTWPTTQ EDEVMRALFTTQLRQETGLRLCGESFS DPIQNG*TPAKWWTCFVKRQFMNKS SGPGTVEGSPGQPTVFPEALGQHFSKM LHNLFAFIS |
| 1543 | 9594 | A | 2495 | 1 | 471 | |
| 1544 | 9595 | A | 2496 | 1 | 1524 | |
| 1545 | 9596 | A | 2497 | 2 | 719 | RPQRAGPVRRAGVMALLDLAEGMAVF GFVLFLVLWLMHFMAIYTRLHLNKKAT DKQPYSKLPGVSLKPLKGVDPNLINNL ETFFELDYPKPLFFSVAPMKRIEKTQM** P*YSTY*YEVLLCVQDHDPAIDVCKKL LGKYPNVDAARLFIGGKKVGINPKINLM PGYEVAKYDLIWICDSGIRGTMEMPSL EQSYDPNVDPYRNNGDADGQHLVLH DFYQQGSGPKCSLINA |
| 1546 | 9597 | A | 2498 | 200 | 370 | |
| 1547 | 9598 | A | 2499 | 295 | 1546 | CVLLDLAEGNVVPVGFVLFLVLWLM HFMAIYTRLHLNKRATDRQPYSKLPGV SLLKPLKGVDPNLINNL\ETFFELDYP/K KFNLHTMLFD*YEVLLCVQDHDPAIDV CKKLLGKIYPNVDAARLFIGGKKVGINP KINNLMPGYEVAKYDPIWICDSGIRIFP DTLTD MVNQMTKVG\LVHGLPYVADR QGFAATLEQVYFGTSHPRYYISANVTGF KCVTGMSCLMRKIDVLDQAGDFIAFAIQ YIAKDYFMAKAIADRGWRFAMSTQVA MQNSGSYSISQFSRWMIRWTKLRINMLP ATIICEPISRMPLLPSLINWDGQAHNVFR WDIMVFFYG/CHCLAWFIFYIPTPGVS QGGTLCFSKGLMQSPWFIRESMITYIFL SALWDPTISWRTGRYRLRCGGTAEIILD V |

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| 1548 | 9599 | B | 25 | 922 | 2057 | XTQTDSPWFMISEKQRNFNAESTIGSHIH GPRIVAGLHAPTLMEEDDALQETVRAS IRKEQRNSRHDGGDGIRKAHAAIPRESRS MKRSPRKEVKKRWNRPKMSLAQKKD RVAQKKASFLRAQERAAES* |
| 1549 | 9600 | A | 250 | 13 | 475 | NGSSLRSPRLR*SRTIPQSS*VAGITGAHH HARLIFFFFFETESCRVSQAGVQWRDL GSLQALLPGFTPFSCLTQSSWDYRHPPP RPANFLYF**RRGFTVLARMVLIS*FRDP PASASQSAGIIGVSHRARPRGRLLAPSYI CRNRGLEG |
| 1550 | 9601 | A | 2500 | 3 | 331 | GAILAHCNLRPL/GFKQFCSLSLPRHS*TS Q*PLTSRLPMVRHG*VKKSEGILCSLPPC TT*VPTSSAPMPWPSRQWERSRTMTVIS SSQLMALGPSCPQRDGSPTSSP |
| 1551 | 9602 | A | 2501 | 15 | 310 | DRVSL/LSRLECSGAILAHCNLRPL/GFK QFCSLSLPSWDYRRAPPHLANFLYF** RRFFRH/GCPGWSLLSSGN/PATLAF*KC* NYGHEPPHPARKIHI |
| 1552 | 9603 | A | 2502 | 3 | 467 | PAPQSLLSARHVSALPTPAS/R/CSGLPP MTPKTMPPRA/VGSPLCVPARRRSSEPRK NSAM/RALLVDIKLEPLAVTPDAA/SQPLI DLPLIDFCDTPEAHVAVGSESRPLIDLMT NTPDMNKNVAKPSPVVGQLIDLSSPLIQL SPEADKENVDSPLLK |
| 1553 | 9604 | A | 2503 | 2 | 273 | FASIPANSSRPLSNISKSGRMGHAMLRPA LPAGPVGASSWQAKRSESSQLNKTIRSIR RRHSCLNSKTKVMPTPTNQFKIPKFSIGD SPKA |
| 1554 | 9605 | A | 2504 | 1 | 472 | VGRVTVHSTPVRSSGPGPQSLLSARRV SALPTPASRRCSGLPPMTPKTMPPRAVGS PLCVPARRRSSEPRKNSAMRTEPTRESN RKTDSTLVDVSPDRGSPPSRVQALNFSF EESDSTFSKSTPLIDFCDTPEAHVAVGSE SKPLIDLMTNTPDMN |
| 1555 | 9606 | A | 2505 | 759 | 1664 | TAGCGLGCASGPQAGHPATAGPQTLLPS AGGRAWSSCPRPALHRWPAGWEGCG YRRWS/RAASYSPWKNKVLLIKPFSIRYK AQSNSYDKPTYQSPSRRLSAA*IPTHP* SLLSSRGCCERRCAPTMRQPGAADTEPMC YHWPVHSLFLPSSCLWGAGVEDKEL VPLWRVFLPGRRSWFPSSQKSRLSHSC LGCCQVSRRGKFEQQNLSSVPDSPGKNK HHGKISGPTCLSGGPGESVPIVHRLSESS HWQMSLLQTRAAAPALSAAGFLKSPPLS SQPGPALCPASRSFQCQSAQGG |
| 1556 | 9607 | A | 2506 | 1 | 377 | ASRRCSGLPPMTPKRCPPGRGSPLCVPA RRSSEPRKNSAMRTEPTRESNRKTD SRL VDVSPDRGSPPSRVQALNFSPEESDSTF SKSTATEVAREEAKPGGDAAPSEVGGLL EPRSSGPAWEMM |

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| 1557 | 9608 | A | 2507 | 3 | 2112 | ILLLADEKFDLSDLSSSSANEDDEVFFG PFGHKERCIAASLELNNPVPEQPPLPTSES PFAWSPLAGEKFVEVYKEAHLALHIES SSRNQAAQAAKPEDPRSQGVRFIQESK LKINLFEKEKEMKKSPTSLKRETYLSDS PLLGPV/VGESCTAHAASQAATQRKPGT KLLLPRAASVRGRSIPGAAEKRTARMPK GRRKRK*QVLF*G*GCCGG*GEG*GCGE AGSSRIAPKKEIPASPSRTKIPAEKESHR DVLDPKPAPGAVNVAAGSHLGQKRA IPVPNKVNNEIFADSVFHFAPLGLKKT LKAPGSTNLARKSSSGPVWSGASSACT SPAVGKGLCCTPVCPARPARPLHSCCK MTPSRPWLMWQCREGLECP*GSGGTWV VRHSCDRRAGRSGSQSPRPHFGSSEVLG* TWRPGERGTGDSPTSSTPKLSRAQRPQSC TSVGSSRH*CCVCRTVHSTPVRSSGP APQSLLSAWRVSALPTASRRCSGLPPM TPKTMPRAVGSPLCVPARRRSSEPRKNS AMRTEPTRESNRKTD SRLVDVSPDRGSP PSRVPQALNFSPEESDSTFSKSTATEVAR EEAKPGGDAAPSEALLVDIKLEPLAVTP DAASQPLIDLPLIDFCDTPEAHVAVGSES RPLIDLMTNTPDMNKNVAKPSPVVGQLI DLSSPLIQLSPEADKENVDSPLLK |
| 1558 | 9609 | A | 2508 | 68 | 2331 | LLTALSMEEGGRDEPSASRAGDVNMD DPKKEDILILADENISTFDLSLSSSANED DEVFF*PFGHKERCIAASLELNNPVPEQP PLPTSESPFAWSPLAGEKFVEVYKEAHL LALHISSRNQAAQAAKPEDPRSQGV RFIQESKF*INLFEKEKEMKKSPTSLKRA ETYYLSDSPLLGPVGVPRLLASSPALPS SGAQARLTRAPGPPHSAHALPRESCTAH AASQAATQRKPGTKLLLPRAASVRGRGI PGAAEKPKKEIPASPSRTKIPAEKESHRD VLDPKPAPGAVNVAAGSHLGQKRAIP VP*NLKGLKKTLLKAPGSYSNLQKSSS GAIVWSGASSACTPQPVAKAKSSEFASIP AN*LPGLCPNISKSGRMGPVAMLRPALP AGPVGASSWQAKRVDVSELAEEQLTAP PSASPTQPQTPEGGGQWLNSSCAWSES SQLNKTRSIIRRDSCNLSKTKVMPTPTN QFKIPKFSIGDSVDSSTPKLSRAQRPQSC TSVGRVTVHSTPVRSSGPAPQSLLSARR VSALPTASRRCSGLPPMTPKTMPRAVG SPLACVPARRRSSEPRKNSAMRTEPTRES SRKTD SRLVDVSPDRGSPSRVPQALNF SPEESDSTFSKSTATEVAREEAKPGGDA APSEALLVDIKLEPLAVTDAASQPLIDL PLIDFCDTPEAHVAVGSESRLIDLMTNT PDMNKNVAKPSPVVGQLIDLSSPLIQLS PEADKENVDSPLLK |
| 1559 | 9610 | A | 2509 | 1 | 353 | DVQLEGAKIGSTEITFTPEKIKGGIHTAY TKTAGSVCLLMQVSMPSVLFASPSQLH LKGGTFKVAQDMATAAVRCIKKEIRDL YVNIQPVQEPKDQAFNGNGNIIIAETSTG CLF |
| 1560 | 9611 | A | 251 | 986 | 1401 | LEQGCNLFHLKHS*LGEVFFFVCFRRSFT LVAQAGVKWGDLSL/HKLPSSLSLPSS WDYRHLPLRLA/NFFVFLVKMGFTVLA RMVSIS*PRDPPTSASQSAGIIGVSPRAGP VAGILMFCRWNISNPKGAVIEKKKKK |

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| 1561 | 9612 | A | 2510 | 29 | 1262 | TKVSELLCGSQRLFFLPLWRRLCRCGLG PRVSPMAGPRVEVDGSIMEGGGQILRVS TALSCLLGLPLRVQKIRAGRSTPGLSMT *RPQHLSGLEMIRDLC DGQLEGAEIGSTE ITFTPEKIKGGIHTADTKTAGSVCLLMQV SMPCVLF AASPSELHLKGGTNAEMAPQI DYTMVVF KPIVEKFGFIFNC DIKTRGYYP KGGGEVIVRMSPVKQLNPINLTERGCVT KIYGRAFVAGVLPFKVAKDMAAAAIVR CIRKEIRDLYVNIQPVQEPKDQAFNGN GIIIIAETSTGCLFAGSSLGKPGFNSDKVV IEAAEWLLANLRHGGTVDEYPARPSLI VFHGH*PNGVSRIKTGPVTLHTQT/API HFAEQIAGK*ILL*RNPEDEEDAIAKDTYI IECQIGIGMTNP NL |
| 1562 | 9613 | A | 2512 | 900 | 1189 | SQHFRPRRADHLSSGVQDQPGQRGKTP SLLKIQKLAGRGGSL*SQLPRRLRQEN RLNPGGGGCSELRSRDCTPAWATEGNS VS KKNK*KKKKK |
| 1563 | 9614 | A | 2513 | 1710 | 2221 | SPLLDVYFKTRLLSRGRREACTLR LNTI GTLLSHCPLGIQPHPGPSGKTCGPFKPR GPGHSCPPD KKKQVPTVLP LPAPLRWA QAGLPYAGISGSPGRPLGAQAG*GSGV IGESNYFVHCMHPRGPGSPHL/PGG*GLQ PKPPRRLPSSSGSTTGLGDRKPCSYSQ |
| 1564 | 9615 | A | 2514 | 205 | 295 | GCNGNKDSCGPIAPSSGDILLTVKRS LP R*NFSPCA/PCSSSSKRAMCSRVCSPWGL *CGPIAPSSGDILLTVKRS LPR |
| 1565 | 9616 | A | 2515 | 1 | 927 | |
| 1566 | 9617 | A | 2516 | 932 | 1688 | KGFKNPTFPCEIPAGQTHKPHHNKHS PPVQKLKLQMKKNEVYETFSYPESYS PTLPVSRRENNSPSNLPRPSFCMEEYQR AELAEEDPI/LSARTPSPVHPSDFSEHNCQ PYYASDGVATYGSSSGALCLGNPRADSIH NTYSTDHASAAAPSVTRSPVENDGYIEE GSITKHPSTWSVEAVVLFLKQTDPLALC PLVDLFRSHEIDGKALLTHGVTVLPEAT WGVKLG TGL*SLCYLH*PDLKQKGKCL |
| 1567 | 9618 | A | 2517 | 3 | 179 | |
| 1568 | 9619 | C | 2518 | 140 | 490 | MAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLP EXSMFEDASVS EGRGTQIEENPLEENILAGEXASQTGDSG NEXANRGDGS DVSSQTPQTSSDWLEX X XLX* |
| 1569 | 9620 | A | 2519 | 194 | 405 | KKILWKKIFWRGKQHLKLVTVVTTAAN RGDGS DVSSQTPQTSSDWLEQVHLV*TA HIWGS KWYRYSVC |
| 1570 | 9621 | A | 252 | 303 | 551 | QEGIKSCKSDENSG LAPGQHGETPSLLK VSKLAGYGGACP*SQLRLRLRQENCLN RDLGGGGCSEPRSCHCTPAWTTEQDSV |

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| 1571 | 9622 | A | 2520 | 1 | 2046 | MRQNSGGNVHLPA AHLVLCGLVPNRPW TGKNKNKRHHLCIPQPTLAKIAKAAK GSAGNFRYPLILGSFPANWVFMNFFQSK ATLDFNLICSLNVKDVAEVFQKWLKIEG KKCHCLSEKTKQNMGNNTTTFRKALIN GDENLACQIYENNPQLKESLDPNTSYGE PYQHNTPLHYAARHGMNKILGTFLGRD GNPNKRNVNHNESMHLLCMGPMISEG ALHPRLARPTEDDFRRADCLQMILKWK GAKLDQGEYERAAIDAVDNKKNTPLHY AAASGMKACVELLVKHGGDLFAENENK DTPCDCAEKQHKKDLALNLESQMVFSR DPEAEIEAEYAALDKREPYEGLRPQDL RRLKMDLIVETADMLQAPLFTAELLRA HDWDREKLEAWMSNPENCCQSRGVQ MPTPPPSGYNAWDTLPSRTPRTTRSSVT SPDEISLSPGDLDTSLCDICMCSISVFEDP VDMPCGHDFCKGCWESFLNLKIQEGEA HNIFCPAYDCFLVPVDIIESVVSKEMDK RYLQFDIKAFVENNPAIKWCPTPGCDRA VRLTKQSGNTSGSDTSLFLLRAPAVDC GKGHLFCWECLGEAHEPCDCQOTWKNW LQKITEMKPEELVGVSEAYEDDRQ/CVC *VMN*TAKPCANCKSPIQKNEGCNHMQ CAKCKYDFCWICLEEWEKT |
| 1572 | 9623 | A | 2522 | 2 | 119 | ESTVSCCEKPTGAMP*MHTACGRPCPSI WRLTKLSMLR |
| 1573 | 9624 | A | 2523 | 159 | 627 | LGRMQDPQGGQMRWAYSITFAKDVCQ LGLSHYFAGAASGGCAQARCGPGRR* GPPAPVPSPLALPPMGTTRKLHPGMWT ALH/VRIP/VPKKEGCVQLIGEISCVLLQK ASWSEASTLCPAKGAIPNGAAFHQRCCR PEAHLGHRLSLAPPREPVE |
| 1574 | 9625 | A | 2524 | 3 | 307 | |
| 1575 | 9626 | A | 2525 | 1053 | 2813 | RTWEKAPEQADLTGGALDRSELSHSL MLPLERGWRKQKEGAAAPQPKVRLRQE VVSTAGPRRGQRIAPVRKLFAREKRPY GLGMVGRLTNRTRYKRIDSFVKRQIEDM DDHRPFFTYWLTFFVHSLVTILAVCIYGIA PVGFSQHETVDSVLRNRGVYENVKYVQ QENFWIGPSSEDLIHLGA*ISPCMRQDPQ GLSFIRSAREREKHSACCVRNDRSGCVQ TSEEECSSTLAVVWKWPIHPSAPELAGH KRQFGSVCHQDPRVCEPSEDPHEWPE DITKWPICTKNSAGNHTNHPHMDCVITG RPCCIGTKGRYVCVPASAAGLWAQSIAL GCEITSREYCDFMRGYFHEEATLCSQVH CMDDVCGLLPFLNPEVPDQFYRLWLSLF LHAGQVTILHCLVSICFQMTVLRDLEK LAGWHRIAIYLLSGVTGNLASAIFLPYR AEVGPAGSQFGILACLFRGSSSRAGQIL GAALACLLQACWLWVLFHLWGLLP WDLTTFAHIFGGSSVALFLSFAFLPYISFG KVRPVPETLPDHLSGGLPRASWLAWW SSSTSILSAVSRVSSSPASPFIDKLL |
| 1576 | 9627 | A | 2526 | 1 | 936 | |
| 1577 | 9628 | A | 2527 | 1 | 1023 | |
| 1578 | 9629 | A | 2528 | 157 | 512 | LG*LQPPPPGFKRFSCSLSSSWDYRMRH HAWLIFVFLVEMGFTLISASRVAGITGM RHHAWLIFVF/CSRDGVSTCLGQAGSQT PDLKVICPLGPPKSAGITGVSHCSWPVIY VLSTLLHAVRNVLFRKTFPLKSSSFLSYD KEIFPILIGLKFYLVLTSTFVKGHILLK |
| 1579 | 9630 | C | 2529 | 11 | 133 | MFCSLQPTDLRKEXMNLQTLRLRSSNKH QRFPGLPRGLCD* |

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| 1580 | 9631 | A | 253 | 3 | 401 | STFGFQGTGWETRWGPT*PGVSAWSLVP SPVLETPDLERKRAHLGVATAGGPAGP YRLSPHTLSSRKEGKGEAASKGTEAELM TIGIENSTCQSCLSFSFHYFWSPRGAGP KAMWLVGDRKGATKNDKRGY |
| 1581 | 9632 | A | 2530 | 367 | 676 | KVVTLIILILQRRKWGA/PGSDPKSPCCSD SKGQASFTAP*CSYLYTADGRLGLAWG* GLNRSAMTSNPDQTHLVAQTSKGPERK HKVSGFLVKVIPATAYDNG |
| 1582 | 9633 | C | 2531 | 156 | 683 | MKLRQRWRHPAHFSGTGKMIGEGTQVS VGTGVTVDTGVGCLSTSSHYANRNADT FRCLCRKRCQRLKSRRGVKKSCISVP HRQLSQALQAMRDSSEPWALSISLRFRE DEALASKHYRRNAPRAALRQFLSDFHR DCLNVFKTKYHTLMYMGRTIMRCEPCA CGGEGKKNVLF* |
| 1583 | 9634 | A | 2532 | 427 | 458 | KNSQYTPLTLIQMMGF*FFVF/ERQSHSV VEAGVQSCSHGSLQPLPPGSSNPPTSASR VAGTTGAHHDDLIFLFL*RRGFALLHRL VSNSWRSRDSA WPSAFPKWLGLWDVEA TTPRPGLFSLVAG |
| 1584 | 9635 | A | 2533 | 57 | 463 | ARTPLQAGAGLVLSRLLSLPLGLSPLPT VSCARWPLCPRPWSSLPGFWD SWHCNH RTGHR TGPGGLDTQSA*VNKLIWGKGN HL*PQATAQLWPIQLGGWQGWTRPS/RW WPLSSPHC*PGYRSLKDSFANTFLF |
| 1585 | 9636 | A | 2534 | 3 | 469 | RKTTTATMTSLCRKVNGGHAG*ETLRL LVVYPWTQRFFDSFGNLSSASAIMGNPK VKAHGKKVLTSLGDAIKHLDDLKGTF QLSELHCDKLHVDPENFKLLGNVLETVL AIHFGKEITPEVQASW/QEDGDWSGQSP VLQIPLSSLAMMQSCQG |
| 1586 | 9637 | A | 2535 | 41 | 676 | APSPRRPWGHFTEEDQGLLSTSLWCKV NVEKCWKEKTPGKGS LVVYPWTQRFF DSFGNLSSAFHHGQT PKVKAHGKVK VLTFLGRCQSTLDDLKGTFQAQLSELHC DKLHVDPENFKLLGNVLT VLAHFGK EFTP/ERLQASWQKMGD*SGQCPVLQI PLSSLPMMQSFSRIRLLFLQAITNNKIS AKRSHMIFFSFFYIFLNI |
| 1587 | 9638 | A | 2536 | 107 | 331 | |
| 1588 | 9639 | A | 2537 | 386 | 1074 | NNPEWRTLIIYVDKENGEPTRVVAKDG LKLGS GSPSIKALDG\RSQVS\TPRFGKTF D/APHPALPKAT*KGFGELSTGATEKSVK DPGDPLKQKNGPAFSGPKKMDLKKDCL KQKS\SVSWPSGLMPNPRNKTFFPLQIL LDF*GVFD/LCPEEHPDLRHLPLSGVPL MIPLTREREL*KSWFQLGPPFHLWKDGP LPPWGIPICLQFSFQGISVRTWGVADLPV CCDIDI |
| 1589 | 9640 | A | 2538 | 1 | 359 | |
| 1590 | 9641 | A | 2539 | 1 | 483 | FQLEVTPQNITLNPFGGPPVFSWRDQAV LRQDGVVVTINKKRN LVVSVDDGGTFE VVLHRVWKGSSVHQDFLG FYVLDSHRM SARTHGLLGQFFHPIGFEVSDIHPGSDPT KPDATMVGLQKDYSKDPWHGAEVSCW FIHNNAGLIDGAYTDYIVPDIF |
| 1591 | 9642 | A | 254 | 1833 | 2126 | EKRKKRGFFKTKPLLKCPGPWGESRFW GPPKGSQV*G/HI*MGPNLGERWKKGP KRPKKPKTKGPPPGVHPPKRNPHLG/ WPGGPTLKKKGKNNLGFC |
| 1592 | 9643 | A | 2540 | 3 | 310 | EVRLANSSQALRMWLDYGFVTPLTSM RGMADQDGLKPTIDKPSSESPPLEMLGP RRTFVLSALQPSPTHSSNTQRLPDRVTG VDT*VVT*PYVLCWNLC |
| 1593 | 9644 | A | 2541 | 1 | 1482 | |

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| 1594 | 9645 | A | 2542 | 37 | 2885 | SMDGAMGPRGLLLCMYLVSLILQAMP ALGSATGRSKSSEKRQAVDTAVDGVFIR SLKVNCKVTSRFAHYVVTQVNTANE AREVAFDLEIPKTA FISDFAVTDGNAFI GDIKDKVTAWKQYRKA AIS*EKA\GLVR ASGR TMEQFTIHLTVNPQSKVTFQLTYE EVLKRNMQYEIVIKVKPKQLVHHFEID VDIFEPQGISKLDAQASFLPKELAAQTIK KSFSGKKTSNGSHSRRFQGHVLFRTVS QQQ |
| 1595 | 9646 | A | 2543 | 159 | 1222 | NNSGVMPPEMPEDMEQEEVNIP**GGFW VTGCHWGFLGRAVHKEFVQQNNL/WHA VGCGFRRARPKF*TG*ICWDSNAVHHIA HDFQPHVIVHCAAERRPDVVENQPRCL PLQLNV\ DASGEF*AKGAAAACLSISPF YI*AQVFVF*WEPNPPYREEDIPAPLNL YGQTK\LDGRKGCPRNHLGAAVLRPI LYGEVEKLEKKCELLMFE*KCQFSQQS PAKQWIHWQARGSPPHMSKDVAPLCAR QLAEKRMLDP\SIKGTFWHWSGNEQMT KYEKGMCQLPDA\FNLPSSHL/RDPITDSP VLGAQRPRNAQLDCSKLETLGIGQRTPF RIGIKESLWPFLIDKRWRQTVVFH |
| 1596 | 9647 | A | 2544 | 211 | 463 | |
| 1597 | 9648 | A | 2545 | 188 | 366 | SCQSACQKNGKIILRLQLLGP*DRLEDTL LNTHGLLQSQILCQFCFLCTCQKVLRI K |
| 1598 | 9649 | A | 2546 | 1257 | 1441 | |
| 1599 | 9650 | B | 2547 | 74 | 733 | MAWKSGGASHSELIHNLKNGIHKTDKV FEVMLATDRSHYAKCNPYMDSPQSIGR VQLVVG DGRMGY AEEAPYDAIHVGAA APVVPQALIDQLKPGGRLILPVGPAAGN PNVGASIPGSRMASIQNEALWMGGDIRA L* |
| 1600 | 9651 | A | 2548 | 45 | 972 | TVQPHVSGSGGDGNSGYSYSGDASGAV TVWEVVSLLGKLLGTVVALKVVLYLLR VCLAMAWKSGGASTSELIHNLKNGIHK TDK\VFVMLATDRSHY/SQKCNPYMDS PQIK*GFQATISCSTHCNAYALRNFLWI QLHHEGSLKLF\DVSGKWESLLACFAR MVG\CTGKIVIG\DAH*RS**DDSVKLMF REGTIPTLLSFRGGVQLVCGGMGRMGY AEEAPYDAIHVGAAAPVVPQALIDQLK PGGRLILPVGPAAGNQMLEQYDKLQDG SIKMKPLMGVIYVPLTDKEKQWSSGMI VKATSA |
| 1601 | 9652 | A | 2549 | 2 | 478 | |
| 1602 | 9653 | A | 255 | 70 | 380 | YSNNPKDRKGETGINEKTNNKMVDLSS YTSVITLNF*ML*/D/KIN*KFVKSP*KKPT LCCLLETYFKYGIGGLVKRWRI*HAH TIGKKT LVAILITKHTSELS |
| 1603 | 9654 | A | 2550 | 392 | 1245 | CTFTKVFLLLRIWYRNMLLKNSVTPLPS CHPSAQCLGTLMRALSQVFRDAW/WWV ASVDVVENEEASASHVKMTDSFTEQAD QVTAEVGKLLGEEKVDA\LCVAGGWA GGNAKSKSLFKN\CDLMWEAEHYWTS HLPSH\ALT KHLKEGGL\TLAGAKAA LDGTPGMIGYGMAKGA VHQLCQSLAGK NSGMPP\GAAAIAALPVTLDTPMNRKS\ MPEVADFSSWITPL*FLVETFDHWITGKNR PSS\GSLIQVVTTEGRT\TPAIFGLISV PMRWPAQKSH |
| 1604 | 9655 | C | 2551 | 60 | 266 | MSWLSCLSNITVWNISPVLLSFFGGNSLI SHLXKIPEEPFLTPLLSSSPSGFXPHVPR VLRSQSATV* |
| 1605 | 9656 | A | 2552 | 1 | 513 | |

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| 1606 | 9657 | A | 2553 | 345 | 2343 | LLGHEEQTRKGKRKAKAAGMVLSQLL TFRDNEAIEFSQEEWKCLDPAQRTLYRDV MLENYRNLVSLGIFSKCEIKELPPKKESN KEYSRQ*CWKDMKSHRHTKIFCFRETQ KNVHDSQCLWKHD*RHYKRVRVITYKG KSH/CVEETMPG*KG*CHKSQPC*KSSLG LNPAVT/CLPRTCQIPSKPEGKIYKYDHM EKSVNSSSLVSPQRISSVKTHTISHTYEC NFVDSLFTQKEKANIGTEHYKCSERGKA FHQGLHFTIHQIHTKETQFKCDICGKIFN KKSNLASHQRIHTGEKPYKCNECGKVVFH NMSHLAQHRRHTGEKPYKCNECGKVVF NQISHLAQHRIHTGEKPYKCNECGKVVF HQISHLAQHRTIHTGEKPYECNCKGKVVF SRNSYLVQHLIHTGEKPYRCNVCGKVVF HHISHLAQHRIHTGEKPYKCNECGKVVF SHKSSLVNHWRHTGEKPYKCNECGKVVF SHKSSLVNHWRHTGEKPYKCNECGKVVF SRNSYLAQHLLIHAGEKPYKCDECDKAF SRNSHLVQHRIHTGEKPYKCDECGKV FSQNSYLAYHWRHTGEKAYRCNECGK VFGLSFLAHDPKIHTGEKPFKCNECGK AFSMRSSLTNHQLRLHTGEKHFKCNECG KLFRDNSYLVRHQRHFAGKKS |
| 1607 | 9658 | A | 2554 | 3 | 517 | STRTQNVLGEKGRRIRELTAVVQKRFGF PAESLRYKLLGGLAVRRACYGVLRFIM ESGAK/GCEVVVSGKLRGQRAKSMKFV DGLMIHSGDPVNYVDTAVRHVLLRQG VLGIKVKIMLPWDPTGKIGPKKPLPDHV SIVEPKDEILPTTPISEQKGNAEPPAMPQ PVPTA |
| 1608 | 9659 | A | 2555 | 3 | 495 | |
| 1609 | 9660 | A | 2556 | 24 | 861 | INPPPPRLSFQSAARWPVQISKRRKF VANGILSKLNLNEFLVRELAEADGVSGV VEVRVTPTRNRKSFIFSHQHRMVLGEK GRRIRIELPAVVQKSFQFPRGAARELY A*KRWPT*/RGLCAICPGQSLCVYKPS*G GLAVRRAL/CYGVL/RGSFIGEVGPKGCE VCGCLGKLRGQRA*NP*SFVDGLMNH GDPVNYVDT*VRHVLLRQGVVLGIKV KIMLAWDPTGKIGPKKPLPDHVSIVEP/ RRDEILPTTPISEQKGKPEPPAMPQPV TA |
| 1610 | 9661 | A | 2557 | 116 | 718 | IFLQAGCLKLVIRSKAGDISHVDTHCQTV HPKAVSISTMTENTPFLTLSPALSPFN PFQIEK*YLILTLIFLIAVEVESLCL*SVF LIYKIFL*PLSNFCCL*V/LLYIILNLLFY MYFPTPLFMKSNFIKVL*KVKGFTF*KCS QIYLFHGYWVLCGLGWECLSYTFITIFFQ YFLLVIFNFHV*FILIFFIHDMDK |
| 1611 | 9662 | A | 2558 | 88 | 811 | GSGGNHVSCCDTMEGGGGSGDKTTGVL AGFFGAGGAGYSHADLAGVPLTRMNPL CPYALNVDPYLVQGYKMFIFITLPELIK TRGQDLKLAFFTIGGCCMTGAAGFAMN GLRLGLKETQNMASKPRNVQILNNG *LGKALWA'NTLGLWALLYSAFGVII EKTRGAEDDLNTVAAGTPAGLLYTCTG GLRGIA'RGGLTGLTSLSLCTIYNTWG AHGKGLASNSSLWKVFAQPP |
| 1612 | 9663 | A | 2559 | 1 | 210 | VIIRLPIGKKLFRCKPG*TWAPPGIL*SGR PRSSSSSPF*N*MHFLFERESSFHRCKWK AGITCVKSWYP |
| 1613 | 9664 | A | 256 | 225 | 353 | RWGFTQLRLRLRQENHLNRGVGGCSEP RLCTPAWATE*DSVL |

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| 1614 | 9665 | A | 2560 | 128 | 687 | THVLWAFPGARVHLQTGWSRAGVAAA ALALGGQASLSYARGKES*GHSPPTHT HKAASGGREKAVSPSVAVVSHGSPSLLS EYTSSQVKHSGPGDPVVTHL/WAPFP DQLPPSPCPLSRKEPEPSPLSHPPQGVTP GQAQIGQLRTSLWGHKRGGWARAEG APVSLLLRGPFDPATVSEAQR |
| 1615 | 9666 | A | 2561 | 246 | 410 | . |
| 1616 | 9667 | A | 2562 | 1 | 414 | AWHEETHKVDLGLPEKKKNKKVVKEPE TRYSVLNDDYFADVSPLRATSPSKSVA HGQAPEMPLVKKKKKKKKVSAALGKE VKRSQSKLRLRNTSP*VMTLRPPQKRK*S PKRR*SSQSSRSQL*KGRKRRRGKRG |
| 1617 | 9668 | A | 2563 | 198 | 531 | RNNPLLSLLALCLVHSSHLCWALPDEG GGQGKERALNSRKIATFFLSSQGTQFGQ WDTAGFENEDQKLKFLRLMGGFKNLSP SFSRPASTIARPHMALGKKAADSLQQNL |
| 1618 | 9669 | A | 2564 | 190 | 510 | |
| 1619 | 9670 | A | 2565 | 1 | 1977 | MEVDFKIRKVGQWTTITLQEHVSVLLFIE ETHPENKPTSTAVEESHISRDVTMVNFQ CQLDWSKGYLEAYLTKINSICSHRFLLD GSVTCHDETGSRRDARDTVGTGVRVND ESVEQLGLRRTMWLGICRGAAMAAVST VTAFAGRPRPGSRNPRGWAGDSK WTS GSRRSWLSRGGGEISPTGMITKTHFVYL GLPEKKKKKRVVKEPETRYSVLNDDY FADVSPLRATSPS*DV AHGQAPEMPLVK KKKKKKKGVSTLCEEHVEPETTLPARRT EKSPSLRKQVFGHLEFLRGKRKNKKSPL AMSHASGVKTSQDPRQGEETR VGKKV SKKHKKEKKGPGPHSLAPVQDPWFCEA REARDVGDTCVGGKDEEQAALGQKRK RKSPREHNGKVKKKKKIHQEGDALPGH SKPSRSMESSPRKGSKKPKVKEAPEYIP ISDDPKASAKKMKSKKKVEQPVIEEPA LKRKKKKKRKESGVAGDPWKEVVPSE MDFAVGELRETDTDLEVVEKKGNMDE AHIDQVRRKALQEEIDRESGKTEASETR KWTGTQFGQWDTAGFENEDQKLKFLRL MGGFKNLSPSFSRPASTIARPNMALGKK AADSLQQNLQRDYDRAMSWKYSRGAG LGFSTAPNKIFYIDRNASKSVKLED |
| 1620 | 9671 | A | 2566 | 1781 | 2148 | VRRFAAAVATLPPGAAPSG/PAPGT/PGP QTRIPGFPWPPLCPLMSGSLGP*TRLLLV PPAPQGPAGSPGPIQAGRGLAAPPQPLS PSRGPCAGSSWELRLEGLSDWGTCPVPC PCHYIHPPKN |
| 1621 | 9672 | A | 2567 | 1 | 345 | |
| 1622 | 9673 | A | 2568 | 1 | 582 | SGRALHASWAAGGVGAYSGRLRSDALE GESFALLSFSSASDAEFDAVVGYLEDIIM DDEFQLLQRNFMKYLLAEFEDTEENKLI YTPWFNEYISLVEKYIEEQLLQRNPEFNM AAFVTTTLQH/HIRDEVAWVTIFGNAGST FHKIFLGF*RKCFLDYRAEKESRGLDLS SGLVVTSLCKSSSLPASQNNLRH |
| 1623 | 9674 | A | 2569 | 2 | 705 | GSVGAATVRPQPNALRCRLRSRAGRSPV LVFGVGIKQPPCPSKKAKTTKTKRPQR ATSNVFMFDQSQIQGVQRGPFNMIDQ NRDGFHSDK/EKVLHDMLASLGKNPH* WHYLDAMMNEGPKGPFKHQCSLTMF WLRKLNGVTRSPEDCHPETAFCFAFD*KK ATGTHFRKDYLRRC*PTHGGIRFPD/ER EVDELYRGGTLLDQKKGNFQITFEHTA SWKHGSQRPKMT |
| 1624 | 9675 | A | 257 | 238 | 512 | HMYVPNLRTSKYMKRTLIELKGEIDSNTI LVGDFNTLSTMGRTFR*DISKETEDLHN TVDPMDLTD/SAELSTQQQNTLSSQAH GIFSRTE |

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| 1625 | 9676 | A | 2570 | 1006 | 1022 | TRNSFLFFIYIYFLRMGSCSVAQGWKCS GTILGHCSLCLRLPGSSNSPTSASHVAG D/SHGMCRRHARLIFALVEMGFHPCWP GLGLELLTLRVIHPTLGLPKCWGL*AGG SAKIGRRAQIG |
| 1626 | 9677 | A | 2571 | 668 | 863 | TFCFFSDLKYSLASCENHLVCFLVCFAP LV*T*NYFCL*TVNLIFSRRVTELCPFIFI VLIIT |
| 1627 | 9678 | A | 2573 | 258 | 579 | FKQICLFLLLFFEMESCSVTRLECSGTIS AHCNLHLPAGSSDSPASASPVGTGTCH HAQLIFLYFYMTGFRHVAQVGVLLG* *AIHLPWLPKVLGLQAPAPDL |
| 1628 | 9679 | A | 2574 | 157 | 371 | |
| 1629 | 9680 | A | 2575 | 1 | 1431 | MHKAGLLGLCARAWNSVRMASSGMTR RDPLANKVALVTASTDGIGFAIARRLAQ DGAHVVSRRKQONVDQAVATLQEGGL SVTGTVCHVGKAEDRERLVATAVKLHG GIDILVSNAAVNPFFGSIMDVTEEVWDK TLDINVKAPALMTKAVVPEMEKRGGGS VVIVSSIAAFSPSPGFSPYNVSKTALLGLN NTLAIELAPRNIRVNC/LAPGLIKTSFSRM LGEPEDCAGIVSFLCSEDASYITGETVVN LSVMFTGGGVCRAASWKEGGTGTPRTP RESPRQREPGETSSDTQENKVWNLPA NPQRPAAEQPVRRKTNKQKGIATSADK SINIRTGKDIHTKTPSIGHQHQRPKVDKT TKMERNQSKKAETSRNQNVSSLPKEYKS SPAREQNW MENKFDDLTDVSFRRSVITN YTQLKEHVLTHCKEAKNLDKMLNEWLT RMKNLEKSLNDLMELITTQELHEGYTS FNS |
| 1630 | 9681 | A | 2576 | 201 | 398 | |
| 1631 | 9682 | A | 2577 | 195 | 434 | |
| 1632 | 9683 | A | 2578 | 150 | 284 | |
| 1633 | 9684 | A | 2579 | 1 | 625 | MHKARLRGHCARAGKSVRLASSGMTRR DPLTNKVALVTASTDWIGFAVAQRLAQ DGAHVVSRRKQONVDQAVATLQEGGL LSMTGTVCHVGKMKDWERLVATGFSKY NVSKTALLGLAQTLPIELAPRNIRVNC/L APGLIKTSFSRMLWMDKEKEESMKETL RIKKV*ASPEDCAGIVSFLCSEDASLHSL GKTVVVDGIGTPSRL |
| 1634 | 9685 | A | 258 | 167 | 408 | DRRITRSGVRDQPGQHGGETPSLLKIEK/L AGHG/GQAPVCGGRSYLRRLRQENRLNP GGRGCSEPRLRHCTPA*VTVRDSVS |
| 1635 | 9686 | A | 2580 | 84 | 1413 | ARKSVRMASSRMTRRDPLTNKVALETA STDGIGFAIARRLAQDRAHVVISRKQQ NVDQAVATLQEGGLSVTGTVCHVGKA EDRGAAWWPPAVKLHGGIDILVSNAAV NPFFGSIMDVTEEVWDKTLINVKGPK P*MTKAVVPEMEKRGGGSVVIVSSIAAF SPSPGFSPYNVSKTALLGLTKTLAIKLAP RNIRVNCLAPGLIKTSFSRMLWMDKEK EESMKETLRVRLGEPEDCAGIVSFLCSE DASYITGETVVNLSVMFTGGGVCRAAS WKEGGTGTPRTPRESPRQREPGENQARS SPRMALRPEFPESASTSWMGPEPVGNR ERPCKPARKVGASPRALRRLGSATRMLS RAALRAGVGARAPRPGGGRGHAHATV WSGLASAAALTARALLKRSLACAAAPQ RCGWRRLCSSLGIRGSGWPCPPWSSI |
| 1636 | 9687 | A | 2581 | 1 | 560 | MVYRQNLPPSSCAPEMGREDGLRALHP AQPPPPRAQQSPPPPLSA/PEPPPPRAQQ SPPPPLLTPHRRHPQSFPAPSAPSALSQR PGLYSAVTFSGSLSGPRTSTCTPSPASSPS AHGLGHIHTDAGVCSLEAQEEAKAPGG RGPSCSAHGALGPTCTSGVAGDSGPVVG SQERALDPRRQGLQH |

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| 1637 | 9688 | A | 2582 | 775 | 1408 | TIPVAYVWADPPLPPKHSCPHPPGSD/D GTRTTGTA/PPCLGFQGDPPVHPAPAPP DW**FPNMGQPGPPPPFTWRAQLQLLK SSVNMGRHRWRNVPSGPHLPEQISLSEL GHSHKPLFLRQNPNTVPWDVMLPFPLL NLLYGKMWNWVSLDLWGCHRNEEWRP TNILLAPWRHGRQLQLKGAGARGRQLPQ LLLALLLILVGYEMSF |
| 1638 | 9689 | A | 2583 | 3 | 560 | GVPPKSASKFLCTRNGKGRWAQSPPPST A/PPRAQQSPPPPLSAQK/KPPPPRAQQS PPPPLLTPHRRHPQSFPAPSAPSALSQRQ GLYSAVTFSGSLSGPRTSTCTPSPASSPSA HGLGHIHTDAGVCSLEAQEEAKAPGGR GPSCSAHGALGPTCTSGVAGDSGPVVG QERALDPRRQGLQH |
| 1639 | 9690 | A | 2584 | 189 | 608 | AFLTENKLRHTDTCRGNKPHPPPPGSK VRKRTWGFAPPGGSPWASLPHGLPPTA GRQGRGR/EGGGPRGGPGKGSAPSSGT RAWRKPMGGCLTEDGPYGGPKGLWP*T TNG*K/PPGARWPPLPLGCPLEPRHPVL GP |
| 1640 | 9691 | A | 2585 | 2 | 847 | LKMAAEEPHQQKQEPGLSDSEGVNCLA YDEAIMAQDRIQQEIAVQNPLVSERL LSVLYKEYAEDDNYYQQIKDLHKYYSY IRKTRANDGNCFYSGFRILPLGRHCWDDS KELQRFKAVS/WPRARVDLGCSQ/WGFT *ISQF*GIFHNKFHGT*LSRWRKQTSVAD LLASFNDQSTSDYLVVYLRLLTSGYLQ RESKFFEHFIEGGRTVKEFCQEQEVAEPMW KESDHIHJMALAQGLNGAIQGEDMDRG EGGTTNPHIFPEGSEPKGYLLYRPGHYDI LYK |
| 1641 | 9692 | A | 2586 | 468 | 1191 | DVSRVGCPLPPSRAMGWTLLALLRRGSAV SALASGLVEEPMGLGPPFHTPRFKAVSA KSKEDLVSQGFTEFTIEDFHNTFMDLIEQ VEKQTSVADLLASFNDQSTSDYLVGYLR LLTSGLL*GPRASSSTSSKGGRDCKEF CQ/QELEPM*KESDHHSHHCAGPGPSAC PSRVGVHGTAAEGGNHQSALSLRASEP KVYLLYRPGHYDILYKIGLGSSPLLCCP PLPGARHVTEVFLWL |
| 1642 | 9693 | A | 2587 | 1 | 326 | HSVNRKRLNRNARRKAAPRIE/CVRGLG FRVAVGLGRDGRDDGSAMSLFAGSSHI RHAWDHAKSVRQNLAEMLAVDPNRA VPLRKRKVLTWQGLGPCLLYSSPAILT |
| 1643 | 9694 | A | 2588 | 879 | 1528 | AAGAVVSAMPKAKGKTR*QKFGYSTL RKRMSRNARRKAA/RAGLECSHIRHAW DHAKSVRQNLA*MGLA/VDPNRA/VPSR KRKVKAME/VDIEEA*KNL YRKPYVLN DLEAEPSPLEKKGNTL/SRDLHLMYRY MV/ENHGEDYKAIARD/ENY/ QDTPK QISELSNVYKRFYPAEWQDFLDSLQK RKMEVKVPGLHHSCPSAEASPGPSEAG |
| 1644 | 9695 | A | 2589 | 1 | 310 | |
| 1645 | 9696 | A | 259 | 660 | 1200 | LTVGKKNRKQQQHQPSPHGPPLKQGQ QPSKVQIEDKFLGR*GKELKNPFTTQKG QSGFVYSKLIHNTSYRQGHSPGWRLRW MN*QK*ASEGG**QTSLS*RSTL*PNILER IPELKDWFISKIRKQK*KRIKRKEENLQ*V WGYI*RPILQITGIPERRVEISMHWVRAC SFSSVKFVIP |
| 1646 | 9697 | A | 2590 | 1 | 716 | SALQRLKPKPRPPERSPRRWVPEPQL EVGGACSAQAQSPSEKLPACLPKPLS*S* IRRRRPTPAMLFRLSEHSSPEEEASPHQR ASGEGHHLKSKRPNPCAYTPPSLKAVQR IAESHLQSYSAILNENQGFGRGREDELGE FWELGYPREDEEEEEDEEEEEDEDSQ AEVLKVIQSAQKTTGQGLEGPWERP PPLDESERDGGSEDQVEDPALSEPGEEPQ |

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| | | | | | | RPSPSEPGT |
| 1647 | 9698 | A | 2591 | 39 | 370 | RGWSLVQTPNPRFKNVPGPPTPQVIAEC EESQCGGLGTLGGL*LSPGP*G*TDSRGPP MMPSEAQGGGAASKGPLPQAAGIHQ GTPLRMGEALEGQAGQTAGPRVQDGL |
| 1648 | 9699 | A | 2592 | 229 | 358 | |
| 1649 | 9700 | A | 2593 | 257 | 386 | |
| 1650 | 9701 | A | 2594 | 217 | 398 | KAWWNLLRKSEPKSCGS*GGLSTSRL VECSSLGLGYCG**LCHLQEPHYGSLH RMSS |
| 1651 | 9702 | A | 2595 | 1 | 3386 | |
| 1652 | 9703 | A | 2596 | 442 | 2093 | CGFLQMGTVINHNIPGPEGYWHFHFNF KALLARAAVGAARGIHIHRCGLTKRPDA RRRRVAGAAGREPAISLPGDRAAGARAT RTRGPGPAPKMPAIAVLAaaaaaWCFL QVESRHLDALAGGAGPNHGNFLDNDQ WLSTVSQYDRDKYWNRFREVEDDYF RNWNPNKPFQDALDPKDPCLKVKCSP HKVVCVTQDYQTALCVSRKHLLPRQKE WGTWAQKHGGLDL*ILVKICKPCPVA QSAMVCGSRWATPNSIPCKLEFHACS TGQK/SFATLCDGVCPCSSQSLEPPKHKG RKGVPCDTELRLNLSRLKDWFGALHE DANRVIKPTSSNTAQGRFDTSLPICKDSL GWMFNKLDNMNYDLLDPSEINAIYLDK YEPCKPLFNSCDFKDGKPLNNEWCLL PSQNPGLP/CAQNEMNRIQKLSKGKSL LGAFIPRCNEEGYYKATQCHGSTQCW CVDKYGNELAGSRKQGAVSCEEEQETS GDFGSGGSVLLDDLEYERELGPKDKEG KLRVHTRAVTEDEDEDDKEDEVGYI W |
| 1653 | 9704 | A | 2597 | 1 | 844 | LHQQAAVWLPTSFLPSQEHCCSTEW APQPAASGVHGICFA/RPFASSTVSTEV GSFCYLPAPWVYGFL*TERPLAWWCL GKYWLQELLGCHPVPLAML*DCLALLK SSLVPMGSPTHCKAIVTEPLHLPEAAA AAHTSSPSSCRCKGCLGWVWPGGSAP GPLGPLSFDPTVSHQSGPSAAPGPTTS SS*RPSAPSHGMQGLADSQGHLCRHSRK GLRSFLLSHTHSTCPHLLQTGMPSPL ISIDADSSPPRIHRLRGQGHFSGLAKGGQ R |
| 1654 | 9705 | A | 26 | 238 | 446 | GFVVSLDSR*QWESRSSIHAWTN*ASS SSSSSSSSVSRIVYPRFIEYLHKDIQSTG QKSPDAWVAGG |
| 1655 | 9706 | A | 260 | 1 | 680 | EQCRSPARARLQPQDPASTEAEERTYP GSIGAPAGEGKVPGLVIYLLWPWQNQDE ALSCLPSEAYSLSRQHGLPLAVNTMSAG GGRAFAWQVFPPMPTCRVYGTVAHQD GHLLVLGGCGRAGLPLDTAETLDMASH TWVALAPLPTARAGAAAVLKGQVLVV GGVDEVQSPVAAVEAFMLDEGRWERR ATLPQAAMGVATVERDGMVY/VSGGNG P*HGPPGPGT |
| 1656 | 9707 | A | 2602 | 144 | 520 | IGKEEIKLLLFPDNLMEYTVNF*MYKPLE LIS*FSKVTEYQVNTK/SNCIYT*QLQIE NEIAKTI*FMIAKSIKYLEISLTKCNKW RDILCICIGRLSIHKVLVLPKLMCGGEKIF NPNPTGFW |

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| 1657 | 9708 | A | 2603 | 105 | 440 | RSTDPVCLGIRSSGCRTADFREP*MLLS DRSSGSFVSEYPAV*SVSLPLLGECLPV RLLRDGHWS*HDSOSS*VFKMADNFPA GFHRLGRSGDGRAEHRRCCLASQRCC |
| 1658 | 9709 | A | 2604 | 1 | 1047 | |
| 1659 | 9710 | A | 2605 | 1 | 690 | |
| 1660 | 9711 | A | 2606 | 210 | 424 | |
| 1661 | 9712 | A | 2607 | 651 | 835 | PRWSRFPDLVICPPRPPKVLGLQA*AIVC ASISITKMWLRNAGLTSSMNWPRRSARY LSVS |
| 1662 | 9713 | A | 2608 | 198 | 755 | |
| 1663 | 9714 | A | 2609 | 1 | 1305 | MMRAHAPPTAVPACTAPRAPPRDHRA GIAREALGRTGRSGFRDCLGTREVALQA REKAQAAAQGEAGCSAHWVRHTRGA APEGRPRVPRAAGVLTGCTVFRRTWIQR DAQIQARQERWAKGESGPWGLRGLAT QPAVRASGRRGRRRLERQDILEVFRCLAA SWNGGFGAVKPPEVADARSGLSGDSF CLVSVSLTKAKKGLELKQNLIEELRKC VDTYKYLFISSVANMRNSKLKDIRNAW KHSRMFFGKNKVMVALGRSPSDEYK DNLHQVSKRLARGEVGLLFTNRKKEVN EWFTKYTEM DYARAGNKEGFHC*AWD PGPLEQFPHSMEPQLRQLGLPTALKRG VVVTLSDYEVCKEGDVADPRARASRS* KLFGVMRWLNFKVTIPNYMWDSSQGRF QQIGKTDLPESAIEFPEESDSEDDDD |
| 1664 | 9715 | A | 261 | 1 | 403 | RTRGQLNRGVYGPRRSLVSPSTLAGAPL AGRLDETSGEETLTLGCGKMSGPTQPP AEGTEGTAPCGGAPVPPNMTSNRRLQQ TKAQVEEVDIIPVNGDNVLRDHLRE LDDRS/DALQARA*PFESSAAS |
| 1665 | 9716 | A | 2610 | 319 | 632 | GEPNIGMSLPWGGPSGSTGMPAPAMPL PAMTPQC/C*GQGPV/GPCAS/CASA/CFR CGL*AGRFC/G/PCPGHC*CFYFSNSVFPN VECMGLREPAVLPAFHLGEEAGRISSGQ GRSQNLPA |
| 1666 | 9717 | A | 2611 | 156 | 621 | LHVPMELOSHSKDEVSPTYLGMSLPGVA PLGSTGDASPCHAPPRPWTQCSKGQGP CCAP/WCP/CCP/PPCPWSHGCL*LLCDP CPPPALPAAEGQQPLCKLASAVSGVVS LGNFATCPWPLMRPASSPRWKAGRTA GSLRPIHSTLGNTFEK |
| 1667 | 9718 | A | 2612 | 1 | 585 | |
| 1668 | 9719 | A | 2613 | 1 | 1047 | |
| 1669 | 9720 | A | 2614 | 1 | 1674 | MRSQGEVRRYLKRQSCRFLGSREKDM VTPSASSVCLIDEQIPAAGESYDIIDPRSK HKFKIHTYGSPTFCDHCGSLLYGLIHQ MKCDTCDMNVHKQCVINVPSLCGMDH TEKRGRIYLKAEVADEKLHVTGKACSSR SSIVGRHLDEGYTDIKAGQLDAFLCISS QPPFGKNAIHTSSSSSIITLLKHGPRRFYSF ASCSCMSSTVSVTNPKILGKGFIDSVVW TCHPGPMDCDWRADMGWGPVRLCIWF S |

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| 1670 | 9721 | A | 2615 | 3 | 2089 | RPQLPGGGKRWLGGMADVFPNDSTA SQDVANRFARKGALRQKNVHEVKDHKF IARFFKQPTFCSHCTDFIWGFGKQGFQCC VCCFVVKRCHEFVTFSCPGCG*GDPTL DDPRRQATRFKIHTYGSPTFCDH/CVGS LLYGLIHQGMKCDTCDMNVHKQCVALN VPSLCGMVHTEKRGRIYLKAEVADEKL HVTVRDAKNLIPMDPNGLSDPYVKLLI PDPKINESKQKTKTIRSTLNPQWNESTF KLKPSDKDRRLSVEIWDWDRTRNDFM GSLSGVSELMKMPASGWYKLLNQEEG EYYNVIPEGDEEGNMELRQKFEKAKLG PAGNKVISPEDRKQPSNNLDRVKLTDF NFLMVLGKGSFGKVMLADRKGTEELYA IKILKDVVIQDDDVECTMVEKRVLALL DKPPFLTQLHSCFQTVDRLYFVMEYVNG GDVLMYHIQVVGKFEQAVFYAAEISIG LFLHKGRIYRDLKLDTVMLDSEGHK IADFGDVQGN*WDGSHGPGTFCGTPD YIAPEHAYQPYGKSVDDWAYGVLLYE MLAGQPPFDGEDELFQSIMEHNVSYP KSLSKEAVSICKGLMTKHPAKRMGCGPE GERDVREHAFFRRIDWEKLENREIQPPFK PKVCGKGAENFDKFFTRGQPVLTTPDQL VIANIDQSDFEFSGSYVNPQFVHPIQSAV |
| 1671 | 9722 | A | 2616 | 1 | 1136 | MTQISNIKQPFAMQHRFFISLLHWTLQIV YPALFLGLCERGRNGRCDQVPEGSVLSL LVWVVPGLAFPEVAPGTCGTSYVPDAQ LHGPEVESKLGDPGSMGTGTQPTRPAQ PAAAEPPALTGPGRVHQEQAVLACGFLG IYHLGAASALCRHGKLVKDVKAFA SAGSLVASVLLTAPEKIECNQFTYKFAE EIRRQSFQAVTPGYDFMARLRSGMESILP PSAHELAQNRLHVSITNAKTRENHLVST FSSREDLIKVLLASSFVPIYAGLKLVEYK GQKWVDGGLTNALPNLPVGRVTISPF GRDISPQDKGQLDLYVNIQKQDIMLSL ANLVRLNQALFPPSKRKMESLYQCGFD DTVKFLLENWFE |
| 1672 | 9723 | A | 2617 | 118 | 1018 | VTARPRASRLKGLVQHGSVPGLHCATA RMKHINLSFAACGFLGIYHLGAASALCR HGKLVKDVKAFAAGASAGSLVASVLLT AP/EKKLEECNQFTYKFSSEEIRRSFGA VTPGYDFMARLRSGMESVLP PSAHELAQNRLHVSITNAKTRENHLVSHFSSRED PQLRSLSPASFVPIYART*SLVEYKIGQ KWVDGGLTNALPHPCPVGRVTISPFSG RLDISPQDKGQLRSVCLISAKQDIMLSL ANLVRLNQALFPPSKRKMESLYQCGFD DTVKFLLENWFGIKCIKVL |
| 1673 | 9724 | A | 2618 | 60 | 388 | GLDSFSATETRRTHNTPEHSQSQEPSNG EPQKEEPAESRDPTPGQQTEDQDTAEI PVRDMEGDLQELASVKHRG*ILDLSISV KVKIIPKEEHCKMPEAGEEQPV |
| 1674 | 9725 | A | 2619 | 1 | 4123 | |
| 1675 | 9726 | A | 262 | 72 | 276 | AIQFSVYICVPGICISPDREKRDRGKDG GRHRTRWRQGE*KGEVGRERRRGRER DRQRDRDRIYSPD |
| 1676 | 9727 | A | 2620 | 71 | 547 | KQIPSLPISRPVLAVMVTMTLKVGAPP MLFIQSVVNSPSCSSESRTTVYFWPPSV SPFMTKLDQSLPTRTPSAGVMLRKVFP PTSREKPTCFSSNA*KELP*GWQESGCSR QCPLSSRETCRASCINESANARGEAVCV LGARVVFLTSETGNS |
| 1677 | 9728 | A | 2621 | 241 | 452 | ENVMLCIIRAKEKNHMITLSYTVKAFGK LKTFFMIYKNKPQKTLSMIRREGNTFNPI KGRFEKNS/AGNIILNGIGLNAF/PIKSEKK VEYLLFFQFSIILEI*INAIK*EK*IKGRFE KNSEVTLY |

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| 1678 | 9729 | A | 2622 | 1014 | 1432 | SARLSLPKCWDYRREPPCPASFLYLKNI LYIIRAKEKNRMITLSYTVKAFGKIENFF MIYNNKPQKMLYMMRTEGNTSNPIKGR FEEPTGNIILNRHKIGCFSEKSEKKVEYLL LLF*FSIILEL*VNAIK*EKLIK |
| 1679 | 9730 | A | 2623 | 55 | 316 | NFWGGGAPKAPPPKKGFFPKIPRGVLNR PPQKEKKLFFPPPVKLGPDKFLKRAPP* TPKFFFFPKP/YKFLGGGGPKSPPPKKR VFSQNPGRGKSPPPKRKKIIFPPPRKIGPP QGFFKKGPPPLFIFFCLFPAFMETTCPSK SLSKKFTTK |
| 1680 | 9731 | A | 2625 | 1 | 963 | PTRPNFHSPHPTSPAAGVSAALRCSGR RSLEVATSLPHSPGPRPAADVKMSSSEE VSWISWFCGLRGNEFFCEVDYHPGT NFNLTDLNKQVPHYRTSSK*SLDPEPD VEELVEDNPNQSDLEQAEMLLWDLIH ARYIPLPTRHRPRCLGKVPKGDGFGYC VPRVYCENPANCPIGLSDIPGEAHGESS YCPQ/CAMDV*HTPSQSRQPSTRMGA*L RATGFPSHGSFMVAIPELPGKRPAPQSF VA/RGFLRGFKIHVPMAYPAGSFQGRPAT FKKPQFKTDSLIPSPTCPAVFCLFSLPT LSGTLYGF |
| 1681 | 9732 | B | 2626 | 44 | 403 | MKALILVGGYGTRLRPLTLSTPKPLVDF CNKPILLHQVEALAAAGVDHVILAVSYM SQVLEKEMKAQEQLGIRISMSHEEEPL GTAGPLALARDLLSETADPFFVLNSDVIC EFPFQAM* |
| 1682 | 9733 | A | 2627 | 159 | 309 | IGPSLALGSKVFLQKKQSLLFIRCWLIA LQDLWPQGWNTAEMGWA*QMG |
| 1683 | 9734 | A | 2628 | 545 | 2302 | AACAPSPRTESSTVSSLPLLECLLGAMK ALILVGGYGTRLS/LTLSTPKPLVDFCN KPILLHQVEALAAAGVDHVILAVSYMSQ VLEKEMKAQEQLGIRISMSHEEEPLGT AGPLALARDLLSETADPFFVLNSDVICDF PFQAMVQFHRHHGQEGSILVTKVEEPSK YGVVCEADTGRIHRFVEKPQVFVSNKI NAGMYILSPAVLQRIQLQPTSIEKEVFI MAKEGQLYAMELQGFWM DIGQPKDFT GMCLFLQSLRQKQPERLC SGPGIVGNVL VDPSARIGQNC SIGPNVSLGPGVVVEDG VCIRRCTVLRDARIRSHSWQESCIGSGG SWKLLTIDQDLMVAQFSTPSLPPTLKVG FLPSAGKEQSVLWVSL EEAEPIDHWGI RVLQPPPRARECAEVRMENVTLGEDVI VNDELAYLNGASVLPKHSIGESVPEPIIH DGGFAEEAVLVVHQVLVDGTSTTGEGM RTALHVPTALPTTKLWGPLLADLWAQG WDTAEMGGGSCCLGRCRGQVRQDLFQ LGQLIGTDIIRIWGVVGSVKSEVAEDVMP LEYSQPTTLLFLRLTRPSRFP |
| 1684 | 9735 | A | 2629 | 124 | 1315 | RARGRARRWECAAGTGQAGCRHLRAR DTPSTSAGAMKALILVGGYGTRLRPLTL STPKPLVDFCNKPILLHQVEALAAAGVD HVILAVSYMSQVLEKEMKAQEQL*IRIS MSHEEEPLGTGVLPLARDLLSETADPF FVLNSDVICDFPFQAMVQFHRHHGQEGS ILVTKVEEPSKYGVVCEADTGRIHRFV EKPQVFVSNKINAGMYILSPAVLRRQLQ PTSIEKEDLPIMGKEGQLYAMELQGFWM DIGQPKDFTGMCLFLQSLRQKQPERLC SGPGIVGNVLVDPSARIGQNC SIGPNVSL GPGVVVEDGVCIRRCTVLRDARIRSHSW VLESCIVGWRCRVGQWVRMENVTLGE DVIVNDELAYLNGASVLPKHSIGESVPEP RIIM |
| 1685 | 9736 | A | 263 | 166 | 396 | PQIPPPGIPRKRENLSREPGG/PNPWGG* A*FPLLEKFLGKKNLGPFGGGPTFPFPF NPNLLGGPKGGDQKAGKKP |

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| 1686 | 9737 | B | 2630 | 162 | 276 | MGRANESNLVIVYHFLQKGVQCRL QLVQVVLQHLLX* |
| 1687 | 9738 | A | 2631 | 2 | 292 | |
| 1688 | 9739 | A | 2632 | 3 | 2111 | SSCGLGGQHGLGAARVRSLFKEARARA PCIVYIDEIDAAGKKRSTTMFGFSNTEEE QTLNQLLVEMDVFYAKIEELKLVNRRAE TGVSLSRCSTQK*KS*NWCILITVFYAAIE ELKLMYPYHGVLCSSRRKLSSCSNKEMT QSEKSQA*YRMTPLGMGTTDHVIVLAST NRADILDGALMRPGRDRHVFDLPTLQ RKGVALSPLRLECSAAITHCGLNLQGS* GARTTMGVRRRAG*FLTESRCVAKAGV QAASAHCNHHLPGA/RKIFEQHLKSLK LTQSSTFYSQLAELTPGFSGADIANICN EAALHAAREGHTSVHTLNFEYAVERV AGPHGFQLWESSGFLPEEWQQLCQTLQ NTPGFSPTALRGREDWRCLCLTENLFSC NHLLCGNRKAFYNSSKAGRTEWEPQA S*KKIHDVLECSGPRADSSCTEWTLTDV WKI*DRK*SLTRTAKKSKILSKEEQVVA FHESGHALEGWMLEH/TEAVMKVSITPR TNAALGFGQMLPKDQHLFTQ/ESSFERR FIALGGRASEHFSLNEVTS/GAQDDLK VTPIAYSMVKQVGMAGPISFPEAQEG LMGIGRRPFNQGLQMMMDHEARLLVA/ KAYRHTKVLQDNLDKLQALANALLEK EVINYEDIEALIGPPPHGPKMIAPQRWI DAQEEKQDLGEEETEETQPPPLGGEPT WPK |
| 1689 | 9740 | A | 2633 | 2 | 2416 | FQANMAVLLLLLRALRRGPGPRPLW GPGPAWSPGFPARPGRPYMASRPPGD LAEAGGRALQSLQRLLTPTFEGINGLLL KQHLVQNPVRLWQLLGGTFYFNTSRLK QKNKEKDKSKGKAPEEDEEERRRRERD DQMYRERLRTLLVIAVVMSSLNALS GGSISWDFVHEMLAKGEVQRVQVPE SDVVEVYLHPGAVVFGRPRLALMYRMQ VANIDKFEEKLRAAEDELNIEAKDRIPVS YKRTGFFGNALYSVGMTAVGLAILWYV FRLAGMTGREGGSAFNQLKMARFTIVD GKMGKGVSKDVAGMHEAKLEVREFV DYLKSPERFLQLGAKVPKGALLGPPGC GKTLLAKAVATEAQVPFLAMAGPEFVE VIGGLGAARVRSLFKEARARAPCIVYIDE IDAVGKKRSTTMSGFSNTEEEQTLNQLL VEMDGMGTTDHVIVLASTNRADILDGA LMRPGRDRHVFDLPTLQERREIFEQHL KSLKLTQSSTFYSQLAELTPRFSVADIA NICNEAALHAAREGHTSVHTLNFEYAV ERVLAGTAKKSKILSKEEQKVVAFHES GVHPLVGMLEHTEAVMKVSITPRTNAA LGFAQMLPRDQHLFTKEQLFERMCMAL GGRASEALSFNEVTS/GAQDDLKVTRIA YSMVKQFGMAPGIGPISFPEAQEGLMI GRRPFSQGLQMMMDHEARLLVAKAYR HTEKVLQDNLDKLQALANALLEKEVIN Y*/EDIEALIGPPPHGPKMIAPQRW/V DAQREKQYLGEEETEETQPPSLGGEPT WPK |
| 1690 | 9741 | A | 2636 | 350 | 1256 | LCLFPLPARKMATNFLAHEKNLVDFK YDDAERRFYEQMNGPVAGC/ASRQENG A/TVILRDIAARENIHKS LAGSSGPGASS GTSGDHGELVVRASLEVENQSLRGVV QELQQAISSEARLNVLEK/TWPGHRA GPQ/TQHVSPMRQ/VEPPSPRSPPTAEG/ DARDDIALFGSDNEEDKGGGTSRE E/RGFREFPGKRPKPRLV/AQLSFLG* NPWDR*KDMAQLEACVRSIQ/LGTGRS WGASKLGAPWATGIRK/LQICVVEDDK |

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| | | | | | | VGTDLLEEEITKFEEHVQSVDAIAFNKI |
| 1691 | 9742 | A | 2637 | 1 | 304 | GKTFDTFCPLGPALVTKDSVADPHTLKI CCRVNGKVQSGNTNQMVFKTEDLIAW VSQDVILTGTTPGVGVFRKPPVFLKKGD EVQCEIEELGVIINKVV |
| 1692 | 9743 | A | 2638 | 1 | 927 | |
| 1693 | 9744 | A | 2639 | 3 | 847 | PSGSDFAAAVVPRLDAVTGASQAQAPAA LDLPPREP*LSAGGPVAAAAARALAAQ LPVLPSEVTFAPVTWPKVVCVGMN YVDHCKEQNPVPKEPIHFKFASSIVGP YDEVVLPPQSQEVDEVELAVVIWKRK ASTSR*SGKGGLPVQSAEAPAPASPSD LTHQHTVPAVPDTRKQSASLLPDTAFPF THLWLALATNMG*QLRDPLP*VLVSPMI *PPVWPNPLP*ATDAMAHVAGFTVAH DVSARDWQMRRNGKQWLL*KTFDTFCP LGA |
| 1694 | 9745 | A | 264 | 3 | 413 | SSYRWPSFPILKTCRGPMAPSLSFPGSFLS GLSVPLPLHHPPCPT*LKAAYPNCQLWP FLASVAPDTAPPECPSCFLLQRAQA/PPF LLDLFPYDC*GLCCT*PHQPRGNPLTPRQ GLWLGLKTHCMGTAKAGPGIPR |
| 1695 | 9746 | A | 2640 | 2 | 562 | ITPRFHLICSDPHNLKICCRVNGEVVQSS NTNQMVFKTEDLIAWVSQ*VTRAVLSAP LHLPHMWRLT*ALHLWLWPLSQPLVSL GPFALLQFVTFYPGDVILTGTTPGVGVF RKPPVFPQGRFSEKQREQGPPKPLAGLPS DLRSTGLCMCV*RKGLTSLWPALLQKG DEVQCEIEELGVIINKVV |
| 1696 | 9747 | A | 2641 | 867 | 1476 | LVPVLRRLPLTSRPASPNQAQEDRLPPP RRQEVNWEGLAGVIGKKGKPIKATDA MAHVGGFTVAHDVSARDWQMRRNGK QWLLGKTFDTFCPLGPALCDQVTGVAD PHNLKICCRVNGEMVPERQTPNQMVIS RQRT*IALGLPSLVTLPPGDVIPNLGPPH LHPGVGVFRKPPVFLAKKGDEVQCEIEEL GVIINKVV |
| 1697 | 9748 | A | 265 | 646 | 1333 | EPGMWQSPPSIGCPHRTGQASCA/SPPS TGLS*IPAFPGWRPAWHLHPLLTSPCTC* L*SLGVFPVPPPPQWSTPSQDLNDIFPV PPSYRWPSFPILKTCRGPMAPSLSFPGSFL SGLSVPLPLHHPPCPT*LKAAYPNCQLW PSSASVAPDTAPPECPLLLCFRGPSPILL TSPICLLRTLQLSPASGESHYPPQGRAV GWA EKPSAWSTRSLALGFPMNNEN |
| 1698 | 9749 | A | 2651 | 28 | 352 | VRVWVGNA GCRLCFRADGVASGVGCA WDGDRMCLPESFIRAPVLSVSTAGPQSS QGSSGRSATPGEGAQGINRTLSPALPSP PMAPPPSYLVGTSPAPHSDDG CW |
| 1699 | 9750 | A | 2652 | 1198 | 1889 | LKLPIFRDLKVQCGWVELENRLTKMLLS TSVLSCFSSRPNMSEVSCNKR YDYLEWP EYFMAVAFLSAQRSKDPYSQVGACIVNS ENKIVGIGYNGKPNGVHNSLFP*RRTPK NKLDTKYPYVCHAE LNAI LNKKFRPDV KRPEVCMFALVPPGK*NGGLSLII/LQAGI KRKLIFHVLINYPG*LTGATAARLLF*YG PGVTFRKFI PKCSKIVIDFDSINSRPSRKL Q |

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| 1700 | 9751 | A | 2655 | 1099 | 1712 | CALGEGNSGHRAFSKDRARLRPGWWSG RAKDELGKPKPLGPS*RRADRR*GQSAC DSSPPSGPGP/TGDGARGRC*AARPGPRA RRRLGPSGEDRSCQMGTEEHGRLW GLSVGPAPKPESAPSSLTCPREETPGRR PPAPQFQSLARSHGIRGAGDKPTEEKSL PQQRHRGGASSVGRGPLGFFPLEEAPLP YPWPPNLQ |
| 1701 | 9752 | A | 2656 | 1 | 900 | |
| 1702 | 9753 | A | 2657 | 465 | 1269 | TSSSCSCHPPNACCRGTSSVLSQKAGQ APHLPGPTGKPLRSSGSLRAVRAPGPIGG GQAPWSDPPVLQAPPRPPQAPRGSWRG AGPRQPGRDAAPRMLLPQPRYRTLQPO RLMPKKNRIAYELLFKAEVGMVPPKKD VPIPKHPELADKNAPNLRVMKPMQVSQ GRGGYVKGQFAWRHFYWYLT*GSK CQLHTEAARLGQP/DIIPTRTRAL*PATG HLSMRARSLEVQRPTAAPSGPSWLSLLQ KGMWTGKNEDLHFRRCR |
| 1703 | 9754 | A | 2658 | 1 | 433 | |
| 1704 | 9755 | B | 2659 | 140 | 480 | MVFEFLYKMCVMAAYFGKISEENIKN NFVLIYELLDEILDFGYPQNSGTALKTFI TQQGIKSQHQTKEEQSQTSTVTGQIGW RREGIKYRRNELFDVLEKVNLLMSPQG S* |
| 1705 | 9756 | A | 266 | 268 | 926 | ASCTPFPTLPVRGRLGYNPDSPGTNAH WAGDNEMSLVGLGPVTKPYPHGALPQG WGSWWVRGLSRTPAVTLSQLCSCVLE TCWGPGEAWFLSPQSVMDLESRSPA DPQDGSGLGVYGLASSWTNVQPTWNTSR IGSACQA/RSEFNKSHLFIFLEGET*GPQK GGGVPPKPHYKAPMQSPGPILWTQPRAP PTGAIYFFLQMGPPWRFSLFGVGG |
| 1706 | 9757 | A | 2660 | 100 | 1674 | SAAMIGGLFIYNHKGVLISRVYRDDIGR NAVDAFRVNVIHARQQVRSPTNIARTS FFHVKRANIWLAAVTKQNVNAAMVFEF LYKMSDEMAAYFGKISEENIKNNFVVH YMELLDEILEFGYPQEFRD/SGALKTFITP AGHSRSSGFRQKEGSSQFTSQVTGQIGW RREGIKYRRNELFDVLESVNLLMSPQG QVLSAHVSGP/VWVMKNYLSGMPECKF GMNDKIVIEKQKGTADETKQEPGSNQL LIDDCTF/HTQCVRLSKFDSERSISFIPPD GEFELMRYRTTKDILPFRVPLVREVGR TKLEVKVVKSNEFKPSLGLQKIEVRIQPP LNTSGVQVICMKGKAKYKAGENSFVW KIKRMAGMKESQIQRGFELLTNDKK KWGC/RPPFPMNFEVPPFAPSGLKVGYL KVLNPKLNYSDDHVIKVVWR*IGRISGIY ENSACKATRQLAQLPQPPFLQVQVPLL PQTHQVSPSLPALLPSLHQARSLRSGP KQHYKVGPEPALGLPGQGEF |
| 1707 | 9758 | A | 2661 | 1 | 356 | |
| 1708 | 9759 | A | 2662 | 303 | 774 | DPKSCGRWRRGRNGNGELADLQAESHR ARAAGRGLPGALARVQPEAAAAEVGAR CGRGA/VAENSIDFVSRELCAHSIRKLQAH VLLIKAVHGYFDPRENYSDKESLSFMDT MKSTLKERFQFVEVPGNHCVHMSEPQH VASIISFLQCTHTLPAQL |
| 1709 | 9760 | A | 2663 | 572 | 902 | GALARA*PPQQRWVSCPR/GVP/GAL*RE FTMFLSLQAENSIDFISRELCAHSIRKLQA HVLLIK*VAQAGAQRSQLTGYGSLTWA CPPLTTVKSHGTAPPHLLHEPSPTSDLPP SMTLLPGGLPKKDLES |
| 1710 | 9761 | A | 2664 | 1 | 398 | PNPLSTQMGTSGGKGHQLLEYSPPGGGP PPGPRKQFHCSPPPNPASGKKGH/SPPL /SPHSFSKVKFNQAPPPPTPTPKQERKS* LKMLFNFSAPVDPTPAQMAPPGLFVPS SPPLHRLPPQAWGQRHSQQ |

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| 1711 | 9762 | A | 2665 | 119 | 496 | TGAVSFQMPEETQTQDQPMEEEEVETFA FQAEIAQLMSLIINTFYSNKEIFLRELISNS SD/GEPMGRGTKVILHLKEDQTEYLEERR IKEIVKKHSQFIGYPITLFVEKERDKEVSD DEAEKEDN |
| 1712 | 9763 | A | 2666 | 1 | 235 | |
| 1713 | 9764 | A | 2667 | 1 | 2424 | RKVREASGKSAARWAGPSLYKAGAGV ARQLLRPGVAVPLVLCGHLAKMPEET QTQDQPMEEEEVETFAFQAEIAQWISLII NTF*LETKRSFLRELISNSSDALDKIPVLN A*HDPHSIRPLGKELHITLLPDQTKIRTL TIVDTWNLE*PKADLINNLGTIA/RS LGT KAFMEALQAGADISMIGQFGVGFYPAI YLVAEKVTVITKHNDDEQYAWESSAGG ISFTVRTDTG*TYGSVGTKVILHLKEDQT EYLEERRIKEIVKKHSQFIGYPITLFVEKE RDKEVTDDAPQEKEDKEEEKKEEEKES EDKPEIEDVGSDEEEKKDGDGKKKKKKI KEYIDQEEELNKTPIWTRNPDILTME EYGEFYKSLTNDWEDHLAVK/HFFQFEG QLEFRALLFVPPTVLPFDLFENKKKKNI NIKLYVRRVFIMDNCEELIPEYLNFIIRG VGDSDELPLNISREMLQKPKF*KFSRK NFGPKKCLELFTELAEDKENYKKFYEQ FSKNIKLGHEDSQNRKKLSELLRYYSI ASGDEMVS LKDFCPRMKENQKHYYIT GETKDQVANS AFVERLRKHGLEVIYMIE PIDEYCVPLAKEFEGKTLVSVTKEGLE LPEDEEEKKKQEEKKTKFENLCKIMKDI KAEKKVEKVVVSNRLVTSPPCIVTSTYG WTANMERIMKAQALRDNSTMGYMAAK KHLEINPDHSIIEPLGPKAEADKNDKSV EGILVIWLKETAPPSAFSLAENPRTHAT RIYRMIKPIGLGIDEEDPTADDYQWLLV TEENPPLEIGDDDSRMEEVD |
| 1714 | 9765 | A | 2668 | 524 | 797 | AVSPSEGEQERGERKAGACGSRL*SQHF VRPRWADHLRSGV*DQPGQHGETPVST KNTKISWAWW*ASVIPATREAEAGEWL EPRRRRLQ |
| 1715 | 9766 | C | 2669 | 102 | 323 | |
| 1716 | 9767 | A | 267 | 599 | 1420 | SHLPSLSLLPRIPPEVIVGSEGPVVFFCP WGSCWGLSRTPAVTSLQGLCSCVLETC WGPGEAWFLSPQSVMCDES PRSPADP /RGWKFRVYGLASSGQMCNHLEYSRML VLARHSELISPTYSFEGETE AQRG*GIPP KPHSRNAEPGYTGHTWPLHTGTFTF SSQMRGPSGLDSSGWIKTEGDKEKAPG LMGLKDRDTGTCYGCVCCKPGQGLQA GGVLYLAQPPALIRLPNGPRPARARERR DWHHREETGFLLEATLLKARP |
| 1717 | 9768 | A | 2670 | 146 | 804 | TETRFSDSVAQAGPGTFGPLLLALPRL TFSPLLSFPTVGTCKGNPLWAPKPCPALA APSGCRMTWKEQGRKMGVNC/PRPVAA CMCV*TKRPPSPMFLSPRFSSETRRAA RGSSLPWWAGAWSASSDSPLPRSTAP RRSVCTHCGLTQPTRHACQKGAGVCVR GPRSEAKGGWRGRALLLAATPCPLSCP NLGLPAKVTPEQGLVRRGGRPAGP |
| 1718 | 9769 | A | 2671 | 1 | 787 | LNSRVEPRVRSRTMETKPVITCLKTLLIY SFVFWITGAILLAVGVWGKLTGLGTISLI AENSTNAPYVLIGTGTTIVVFGLF GCFAT CRGSPWMLKLYAMFLSLVFLAELVAGIS GVVLRHEIKDTFLRTYTDAMQTYNGND ERSRAVDHVQRSLE/SCCGVQD\YTWW STSPYFLEHGIPPSCCMNE\TDCNPQLH NLTVAATKV\NQKGCYDLVT*FSWETN MGVHAGSGRLGIVAFSQLIGHAGWACCL SRFHHGPIQY |

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| 1719 | 9770 | A | 2672 | 1 | 670 | YKVLIFT/SPCS/VDQLCSALCSCFRPKDT ER/LRG/APEGFSRTDLHLA/VVPVLTALI SYHNYLDKTKQREMVYRLEQGLIHRCP/ RQCVVALSICSVEMPDIIIKALPVLVVKL THISATASMAVPLLEFLSTLARLPHLYRN FAAEQYASVFAISLPYTNPSKFNYIVCL AHHVIAKPLHRLQSPHLMRWASGSAS SPRWRTSPSLCEAGALPPALALDGIACQ |
| 1720 | 9771 | A | 2673 | 1 | 154 | |
| 1721 | 9772 | A | 2674 | 237 | 410 | |
| 1722 | 9773 | A | 2675 | 1 | 414 | |
| 1723 | 9774 | A | 2676 | 1 | 6371 | MPDSCGLHIPAAHAAPSRDARIAGLSAR GRHRTTTPSKLPRRPSAQCRYRKCGSRF RRRPGARGVRLSPRRGGPERGGAAREGF SGASWSTMAKPTSKDSGLKEKFKILLGL GTPRPNPRSAEGKQTEFIITAEILRELSME CGLNNRIRMIGQICEVAKTKKFEHAVE ALWKAVADLLQPERPLEARHAVLALLK AIVQQGERLGVLRALFFKVIKDYPNSNE DLHERLEVFKALTDNGRHITYLEEELAD FV |
| 1724 | 9775 | A | 2677 | 1 | 5405 | MAKPTSKDSGLKEKFKILLGLGTPRPNP RSAEGKQTEFIITAEILRELSMECGLNNRI RMIGQICEVAKTKKFEHAVEALWKAV ADLLQPERTLEARHAVLALLKAIVQQGQ ERLGVLRALFFKVIQG/DYPSNEDLHER LEVFKALTDNGRHITYLEEELADFLQW MDVGLSSEFLVLVNLVKFNKLVTLDE VQSQRNGFKMICLLCVRTASSVDIEVS LARLLDAVGLANNCLPAESLPLFIV |
| 1725 | 9776 | A | 2678 | 1 | 5469 | GASWSTMAKPTSKDSGLKEKFKILLGLG TPRPNPRSAEGKQTEFIITAEILRELSMEC GLNNRIRMIGQICEVAKTKKFEHAVEA LWKAVADLLQPERTLEARHAVLALLKAI VQQGERLGVLRALFFKVIKDYPNSNEDL HERLEVFKALTDNGRHITYLEEELADFLV LQWMDVGLSSEFLVLVNLVKFNKLVTLDE DEYIARMVQMICLLCVRTASSVDIEVSL QVLDAVVCYNCLPAESLPLFIVTLCRTIN V |
| 1726 | 9777 | A | 2679 | 35 | 239 | SPSSQPPVPVIPH*PVCKQPTSCRSRKR V LNLVGGGEGAASY |
| 1727 | 9778 | A | 268 | 1755 | 2524 | VPWGNPGSESVGLPGGRGLVTAPAVFLP PKPAPGFGAQHVRSRK/PSRRGQLIRAA WLTGSPVRPGQEMLGAGRGASGRAG* GPAPYRKLSSASARGAGHPESGNCSSG SGSTWSSSWGSGSGSSWGSRLSQEMV EEVL/HFIQGGAG*AGGTLQWALVSNLG FGVRQGDIVVVTLLGLHGSIEDGAGVQ GRSEAMEPRQAG/RTEGWLGHSSETP HPPAGTSFCNLRPTVSREAAPAGRRGAE SQTSLPSTSA |
| 1728 | 9779 | A | 2680 | 118 | 359 | AVCKQPTSCRSPPCSPGQASPC*AFRR LEI/CRAGF*A*ALGPGKSQGGNCPRSSP PSP/CPLLYGQNCG*KCPQRLH |
| 1729 | 9780 | A | 2681 | 229 | 455 | TMQGSNLKPLPSP*PRAATKIPNP/SPSP PQAPQTTPHSILSTKAMTPVTIQALFSRI VRYLCDCRDRLTQSF |
| 1730 | 9781 | A | 2682 | 1 | 373 | |

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| 1731 | 9782 | A | 2683 | 72 | 1031 | GCPRLILLRGRSGLEPGTFRKMAAARPSL GRVLPDSSVFLCDMQEKFHNIAYFPQ IVSVGSRMLKVARLLEVPVMLTEQYPQ GLGPTVPEAGD*GPSAAWQKTCFSM/CC LPLQQELDSRPQLRSVLLCGIEAQACILD PRSYPGLALTSYPQNTTWDLDRGLQ VHVVDACSSRSQVDRVALARMRQSG AFLSTSEGLILKLVGDAVHPQFKETQKLI KEPAPDSGLLGLFQQNSLPPLNSNPALR EDHPPVHPGPQWEARFPPSLGFPRVGAIP PGSCRPLVGGGWCCLPQQLPEMQM RLLETGWEMG |
| 1732 | 9783 | B | 2684 | 1 | 792 | MGVLP SYFWDEEA EAQEGICLSLKQRM PVGRAGHSGHFLADATSRALARREEW GKQEERG VKESSESTNTTSRMKTPKEDV RPGMTAFEPEALGNLVEGRTSIDSILKTV SNSFSLGACCLLSFHVLLDGTAGRGSDR DEQNAHSV VPEQQARAHHPHSHIHL GDESACIAYIRTRSTWTLAASHAPPSRRD PCLAPPGWQMADRPLHRSGAPSVLPHSQ DTDTEMNQERYMNASISFPKPPHSTSQQ VLFIQPGEEEREI* |
| 1733 | 9784 | C | 2685 | 10 | 126 | |
| 1734 | 9785 | A | 2686 | 2 | 370 | HCIQQILEAVLHCHQ/MGVVHRDLKAPGE KKNQTLGRAVLLSFT*RRQLSLGLHQLH SLAPSAGTSWISLLIMVSVAGFAGT/PG YLSPEVLRKDPYKGP/VDLWACGG*RFS GPLPGVILYILLV |
| 1735 | 9786 | A | 2687 | 1 | 1593 | |
| 1736 | 9787 | A | 2688 | 3 | 1607 | IPGSTISCSSVKPVLCLHSAARACKWSLG SGAEQQRSLSPGPPVPSLTCLPSARMATIT CTRFTEEYQLFEELGKGAFSVVRRVCVKV LAGQEYAAKINTKKLSARDHQKLEREA RINCRLKHPNIVRLHDSISEEGHHYLIFD LVTGGELVEDIVAREYYSEADASHCIQHI LEAVLHCHQMGMVVHRDLKPENLLASK LKGA AVKLADFGLAIEVEGEQQACVGF AGTPGYLSPEVLRKDPYKGPVDLWACG VILYILLVGYPPFWDEDQHRLYQQIKAG AYDFPSPEWDTVTPEAKDLINKMLTINPS KRITAAEALKHPWISHRSTVASCMRHQE ARGPA*KKFNARRKLGAILSTMLAT RNFSGGKSGGNKSDGVKESSESANTTI EDEATKVRNQEIHKVTEQLIEAISNGDFES YTKMCDPGMTAFEPEALGNLVEGLDFH RFYFENLWYRNSKPVHTTILNPHIHLMG DESACIAYIRITQYLDAGGIPRTAQSEET RVWHRRDGKWOIVHFHRSGAPSVLPH |
| 1737 | 9788 | C | 2689 | 6 | 167 | XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX KH* |
| 1738 | 9789 | A | 269 | 3 | 389 | GVSPCWPGWS*TPDLK*STRLGFPRCWD YRLLEVDPC TGHSLYL*KDPPVLP LPAEG CDYQGKEYALSSCCDKSYLLPDYRTKFL CCHPERGTWKLGTVGGCYAPIQSFGIAD EQAWLQHGSGAVYLC |
| 1739 | 9790 | A | 2690 | 310 | 593 | LQVISEYLFWRINFFLFLF*TVSLSVAQA RVQWRDPGSLQPLLP GFKRFLASASRV ARVTGAHHLHAQL/ILYF*VETGFHHVG QAGLELLTSGK |
| 1740 | 9791 | A | 2691 | 58 | 481 | LQVISEYLFWRINFFLFLF*TVSLSVAQA RVQWRDPGSLQPLPPGSRDS*ASASRVA RVTGAHHLHAQLFCIFK*RQGFHPGWSG WSSNLPDLQANPAASALPKVPGITGTSP LHPPWSINFKNIKIWNQETSILVFFRL |
| 1741 | 9792 | A | 2692 | 1 | 398 | |

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| 1742 | 9793 | A | 2693 | 3 | 267 | AMVGGGGVGGGLENANPLIYQSRGER PVTAGEEDEQVPDSIDAREIFDLIRS*AW PLTPQPAYWYPGPSSCQGCYRCFLESLT MRN |
| 1743 | 9794 | A | 2694 | 1 | 942 | |
| 1744 | 9795 | A | 2695 | 3 | 707 | AMVGGGGVGGGLENANPLIYQSRGER PVTAGEEDEQVPDSIDAREIFDIRRCWAR AGSGGLRWGEQ*YRAAGGAASQQGVP GRGF*VGKGAESLFLHFPQLIRFLNDPVE HSLTLEELNVVEQVRVQVSDPESTVAVA FTPTIPHCSMATLIGLSIKVKLLRSLPQRF KMDVHITPGTHASEHAGKCGLVVRVLA RAPPKQSEASPLHRSWARLEMGNVCVSE IARDSSVWVIA |
| 1745 | 9796 | A | 2696 | 2 | 604 | ARSHRISGGGSAMVGGGGVGGGLEN NPLIYQRFGERPVTAGEEDEQVPDSIDA REVFDLIRSHQMTPEHPALTLEELNVVE QVRVQVSDPESTVAVGFPPKTHSGTCR HGPPILGLSVKVKLLRSLPSAFSRWDVA HLLPGDPLPQEHAVEQATLQIKEAGWAT ALGRTPHLLVVNQCLSSPAPGTWAFV PLSLA |
| 1746 | 9797 | A | 2697 | 79 | 690 | KVSKAIAGCLRNYGVCLAHLRTWAIPEP PKMNPVVEPLSWMLGTWLSDPGAGT YPTLQPFQYLAEVHISHVQAMLNFSF NSFHPDTRKSMHRECGFHFASKPDTNK VGLCQAPQNTGLGWNWKEGEVKRARS LCIRIPLPFARISFRQKPHVEQIT/RGKFR LASEGKL*ADGSPMGNPRHSPMTQHH HDTYQEGEHRKP |
| 1747 | 9798 | A | 2698 | 1 | 405 | |
| 1748 | 9799 | A | 2699 | 1 | 1437 | |
| 1749 | 9800 | A | 27 | 244 | 309 | NPKGQKDREAPLSRSVFLKIKIKRAFAL LLHGRF*PSTPAASASPASKSPRGSGKAL ASALFYIVQLTK |
| 1750 | 9801 | A | 270 | 555 | 1181 | RGPMERPKQMTAVHCQGHQRGDSEIRN FRCHGPNSCTRWGSPPHASASFSTCL*N KPKYFPWGISLFFLSRRSL/DSVAQAR VQWCNLGSLQPLPPRF*QFSCIRLLSS*D YRCMPPCPA/NYL*F**RQGFTI*ARLVLN S*PRDPPVLASQSAGITGVSHQARTFFLF FETTFHSAHAGVQWHDLSLPPPPPRF KRLSCLSLSS |
| 1751 | 9802 | A | 2700 | 78 | 399 | FIHRPSDGGPPAERSPCRGRVCISGKKHS YPSCWYPLPKHTASCPISTSILTPLPLDL RIPLMWKDTHEYFKNKGDHLRWAVFLL QLGEHIQDTEMIIVDRTLTYCI |
| 1752 | 9803 | A | 2701 | 2 | 368 | VVAGALGCSWLIGAGFLSGREGACRR ERGQQQTGTPLPSSLPLLSLEKRAGRTA ATKARLDTLCLEPPLQLAFPPGDPTYPT SLSFSSLPLGLPA/WPPEQQWGEENLSQQP EGV*QELQRDKGSFCPLPKSWPPL*RG GARLQLARNRGWFPVWKGRLQKAGAG TAADRHTPAFLSPSPFSGKASWENSCH QSETGHSVPRAPSAAGLSSWGPHLSSLR FLFLPCLGSRQAPGAAGVGRKFVTAARG GLTGVAEG |
| 1753 | 9804 | A | 2702 | 1 | 588 | VRAGELDQALGRPFTLSISNQYGDDEV HTLQTESREALQSWMEALWQLFFDMSK REGGWVEPLGRTGVCHFY*RPFLQDYV EGNVAGERAAWLSLLISALLPGQWKQC CDEIMKIETPAPRKPPQALAKQGSLEYE MAIEPLDDIAAETDILTQREGARLET WLAMFTDQPALNPCSPASVAPAPDWT HPL |

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| 1754 | 9805 | A | 2703 | 46 | 1825 | AAAGSETGLGSCLEGKGAEGSGDSSRQ AHPCLPLSLSSLLWKSEDELQRKLDHEI RLRKGPCKLLANLLPSEKQALEATKSL LVCNSRLASYMGEILQRARKEAQLLGKT SRRPSDSGPPAER\SPCRGRVCISDLRIPL MWKDEYFKNKGDLHR\WAVFLLQL GAEHQDTEMILVDRTLDISFQSNVLF AEAGPDF*TCGLELYGACVEEEGALTGG PKRLATKLSSSLGRSSGRRVRASLNSAG GSR/GAIPFMLPTPEVGGRYHLLAHTTL TLAAVQDGFRTDHLTLASHEENPAWLPL YGSVCCRLAAQPLCMTQPTASGTLRVQ QAGEMQNWAQVHGVLKGTNLFCYRQP EDADTGEEPLLTIAVNKVMGPLVETRVR AGELDQALGRPFTLSISNQYGDDEVHTHT LQTESRGSTCRAWMEALWQLFFDMSQ WKQCCDEIMKIETPA\PRKPPQALAKQG SL\YHEM\ALFEPLDD\AAVTDILTQREG ARLETPPPWLAMFTDQPALPNPCSPASV APAPDWTHTPLPWGRPTFSLADAVPPDH SPRASLRFAPLPTFSESPRTRGLLQAKGQ PRTWLQSPV |
| 1755 | 9806 | A | 2704 | 1 | 370 | |
| 1756 | 9807 | A | 2705 | 1 | 363 | |
| 1757 | 9808 | A | 2706 | 158 | 301 | IIMTLAEDLLCSAAQNSRLSAQRTQAGW LLISALMTLGNL*KVYIP |
| 1758 | 9809 | A | 2707 | 182 | 395 | |
| 1759 | 9810 | A | 2708 | 1 | 434 | SSYIPFSIQILFPTHTFTL*HPVSWKNC RK*TRENK/ITAELEIFQEGIKVLETLVT VAEEHHRAQLVACLLPILISFLLDENSLG SATSIMRNLHDFALQNLMOIGPQYSSVF KSLVASSPALKARLEAAIKGNQESVKVK I |
| 1760 | 9811 | A | 2709 | 112 | 501 | |
| 1761 | 9812 | A | 271 | 80 | 599 | SIQEKRLGGEQSPFLKELQEGTSWLLM AKLYEAVTFKDVAVIFTEELGLLDPAQ RKLYRDVMLENFRNLL/SQWGINHAMEI LSTS*GKEKLWVMGTSSQ*ERNLGGKIQ TEMETVPEAGTHEEFSCKQIWEQIASDL TRSQDTTISNSQLFEQDDNPSQIKARLST VHTR |
| 1762 | 9813 | A | 2710 | 1298 | 8400 | FPTNTTFPLLKVCYRFHYAEPVPGHCR AGVRREGADWGTGSADKQRPFFLLDY GKVWLAPCAQQNDVREKQKTLVEQLLSL LNSSPGPPTRKLLAKNLAILYSIGDTFSV HEAIDKCNDLIRSKDDSPSYLPTKLAHV VCLGSLYKKLGRILGNTFTDTVGNIKA MKSAESQGRYEIMLSLQNLNGLGAAAA PCHRDVYKAARSCLTDRSMAVRCAA CLLELQNEAIFMWSTDLDVATLCFKSF EGSN |
| 1763 | 9814 | A | 2711 | 2107 | 2424 | TTRYLKKTSTTGQRKKRGRNGSFPTEN LVPSGTVTGSQQLGPPFR*N/HTEECWGP PTADGRAGKGPRQPGRAQRIYRWDP DGTTWHHRPCSGRGTDQPETK |
| 1764 | 9815 | A | 2712 | 1 | 368 | FRREGRPAGAGAGFADSGGAPSSCCGPT VRPVAATAENVLHVGAQFQEPVQCAG VQWRNHGSLRPPPPGSSHPPIAS*VVET TGMCHHVWLIF**NFFVETGSPYVAQAL ILLMLGIKTL |
| 1765 | 9816 | A | 2713 | 1 | 278 | |
| 1766 | 9817 | A | 2714 | 188 | 406 | |

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| 1767 | 9818 | A | 2715 | 123 | 914 | PRAGGCGSGRVTACLACATLVWPPR FQEVLLVLSGLVHARGCTYSQLWSRSH FCCSRGPLAMAGILFEDIFDVEGY*PEGQ EVWTECSRLHCESESEFRMDLILDVNIQY PVDLGDKFRLVIASLTLYEDGTLDDGEYN PTDDRPSRADQFEYVMYGKIVYRIEGDVE TSTEATR\AAYVS\YGGLL\MRLQGD\A NNL\HGFEVGLPRVYLLMKKLSLLNLAL NQPSLPSHSGRGHCSSLSGQPLFAHLLRK GWLTVHRWRHL |
| 1768 | 9819 | A | 2716 | 1 | 2415 | |
| 1769 | 9820 | A | 2717 | 2 | 964 | |
| 1770 | 9821 | A | 2718 | 276 | 482 | |
| 1771 | 9822 | A | 2719 | 329 | 3354 | PVRQFIFPKLPIRHCLAEVGGRGQTCAP PRKWAVPIGLHSRATSQSGCGGGRSWL CSSLKMAAQPPRGIRLSALCPKFLHTNST SHTWGHVSQLELIG*CLWIPDVNAKQI WGLTKQWINDHICLTFDNGNGMTSDK LHKMLSFGFSDKVTMNGHVPVGLYNGG FKSGSMRLGKDAIVFTKNGESMSVGLL SQTYLAEVIKAEHVVPVIAFNKHRQMIN LAESKASLAAILEHSLFSTEOKLLAELDA |
| 1772 | 9823 | A | 272 | 1321 | 1913 | VEMRRNQCKNSSNSNGLCVICPSNNHTS SPTRVLATWMNCLELHKYNV*IWIGKKII *TQENGKTQSEENKNNIKVLQELKDKVA GIIKKNLTDLNAPKNTLLEFHNAFTSINS RK/DKSDERISELEDWVSNIRWTKVN*NE QILHGGWDDIMRPILQITGISEREVEKSN NLENVVQDIIFESFPNLARKANSQIQE |
| 1773 | 9824 | A | 2720 | 1135 | 1476 | HGVSLLLPRLECTGH/VISAHCDPRLPGF ERFSCLSLPSSWDYRHAPTHAQAKFCI FKWRRGFSHVGGAG*HFYFPSQVLGTN MEDFFLTGLLHGLFQEDSNAPYSFKWG SLR |
| 1774 | 9825 | A | 2721 | 670 | 1253 | ACYALNLFPKHTDIFYFFIYFFCRDRGP RYITQAGLKFDVK*ILPPWPYQSVGHISV SHPPGPH*CILNAINKNYRYRN*LLY/IQ YPMLFGVFLRQGFAVT/SAAVQWYDHG SMQPQLPGLRWFSHLSSGWEHRRTPP RLG*FCIFSRESFVMLPRLVLNSWGSNDT PALASQSVVITGMSHHAPAFPMFLF |
| 1775 | 9826 | C | 2725 | 95 | 310 | MREYNLVVLGSGGVGKSALTQFVQGI FVEKYDPTIEDSYRKQVEVDCQCML LDTAGTLPRLTTYRT* |
| 1776 | 9827 | A | 2726 | 1 | 1101 | |
| 1777 | 9828 | A | 2727 | 53 | 772 | IPRSGITGSEGDPVYKSMCLTAPSMALS RSSVFKQITSLREYKLVVLGS*GVGKSAL TVQFVHGIFVEKYDPSIEDSYRKQVEVD CQQCMLEILADTAGTEQFTAMRDLYMKN GQGFALSIFYLQLQSTFNGLYRDLEGNQ ILRV*GTRE/VMFPMILVGKCDLEDERV VGKEQGQNARQWCTLALLESA/RRSE IQVNEVLAYDPVRQINREY/TPVEKKKPK NSMSTLLGPVRRQL |
| 1778 | 9829 | A | 2728 | 377 | 615 | VPAQCSF*DTASCLLVKRMRLDAVAH AYNPSTLGGGGWI/TRGQEFKTSANM VKPVSTKNKKISRVVWHNRNPSYSGG |

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| 1779 | 9830 | B | 2729 | 1 | 1224 | MPTVGKAQARRRTRDLLLLDITQVLIDQ SPRKDTGLAQQTGVIVPSKGIVKYWRAQ LKGDMMKYASPAFELFYFSVRAQSTDGIV TLLDPTTREDCDISSAPNPEVRTQRQAEV AGVGLLAVKVPRDEEGVLGGAPGPQKR SRVCGEPTLQRRSGPLPVARPGSRCPPT SVSSPVPEDYGRVVMIRLDNPGISGRT IENNPPLEKQLPGEPSENSPYLGPVQLF LLRDPREDVMLLLNQPTTTAEKQAVLQ AAEIFRNEQQISYNTSKGKKGDRECEIA ETPFQIGSEAVPLDNPWNSSSSAGEWK RRHFLICILEGLERTKAKFLNCSKLSMVD QKPDENPAAFMERLREALIEQTSLSPDSV EKQLILKDKFVTQSASNIRRLKQQAIGP ISTLKNLLK* |
| 1780 | 9831 | A | 273 | 193 | 310 | |
| 1781 | 9832 | A | 2730 | 877 | 1536 | TNFLFALSPSCLAGLLPPKFQFSCSLLS SWDYRNFIYIFW*RWGFTMLARLVNS*P Q/CDPHTSASHSAGITGMSHCAWS*TLNF FSYELFFSFTSALS*KDHCKGGHNMGCQ FT*MHQ*L*EKPP*LLFETESRVA/QAG VQWRNLGSLQPPSPGFKRFSCLSLPSSW DYLRTPPRPANCCIFSRDGVSPCWPGW SQSLDLVICPPWPVKVLGLQA |
| 1782 | 9833 | A | 2731 | 3 | 643 | RLEEDLGRRLAPVGVVETVYFTVVL WITTMGIQAGSVLFGALLVLAVLCVHS GH*PCQC/YNGFLPQTADCQKQPFNCSS GFWMRVFITQKLGYQVYNKICWKFHC NFNDRHNP*A*RKMGILTLLCKKG/LRCN FTEARLENGGTSASEKTVLLGELHFWA AAWEPSIPKSNTRCFLTKLPRSLRSSVF PLGWPHSKGLDIFQMGSWLGKE |
| 1783 | 9834 | A | 2732 | 11 | 431 | RHLLAAPPAPPAAPAAAAALSHCLRSSG RLAPHTSRRLPRVVKRRVNALKNLQVK CAQIEAKFYEEVHDLERKYAVLYQPLFD KRFEIHAIYEPTTEEECEWKPDDEEISEE LKEKAKIVDEKKDEEKEDPKGIPEFW |
| 1784 | 9835 | C | 2733 | 257 | 358 | MILLVFLPXHQVFLERXQSEILHHLNTL ADVL* |
| 1785 | 9836 | A | 2734 | 2 | 387 | |
| 1786 | 9837 | A | 2735 | 64 | 467 | PAAWLPILVAARQLTVQMMQNPQILAA LQERLDGLVETPTGYIESLPRVVKRRVN ALKNLQVKCAQIEAKFYEEVHDLQRY AVLYQPLFDKRFEIHAIYEPTTEEECEWK PDEEISEELKEKAKIEDEKKD |
| 1787 | 9838 | A | 2736 | 1 | 795 | |
| 1788 | 9839 | A | 2737 | 1 | 982 | |
| 1789 | 9840 | A | 2738 | 2 | 138 | SARGAASCSSRCCRCRPESLPAQLRAA WLPILVADIWSSYNMADIDNKEQSELDQ DLDDVEEVEEETGEETKLKARSA*LFR MMQNPQILAAALQERLDG/LWVETPTG YIESLPRVVKRRVNALKNLQVKCAQKE TQFYEEVHDLERKYAVLYQPLFDKRFE IHAIYEPT/EKECEWETR*RKDEDFGGN WKEKGQIEDEKKDEEKEDPKG/IFPEFW LTVFKWVDLLSDMVQEHDEPILKHLKDI KVKFSDAGQPMFVLEFHFEPNEYFTNE VLTCTYMRSEPDSDPFSDFGPEIMGC TRVPR*DWKKGKNVTLKTIKKQKHKG RGTVPYCDLKPVSNDSFFNFGPLPESSL RSGDLDDAEAVLAADFIEGHFYRERIIP RSVVNFTGEAIEDDDDDYDEEGR*RS* GRLAPHTSRRYLEFLQHGRH |

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| 1790 | 9841 | A | 2739 | 1 | 435 | PRARAERPAPASCSSTSTRITPTDTEVC IVERLFSSSLVAIVSLKAPRKLKVCHFCK GTEICNYSYSNTILAVKLNQRQLIVCLEE SLYIHNIRDMKVLHTIRETPPNPAGLCAL SINNDNCYLAYPGS*SGEAGAGQLLFAN FNQDNTDTEVCIVERLFSSSLVAIVSLK APRKLKVCHFCKGTEICNYSYSNTILAV KLNQRQLIVCLEESLYIHNIRDMKVLHTI RETPPNPAGLCALSINNDNCYLAYPGSA TIGEVQVFDINLR |
| 1791 | 9842 | A | 274 | 831 | 1102 | HFGRPRQVDCSSGVQDQPGQHGEVQS VLKLKLAGHGAHL*SQLLWRLRHEN HLNLGGRGCSEPRWCHFTPWTTEQDS V*NNNNNNK |
| 1792 | 9843 | A | 2740 | 3 | 438 | |
| 1793 | 9844 | A | 2741 | 1 | 1336 | MLLRLQRIKTLRPPGCPHMTTCSAGTLS AVPCVSPRQVVFERRFCLWHSVEMFT HVLFPVISADTEVCIVERLFSSSLVAIVS LKAPRKLKVCHFCKGTEICNYSYSNTI LAVKFNRQLIVCLEESLYIHNIRDMKVL HTIRETPPNPAGLCALSINNDNCYLAYPG SATIGEVQVFDINLRAANMIPAHDSPLA ALAFDASGKLTASEKGTVIRVFSIPEG QKLFERRGVKRCVCSICPLAFSMDGMF LSASNTEDTVHIFKLETVKEKPPEEPTT WTGYFGKVLMASTSYLPSQVTNMFNQ GRAFATVRLPFCGHKNILLG*PTIQKIPR LLVGAADGYLYMYNLDPOEGAGECAL MKQHRLDGSLTNEILDSASHDCPLVT QTYGAAAGKAYTDDLGAVGGAACLEDE ASALRLDEDEHPPMIIRD |
| 1794 | 9845 | A | 2742 | 152 | 1616 | VQDPSPSRARPPRPGPLAARPAMNLSAQ SGEAGAGQLLFANFNQDNTNTEVKASRA AGLGRRAVWWSLAVGSKSGYKFFSLSS VDKLEQIYECDTEVCIVERLFSSSLVAI VSLKAPRKLKVCHFCKGTEICNYSYSN NTILAVKLNQRQLIVCLEESLYIHNIRDM KVLHTIRETPPNPAGLCALSINNDNCY LAYPGSATIGEVQVFDINLRAANMI PAHDSPLAALAFDASGT*LATASEKGT VIRVFSIPEGQKLFERRGVKRCVCSICSL AFSMDGMFLSASNTETVHIFKLETVKE KPPEEPTTWTGYFGKVLMASTSYLPSQV TEMFNQGRAFATVRLPFCGHKNICSLATI QKIPRLLVGAADGYLYMYNLDPOEGGE CALMKQHRLDGSLGKRPNEILDSASH DCPLVTSDITAQLAGKGTYPVSSPTETCP TRDDVGAVGGAACLEDEGPAALRLDEDS EHPPMILRTD |
| 1795 | 9846 | A | 2743 | 122 | 1162 | LGLEGGASQWVGGRQLQDCRNRSL QGSPETLIPP/SLQITVPSRTCFP/SLQVGL T/FPPRAVPSAAAALGRNLRL*RGWHRRI IPPVWASISRAASSWG/TKPPLFKVPSQPE TLGETWVIKAMAGTYGGSNTLPRSPGG NFRSTVPR*VQTTPRQPGAGLPKPVVVA TSSD*QASRSSPGRSRKDGPSFPALPVS/ RGEPEPSLQPPPPSTR*PSRLRGPRPSPA LSGPLRAPEHAQSSTSPSRWTTSPRMLR APARAPPCPSPTLVVSTPSPFP*RSQ* SGHTPGRFFPCSPPRIRASACASLSTTD GSTAYQIAHAPHHVFLTSLRAFLRLAGS CTNHG |
| 1796 | 9847 | A | 2748 | 54 | 188 | NMTKLQVVSKNLLLLKMLIKERETQRK GGSS*KSTQGAKGGAPR |
| 1797 | 9848 | A | 2749 | 572 | 857 | GQKKGFSGMG*GEKGLGNPSWGTAGG QAPVPPQGLTGTRFTQGSSGTAGPPAST FCLGGHGAUVGTYGRQMYMYEFVFC VGVAQKKDLCPRE |

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| 1798 | 9849 | B | 275 | 53 | 403 | ALVTEFQETHSQDAIEHVLNLANFAYD PSNYQYLRQLQVLHFLDSLSENETLV EFAIGGLCNLCPRANKEHILHAGGVPLI INCLSSPNEETVLSVITTLMHLSPPGRSFL P* |
| 1799 | 9850 | A | 2750 | 3 | 127 | |
| 1800 | 9851 | A | 2751 | 1 | 359 | LILVKAAAALDTGHLSPWFGVRCAFQNP GRRGCS/PEGKQLQSRVI*G*EFQSTAAC EEHYMASIRRSVSPSLSVCTSPPLPSVDIL PPTDLYFEQHSPIL*LKVKGSLH*RSSPLR KES |
| 1801 | 9852 | A | 2752 | 1 | 1270 | MGATTMDQKSLWAGVVVLLLLQGEMG FCYVARAGLELLGSRPPASASQSAGITG SAYKLVCYFTNWSQDRQEPGKFTPENID PFLCSHLIYSFASIENNKVIHKDKSEVMLY QTINSLKTKNPKLKILLSIGGYLFGSKGF HPMVDSSSTRLEFINSIHLFRNHNFDGLD VSWIYPDQKENTHFTVLIHELAEAFQKD FTKSTKERLLLTAGVSAGRQMDNSYQV EKLAKDLDFINLLSFDHGSWEKPLITGH NSPLSKGWQDRGPSSYNNVEYAVGYWI HKGMPSEKVVMGIPITYGHSFTLASAETT VGAPASGPGAAGPITESSGLAYYEICQF LKGAKVTRGSRDQQVPYAVKGNQWVG YDDVKSMGDQGSVL*RFKTWGGAMIW SIDMDDFTGKSCNQGPYPLVQAVKRSLSL |
| 1802 | 9853 | A | 2753 | 385 | 570 | KLGEQDKGRIILLVWAKLHQLSY*HI RVLSIGGN*GPGE*MGMPGVHLLFFRT KIRIQI |
| 1803 | 9854 | A | 2754 | 1 | 1022 | MTLAPSDQDLFVFRSGPPAAAGMPCLF PEVPFCTRVHQPTGRDGSKNLLNELFIAC PGGLMAQGPLDPTESSVPNTKALCGIFS DVAATAENRQTFMQSAIQFLRKYNFDG LDIDWEYPCNRGSPADTQQLFTILLKEM YEAFAQESTRSKKPRLLMSAAVSAGKGT IETACQIPEMSSSTPSRKEPPRVWNAPE VPYVYKGNQWIRYDNSKSFTLKAVLPH SKDKV*TTEFFALLCLSPAHGKFTQAEPK SGGDRASGLLQSTHLYPGHQAAPITAA PGGGSTGGSGFCTGKSKGLYPVPHSKH AFYNCVDEHTYEEACQEGLVFDTSCASC CNWA |
| 1804 | 9855 | B | 2755 | 143 | 867 | XVVVLLLLQGGSAYKLVCYFTNWSQDR QEPGKFTPENIDPFLCSHLIYSFASIENNK VIHKDKSEVMLYQTINSLKTKNPKLKILL SIGGYLFGSKGFHPMVDSSSTRLEFINSII LFLRNHNFDGLDVSWIYPDQKENTHFTV LIHELAEAFQKDFTKSTKERLLLTAGVSA GRQMDNSYQVEKLAKDLDFINLLSFDH HGSWEKPLITGDNPSPLSKGWQDRGPSSY YNCEICCGVLD* |
| 1805 | 9856 | A | 2756 | 2 | 394 | CSAHSTALRVVRNHFYFTITATQVHKGS SSHPCDRGNEMMASSQPQSAFGIPGWG AR*PAPAPLPHRRGLPGSVTG*WRPIVGQ */PSPHTHCKASTKAQPEPGTPPPGKPS WKELPESHKKSLAPSPF |
| 1806 | 9857 | A | 2757 | 499 | 1592 | QPSQPFLSAGLNQTVPWGTCLHRAELSP STENSSQLDFEDVWNSSYGVNDSFPDG DYDANLEAAAPCHSCNLLDDSAFFIL NQCSWGILASRTGLFMPFRPFRRWQLCP G\WPVLGTAGCGAVAFQHLWVPVFGP QGYGS\TRSSALL*LGATGVWYGSAFAQ ALL\GC\HASLGHRLGAGQVQGLTLGL TVGIWGVAAALLTLPVTLASGASGGLCTL IYSTELKALQATHTVACLAIFVLPLGL FGA\KGLKEGIGLMGPGPLDEISLWA\WF IFWWPHGVVLGLDFLVR\SKRLLSTCL AQQALDLLLNLAELAILHCVGTPLLLA |

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| | | | | | | LFCHQATRLLPSLPLEGWFFHLDTLGS KS |
| 1807 | 9858 | A | 2758 | 1541 | 1830 | KRFLHLHQHTSGKSGRGFHLCCCGFSS KSP/GS*PGAGGASSSSQSKSPGPRPARV RRRLWVRAPPATSQEEASAGRRVRPPSS VHVNIPPPSVRPA |
| 1808 | 9859 | B | 2759 | 4 | 1698 | MGDFNTPLSTLDRSMRQKVNKDIQELNS ALHHMDLIDIYRTLHPKSTEYTFPSAPQR TYSKIDHIVGSKALLSKCKRTEIITNCLSD HSAIKLELRIKLTQNHSTWKLNNWLL NDYWVHNEMKAEIKMFFETNEIKDTTY QNLWDTFKATLNQEEVESLNRPTGSEIQ AMINSLGTKKLQDQTSQPSSTRDDMIV YLENPIVSAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSKLPFTIASK IHKYLGVLTRDVKDPFKENYKPLLNEIK EDTNKWKNI PCSWIGRINIMKMAILPKVI YRFNAIPIKLPMTFFTELEKSTLKFIWNQ KRACIARSILSQRNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWNITEPSET MPHIYHYLIFEKPDKNKKWGKDSL FNK WCWENWLATCRKLKLDPFLTPYTKINS RWIKDLNVRPKTINTLEENLGNTIQDIGM GKDFMSKTPKAMATKAKIDKWDLIKLLK SFCTAKETTTRVNRQPTWEKIFAIYSSD KGLISRIYKELKQIYKKKTTTPSTSG* |
| 1809 | 9860 | A | 276 | 842 | 2432 | SLISCSEGS SPKASGPSS*EHCPAKPLGPG TWLLTPGPESGGGGPDVGLRAGQPMN AAPV*SSPCL*N/PGFLTSPGVSSV*MPVL LKEPAFQMAEKAPNGAVCAP/SFPASTS GLWSPAVGVPRSRSLHGSALPWGHAPR Q/SGYPGQSAPAGCGPRPPGGGSRSPGR SVPGSGAWRWPRGRSEACTAPRAWRSA LGESCPAGSGA*AW*WQTAPSPHWGW IGS***VGHLLRAGCAPCWPCLTGTGCTG LPSRSGHKSLSLSVQQVQWLIRFFPLS* M*KPAACLPS*RERPSCAHWTAGGVMG FLSV*SVIR*SLSHCLAAESSPHPGAPQG TATQIGGGGSRVYVQRG*NHRPCRS*PIQR PCGQAGSGGRVASTWCAQ*QTPPGSHSP PTANREINPGPAAAADTRSCWGHKRSW RGWRGLAPWRLGFGSPWNSRDQGPAGI PAARRGGPTFGFLAHGPR*RRTPRDGRE GKGAGAKPSETLTRSPVVRGKRGSA NGFLSWVQILQYFAAGNGIWEMGRGLRI L |
| 1810 | 9861 | B | 2760 | 1 | 1044 | MGRNRSRKDENSKNQSASSPPKDRSSSP ATEQSWMENDFDELTEVGFRRLNQEEV ESLNRPIRGSEIEAIINSLPTKKSPPGDGFT AEFYRRYKEELVPFLKLQSYEKEVILP NSFYEAIIIPKPGRDTTKKENFRPISLM NINAKILNKILANQIPQHIKKLNHEDQVG FIPGMQALFHIQESINVIHINRTKDKNHI IISIDA EKAFDKIQRFMLKTLNKLDDMI VYLENPIVSAQNLLKLISNFSKVSQYKIN VQKSQAFLYTNNRQTESQIMSELPFTIAT KRIKYLGIELTRDVKDLFKENYKPLLNQI KEDTNKWKNI PCSWIGRINIVKRATLPK* |

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| 1811 | 9862 | A | 2761 | 1331 | 2175 | TEPKTKTT*LSQ*MQKRPLTKFNNPSC*K LSIN/IVLEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIISAQNLLKLISN FSKVSGYKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPCSWIGRIN IVKMAILPKVIYRFNAIPKLPMTFFTELE KTTLKFIWNQKRARITKSILSQKNKAGGI TLPDLKLYYKAIVTKTAWYCYQNRDID QWNRTEP*EIMLHIYNLYIF |
| 1812 | 9863 | B | 2762 | 1 | 2898 | MRQKVNKDTQELNSALHQEDLIDIYRTL HPKSTEYTFFSAPHHTYSKTDHIVGSKAL LSKCKRTEIITNCLSDHSAIKLELTIKKLT QNHSTTWKLNLLNDYWVNNEMKAEI KMFFETNKNKDDTTYQNLWDTFKAVCKG KFIALNAHKRKQERSKIDTLTAQLKELE KQEQTHSKASRRQETIKIRAEKETETQK TLQKINESRSWFFERINKIDRPLARLTK KRKKNQIDAINKDKGDITDPTEIQTII |
| 1813 | 9864 | A | 2763 | 3 | 668 | |
| 1814 | 9865 | B | 2764 | 64 | 1242 | MINS LGTKKLQDQTD SQPSSTRDDMIVY LENPIVSAQNLLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSKLPFTIASKII KYLGVQLTRDVKDPFKENYKPLLNEIKE DTNKWKNIPCSWIGRINIMKMAILPKVIY RFNAIPKLPMTFFTELEKSTLKFIWNQK RACIARSILSQRNKAGGITLPDFKLYYKA TVTKTAWYQYQNRDIDQWNITEPSETM PHIYHYLIFEKPKDNKKWGKDSL FNKWC WENWLATCRKKLDPFLTPYTKINSRWI KDLNVRPKTINTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIKLSF CTAKETTRVNRQPTWEKIFAIYSSDKG LISRIYKELKQIYKKKTTPTSTSG* |
| 1815 | 9866 | B | 2765 | 287 | 898 | MNINAKILNKILANQIPQHKKLNHEDQV GFIPGMQALFHIQESINVIHHNRTKDKN HIIISIDA EKAFDKIQRFMLKTLNKLDD MIVYLENPIVSAQNLLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQIMSELPFTI ATKRIKYLGIELTRDVKDLFKENYKPLL NQIKEDTNKWKNIPCSWIGRINIVKRATL PK* |
| 1816 | 9867 | B | 2766 | 1 | 1443 | MKLPEEASGSNICCYAIFAVLQPLLVIPK ETVSGVDLQQTPTDLQLSDLTPGRKTNK QKGIASPSTKRTSTPKPHLQANAQRFCF HQACVTRVPKGSTKHGKEQLVPATAKT CQIVKNINAMKKLHQLTEIQTIREYHKH LYANKLKNLEEMDKFLDTYTLPRLKQEE VESLNRPIMGSEIEAIINSLPTKSPGPDG FTAKFYERYKEELVSFLKLFQSIEKEGIL PNSFYEASHILPKPGRDITKKENFRPISLK NIDAKILNKILANRIRQPIEKLIHHDQVGF IPEMKGWFKCKSINVIHHNQTNNDKNH MIISIDA EKAFDKTQPPMLKTLNKLGTI RQKKEIKGIQLGKEEVKLSLFADDMIVY LENSIVSAQNLLKLISNFSKVSRYKINLQ KSQAFLYTNNRHMESQITSELPFTIDTKR IKYLGIQFTRDVKDLFKENYKLLLNEIKE DTNKWKNIPCSWIEESIS* |
| 1817 | 9868 | A | 2767 | 1 | 966 | |
| 1818 | 9869 | A | 2768 | 1 | 216 | |
| 1819 | 9870 | A | 2769 | 3 | 2074 | |
| 1820 | 9871 | A | 277 | 721 | 1027 | |

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| 1821 | 9872 | A | 2770 | 1 | 1632 | MHCILPTPSGSGSPVYTSQSQPKTPGAF SGTLSVREPLSPEPDVLLPGSAKCAALC WVSVLDAAASPVTRWPVSRSPWECRCV PSPPVREAPVSPPFQCAPPYTDCLSPYL YEYTVCPSPCARVPIPSSTHPWEYKVPPP HAERLCPVSEDPCLCNWKTRAAGARES SLVPCPYAARYPPSPPRVAWSSHFSYRG LSPSLGPNKPGNPRGPSESPAAAASRPRA AAASAPPPGAARLPASPTPRLARDRGVS |
| 1822 | 9873 | A | 2771 | 842 | 2353 | TEPKTKTT*LSQ*MQKRPLTKFNNPSC*K LSIN/IVLEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIISAQNLLKLISN FSKVSGYKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLATRDVKDLF KENYKLAFLIKEIREDTNKWKNI PCSWIG RMNIMKMAILPKVIYRFNAILIKLPLTSFT KLEKTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKAIVTKTAWYCYQN RDIDQWNRTEP*EIMLHIYNYLIFDKPEK NKQWGKDSL FNKWCWENWLTICRKLK LDPFLT SYTKINSRWIKDLNVRPKTIKTP EENLGNTIQDIGMGKDFMTKTPKAMAT KAKIDK WDLIKLSFCTAQETTIRVNRQP TEWEKISAIYSSDKGLISRIYKELKQIYKT KTNNPIKKWAKDMNRHFSKEDIYAAKR HMKKCSSSLAIREMQIKTTMRYHLTPVR MAII/RIKSGNNRCWRGCGEI |
| 1823 | 9874 | A | 2776 | 3 | 2077 | |
| 1824 | 9875 | A | 2777 | 3 | 1038 | TAEGTWIAVRRRLRLEGTGGEMSRVPAFL SAAEEVHLRSSSLIPPLETALANFSSGP EGGVMPQVPTVVPVTKHRGYLGVMMPA YSAAEDALTTLVTLRGPRHHLRSLP TRVIVVTLSPAMGTLLAVMDGKCS*IA KRTAAVSVCHLPPSFLKPPSSEVLCLGAG VQAYSHYEIFTEQFSFKEVRIWNRTKEN AEKFADTVQGEVRVCSSVQEA VAGADV IITVTLATPEILFGEVVKPGAHINAVGA SRPDWRELDDELMKEAVLYVDSQEAAL KESGDVLLSGAEIFA*AGEK*FKGVKPS /YCEKTPRC SKSLGMAVEDTVAAQTHP MIPWSSGK |
| 1825 | 9876 | A | 2778 | 2 | 2037 | |
| 1826 | 9877 | A | 2779 | 3 | 194 | TFFQVKPDGTYVKPLSNKLTGYTMV FVRSFLVGEAARALS KACTIAIRYSAVR HQSEIKPG |
| 1827 | 9878 | A | 278 | 615 | 2182 | PQVIRPPWPKVLGLQGLLTFRDVAIEFS QEEWKCLDPAQRTLYRDVMLENYRNLV SLDTSSKMMKMFSSTGQGNTEVVHTG TLQIHASHHIGDTCFQEIEKDIHDFVFQW QENETNGHEALMTK/YQKVDECTERHD QRHAGNKPLKMSLDQAFIRICLKCTYFT PKGKLVIKLRLSTMLS/HVSASQRISCRP KTRISNKYRNNFLQSSLLTQKREVHTRE KSFQRNESGKAFNGSSLLKKHQIHLGD KQYKCDVCGKDFHQKRYLACHRCTG ENPYTCNECGKTFSHNSALLVHKAIHTG EKPYKCNECGKVFNQSSNLARHHRVHT GEKPYKCEEDKVFSRKS TLERHRIHT GEKPYKCKVCDKAFRRD SHLAQHIVIH TGEKPYKCNECGKTFVQIHLVMHKVLA HTGEKRYKCNECGKVFNHKS NLACHP* TSIPGRETTVRVMECGQGFNRKSNLER HHRLHTGKKS*KC/EICKVFRQSSNLAC HHRLYTGEKPYKCEEDKSFQFQITP |
| 1828 | 9879 | A | 2780 | 1 | 903 | |
| 1829 | 9880 | A | 2781 | 133 | 402 | |
| 1830 | 9881 | A | 2782 | 2 | 242 | |

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| 1831 | 9882 | A | 2783 | 26 | 2229 | RFRAGAADLDCHCHLGRCLLRQCLVVA MNPDLRRERDSASFNPPELLTHTLDGSPE KTRRRREIENMILNDPDFQHEDLNFLTR SQRYEVAVRKSAIMVKMREFGIADPDE IMWFKNFVHRGRPEPLDLHLGMFLPTLL HQVATAEQQERFFMPAWNLEIIGHFIAQ TEMGWHGVTHLSRLSETTATYDPETQEFIL NSPTVTSIKWWPGGLGKTSNHAIVLAQL ITKGKCYGLHAFIVPIREIGTHKPLPGITV GDIGPKFGYDEIDNGYLKMDNHRIPREN MLMKYAQVKPDGTYVKPLSNKLTGT MVFVRSFLVGEAARALS KACTIGILYSA VRHHSEIKPGEPEPLILDFQTQQYKLFPL LATAYAFQFVGAYMKETYHRINEGIGQG DLSELPELHALTAGLKAFTSWTANTGIE ACRMACGGHGYSHCSGLPNIVNFTPSC TFEGENTVMMLQTARFLMKS YDQVHSG KLVCGMVSYLNDLPSQRIQPQQVAVWP TMVDINSPESL TEAYKLRAARLVEIAAK NLQKEVIHRKSKEVAWNLTSDLVRA EAHCHYVVVKLFSEKLLKIQDKAIQAVL KE/SLCLLYSLYGVSQWAGDFLQGSIMT GPQITPSNPAV*RELLTLIRSDAVALVDA FDFQDVTLGSVLGRYDGNVYENLFEW AKNSPLEPKAEVHGIFTRHLEVHCQSQA LEVFRDCKFKSGFQKAPVWQLQILWESF SNSNRL |
| 1832 | 9883 | A | 2784 | 61 | 241 | |
| 1833 | 9884 | A | 2785 | 60 | 341 | |
| 1834 | 9885 | A | 2786 | 70 | 428 | IGGPQGFSP TSLKPRPRIFKTPPIRGNWG PRPPGVSPQFQFGGDTKFNLEILFVVL TFSV*AQSGDPAAPPRSGP/RPGGRGERE G*NEKSPVLPQCWGGWRHPPSAALLW ALIW |
| 1835 | 9886 | A | 2787 | 38 | 243 | TPSTIDKSLTSLIKKKKA*INNFRDCKGN IAKDIPEM*KIIREYYENIHANTFENLGDI DKNKIDQN |
| 1836 | 9887 | A | 2788 | 2 | 114 | |
| 1837 | 9888 | C | 2789 | 50 | 214 | |
| 1838 | 9889 | A | 279 | 403 | 933 | QQRWQQGW WQAWGGQVPVQEVGFWF LLSWLLSRL LGVPAQGPARGVDPRPGS RGARGGCSASAAPPARASPGRPCCWNG SRPPAQHRTSPATRVGEAGQGEVRGVR RLPAPLLQAVQPRLSDRSYPAAPARPTA TSP/APPPSPAPKAPIVGALS*GTADPGSD SYPPSRSHAPRP |
| 1839 | 9890 | A | 2790 | 1 | 624 | |
| 1840 | 9891 | A | 2791 | 2 | 851 | |
| 1841 | 9892 | A | 2792 | 1 | 1116 | |
| 1842 | 9893 | A | 2793 | 53 | 1408 | HRCCLWTFQCLSISLGITFLIKEGKEGKL EPAREGPYLVLLTTETAVLLISITPTTSNS NPTLERFCGLGAEVTGKDPMGFFKVL RQ SLDADEGTAVDIQSFRPQKDFGRRRTLE ECHVTGKGGTGTKMSNRVVCREASHAG SWYTASGPQLNAQLEGWLSQVQSTKRP ARAIAPHAGYTYCGSCAAHAYKQVDPS ITRRIFILGPSHHVPLSRCALSSVDIYRTPL YDLRIDQKIYGELWKTGMFERMSLQ TDE DERSIEMHLPYTA KAMESHKDEFTIPLL VGALSESKEQEFGLFSKYLADPSNLFV VSSDFCHWGQRFRYSYYDESQGEIY*SI EHLDKMGMSIIEQLDPVSFSNYLKKYHN TICGRHPIGVLLNAITELQKNGMNMMSFS FLNYAQSSQCRNWQDSSVS YAAWEHS RATEALNPQGCHLPSSYSVRGSPA |

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| 1843 | 9894 | A | 2794 | 53 | 699 | SLPSLTPPGSRQPPAGRLLNTEHHINEHIL MYSLDLNSSSQMPSIKAQTSDEIFEVD GEMPNHLLPIKAHVEDLGMDDEGDDD PVPPLPNVNAAILKKVVIQWCT/HPHKDD PPPPEDDEEQRSVPDDIPVWDQGIPIGK FDQGTLF*NSFLGLQTYFRTSKGLDVTCTC KTVQCYDQKGKLP*EIRKPPFKSKMTFT EEEEAQVRKVENQWCEEK |
| 1844 | 9895 | A | 2795 | 162 | 522 | WVRRGTISPARQRQDGVGAAPANYAKV LEWQLAPSPRHKCQQRPGTHLGCDSIGP LSPVGLPGLKG*PDNSSEGCPS/QALPVP SSPGHPGSGGPKGQARSLLNCRGCPINW QHRCCRKI |
| 1845 | 9896 | A | 2796 | 2 | 1214 | QPFQSGSCVAILGRKMFSSVAHLARAN PFNTPHLQLVHDGLDLRSSSPGPTGKP RRPRNLAAAAVEEQYSCDYGSGRFFIL CGLGGIISCGTTHLALVPLDLVKCRMK VDPQKYKGNFNGFSVTLKEDGVVRLA KGLAPTFLGYSMQGLCKFGFYEVFKVL YSNMLGEENTYLWRTSLYLAASASAEFF ADIALAPMEAAKVRIQTQPIGYANT*EGI SFPKCIKEKGLKAFYKGVALLWMRQIT YTMN*SSPCLERTV*SHCTSLGVKPRSE VCSKPEQTGCNHLVAGYIARVFCIVVSH PC*FVWYLVLNKE*SVAVSLLVFSVTLT FKGVWKGLFARIIMIGTLTALQWFIYY SVKGYFRT/LPRPPPPRDGQSLNNKFGL TPVVRSKQIVD |
| 1846 | 9897 | A | 2797 | 276 | 728 | CFGFVFPSPWPYGPLSTGDVPLGPPN* AMGGFRPGKQVSLPGFAGGHACSPAS LPSGPGPAPPRACLPSPRGGRKSLGAPGG FPPGDSHGAPCSRVTTVSPGNDLKPGHS PRTLQRGSLPGRRWVWSCGVVCPVW WPVLSASISGWI |
| 1847 | 9898 | A | 2798 | 451 | 1030 | VPEALSPFEMEGPQFPTMCCCSAPPAMP FPTT*QPSEAAAGQGVPGPHRL*GGLAP AGRS*APAGAFWGGQPAQRGEPAYSSK GGAAASTQRVL*HRRGHRGDASRGCP GDQNLQ*KLCSSRAEGGAVSQPGWPAL PHAAAGEPLASALPGLHAAQAPAPAVVSG PTTIRSCSGNSGKIFPSSCLDSCFPFS |
| 1848 | 9899 | A | 2799 | 1 | 933 | |
| 1849 | 9900 | A | 28 | 1230 | 1820 | QEYRPSQTPHLALSPERVAPGRRAAGRL APEARAPRGSP/LPPHRVSEKTIRVVVFH PGARKAGGTPPRAPRGDTGGAPGAPTY STPLMSLHRARLESSSTGSSFPADSAPV PLAVVSLDSR*QWESRSSIHAIVTN*AS SSSSSSSSSVSRVYPRFIEFLHFDIQSTG Q/RITSRQHPPR/DLRDALF*LNSRIPL |
| 1850 | 9901 | B | 280 | 73 | 207 | ELGTQLRTCTLSGLASQVEAHHSLVLS HLKTLWKKISNTKYS* |
| 1851 | 9902 | A | 2800 | 1 | 1563 | MRREGFKFSRSKVVFQDEMTKKWHKSD LHWVSRIQCTVLGVLTNATEMRSLPIES LFLIQCFVVSGASRNEATDCSGECYSSM RETRGSKECAAARFIKVKGVQKQVESY KLYHPYFLANWFSASFVKVGLVEMRG QEEETLGTFAHVLMTFQAASSRALVLPPT MQLELQNFNTCSYRKPNMASSMRSLF SDHGKYVESFRFLNHSTEHCQMQEFM DKKLPGIIGRIDTKSEIKILSIGGAGEI DLQILSKVQAQYPGVCIQH*SCLRPSAG TNWPNYKELVAKTSNLENVKFAWHKE TSSEYQSRMLGEKGAFKSWDFYSI*FKM LYYVKDIPATLKFHSLALGTNAKMLIIV CVQGSSGWDKLWKYGSFPPQDDLC QYITSDDLTQMLDNLGLKYECYDLLSTM DISDCFIDGNENGDLLWDFLTETCNFNA VTAPPDLRAELGKDLAQEPEFS/ALRKEG KVLFNNTLSFVIVIEGITIQSQYIQKLYFE |

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| | | | | | | QLESLIYFHIKITNSSH |
| 1852 | 9903 | A | 2801 | 1 | 6750 | |
| 1853 | 9904 | A | 2802 | 3 | 91 | KKNIN*EILN*KQMEEPTLYVGNFPIQLT |
| 1854 | 9905 | A | 2803 | 3 | 7501 | |
| 1855 | 9906 | A | 2804 | 3 | 3223 | PPPEAAVVAFEWLKSTLTGLHPQLPLSL PQPECALPYLVRAFSRGDYMGRIQEVG WVTAGLVIWAGTCYIIYKFTKGRAQSV RTLARNGSTVKMETVVGVSQTLAINEA EIKTKPQVEIGAETGARSGPRAEVETKAT AIAIHRANSQAKAMVGAEPETQSESQVV AGTLVMTEAVTLTEVKAKAREVAMKEA VTQTDAGKIVKKEAVTQTKAKAWAL VAKTEAKREAMTQTKAETHILAEKETEI NRVMV |
| 1856 | 9907 | A | 2805 | 1 | 374 | NYFLSLRFDWHSSKS*GHPTCVHCF*/TK NE/CASCHCGAGLLGFLGSGEGASHPC PSCLPLEYRSLHCSLGHCGECMPGASGW GPWTGPGHCPNLCQDKGSKRISWRVGR NGWGRPSFDNAPVAL |
| 1857 | 9908 | A | 2806 | 162 | 789 | AGQNGVSGSAERCLSLLIPLALWSHINI LLYIPNGHTFYASSNKLNTNYVWYSERI*L SGIMMLIVTTVLLVLENNNNYKACQSE NCSKKYVTLLSIIFSSLGIAFSGYCLVISA LGSCP*AIC/LAPLMGWGVCF*RALLGRF LTDSSIWDSVPGNLAHVVEWNIILFSILIT LSGVQVHICLIRVVMQLSKILCGSYSVIF QPGII |
| 1858 | 9909 | A | 2807 | 1 | 3282 | |
| 1859 | 9910 | A | 2808 | 136 | 447 | |
| 1860 | 9911 | A | 2809 | 3 | 3593 | SSDPRPSSFVLVWVGLWSMVWRVPPFL LPILFLASHVGAAVDLTLLANLRLTDPQR FFLTCVSGEAGAGRGSDAWGPPLLEKD DRIVRTPPGPPLRLARNGSHQVTLRGFSK PSDLVGVFSCVGGAGARRTRVIYVHNSP GAHLLPDKVTHTVNKGDTAVLSARVHK EKQTDVIWKSNGSYFYTLDWHEAQDGR FLLQLPNVQPPSSGIYSATYLEASPLGSA FFRLIVRGCGAGRWGPCTKECPGLHG GVC |
| 1861 | 9912 | A | 281 | 276 | 565 | WTSSVSTGQSDQA/GPAPALIQMQRPGC GPSPVPGGWLE*RDGQAGMGAAPAA WVLLCIPAGQGPLPGPRLPFHILKFCYC GILVEKKEPRGCF |
| 1862 | 9913 | B | 2810 | 85 | 283 | MEKTELIRRSARWRVISSIEQKTDTSKKL QLIKDYREKVESELRSICTTVLELLDKYLI ANATNPEX* |

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| 1863 | 9914 | A | 2811 | 1 | 932 | KAKSRSEVGLASRPRRRGSSRGSSRCG SALALALLALRPGPGPAPAMEKTELI QKAKLAEQAES/RYDDMATCMKAVTEQ GA/QSLSNEERNLLSVAYKNVVGRRS A\WRVSKHPSRKTDTSK\KLQLIKDYR EKVD\SELR\NCTTVLGICLDKYF/ILANG NLIPESK\VFY\KMKG*FTFR\YLCLEVA CCADDRK\QTIDNASQGAYQEAFDISKK\E MQPTVHPIRLGALLLTFSVFYYE\LNPE AC\HAWLKTA*WRAIA*LDTLNEDSY KDSTLIMQLLRDNLPLWTSDSAGEECD AAEGAEN |
| 1864 | 9915 | A | 2812 | 199 | 214 | PPSPLNSSTCCLAKTDEK*CKEKGSHLLH |
| 1865 | 9916 | A | 2813 | 1 | 2176 | QGPKLFMDAGIEVFSQDEWKCLDPAQRT LYRDVMLENYRNLVSLGICLPDLSVTSM IEQKRDPWTLQSEEKIANDPDGRECIKGV NTERSSKLGSNAGNPKCKNQLGFTFQLH LSDLQLFQAERKISGCKHFEKPVSDNSSV SPLEKISSSVKSHLLNKYRNNFDHAPLLP QEQKAHIREKAYKCNEHGQVFRASASLT NQVIHNADNPYKCECGKVFSKSSKLV HRRMHTGEKPYKCECGKLFSSNSNLSQ HQRHTGEKPYKCECDKVFRSSSKLAQ HQRHTGEKPYKCECDKVFNQIAHLVR HQRHTGEKPYSCNCKGKVFSRHSYLA HQT VHTGEKPYKCECGKAFSVRSSLIT HQLIHTGRKPYKCECDKVFRKCFLLTS HQRHTREPRPYGCSQCGKIFSQKSD*R HRKTHTDEKPYNGNCKGTA\REFSDLT HFLIHSGEKPYECKE\CGKVFRYKSSLTSH HRIHTGEKPYQM/CNRCGKVFSRSSNLV CHQKIHTGEKPYKNQCGKVFNQASYL TRHQIHTGERPYRCSKCGKA\FRGCSGLT AHLAIHTEKKSCHECKE\CGKIFTQKSSLTN HHRIHIGEPYKCTLCS*GLSVTILTLHSF RGFHHGEPYKLC/DGKTIIMSSSINHQ* VHTKWKS*NVCDTGFIKACQITGHHH ITVEDESTQMNCVYLGYYSTIAEHDR YTRSNSVSGSLILIYDIA |
| 1866 | 9917 | A | 2816 | 26 | 736 | EPIPVTPDHLVMTMTHIVANLLSCQQRPR LPNYEMLKEEQEVA\K\GAPQKPLPEC PPVIH\IRNETSWPDHVRLVPVQ\HPLHE HLLRLGFIRFA\YSVKS\LRDRK\MVGEVN RGPKA*CLHRQSA*KIWGPDFG\HLHEPI LAHQSSPPKFWVVPGPANDREASLRPG ALPVTCP\PRTLASSIPRPAPRGQEV\PLTCI PLTPPSIPRPVPTAES\CSPLSSHAFLQWH SIKICIFW |
| 1867 | 9918 | A | 2817 | 748 | 1637 | DIMESGFTSKDTYLSHFNPRDYLEKYYK FGSR\HSAESQILKHL\K\NLKF\CLDG VEGETCLADIGFWAPLILSSSSCFVESF* GRIVRSLDYFR\TQEPGRELGRK\WLEGKE ARGLFDWVPPMVTMCLNLERETE\VKG PRRRRK\K\QAVKARCLKM*M*TQKPS HLGAVPLPPG*TAVPQAHLCLGCPPCPR PPQPTCKGASGTLGQPYLKPRG\PSLVIM DAAQEPTYMIGE\QKFS\SLPLGREAVK AAVKEAGYTIEWFEVISQSYSSTMANN EGLFSLVARKLSRPL |

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| 1868 | 9919 | A | 2818 | 1 | 1538 | MENPIVKSLAKARERLEDSKLEAVSDNN LELVNEILEDITPLINV DENVAELVGILKE PHFQSLLEAHDIVASKCYDSPSPSPMNN SSINNQLLPVDAIRILGIHKRAGEPLGVTF RVENNDLVIARILHGGMIDRQGLLHVGD IIEKVNHEVGNNPKELQELLKNISGSVT LKILPSYRDTITPQQVFKCHFDYNPYND NLIPCKEAGLKFSKGEILQIVNREDPNW WQASHVKEGGSAGLIPSQFLEEKRAKAFV RRDWDNSGPFCTISSKKKKMMYLT RNAEEDRHEIQIYEEVAKMPFPQRKTLV LIGAQGVGRRSLKNRFIVLNPTFGTTVP FTSRKPREDEKDGQAYKFVSRSEMEADI KAGKYLEHGEYEGNLYGTKIDSILEVVQ TGRTCIL DVNPQALKVLR TSEFMPYVFI AAPELETLRAMHKAVVDAGITTKLLTDS DLKKTVD ESARIQRAYNH YFDLIHNDNL DKAFEKLQTAIEKLMEPQWVPISWVY |
| 1869 | 9920 | A | 2819 | 1 | 1749 | EFVLNYEPRVCRWGCSAAPVAEGEQR RGATGSGSGGAEAAEVRAAMQQVLEN LTELPSSTGAEEIDLIFLKGIMENPIVKSL AKAHERLEDSKLEAVSDNNLELVNEILE DITPLINV DENVAELVGILKEPHFQSLLE AHDIVASKCYDSPSPSPMNNSSINNQLL PVD AIRILGIHKRAGEPLGVTF RVENNDL VIARILHGGMIDRQGLLHVGDIIKEVNGH EVGNNPKELQELLKNISGSVTLKILPSYR DTITPQQVFKCHFDYNPYNDNLIPCKE AGLKFSKGEILQIVNREDPNWWQASHV KEGGSAGLIPSQFLEEKRAKAFVRRDWDN SGDELDTIKFDRHEIQIYEEVAKMPFPQR KTLVLIGAQGVGRRSLKNRFIVLNPTFG TTVPFTSRKPREDEKDGQAYKFVSRSEM KADIRAGKYLEHGEYEGNLYGTKIDSIL EVVQTGRTCIL DVNPQALKVLR TSEFMP YVVFIAAPELETLRAMHKAVVDAGIHH PRL*PNSDLKKTVD ESARIQRAYNH YFD LDPSINDNPRPKPF EKLQTAIEKPENGPP QWVPQSAWVYLMIQ |
| 1870 | 9921 | A | 282 | 1466 | 2353 | RNVHLNLLIHFIYFKINVFHIDFPLGGEK NSGVLGFQAVQKQPRGSFPLPRIPQ*QN LRIGI*KGRRGPGSGPWPAGDTQQHPSK GKGLPPLPACPSL**QQGRRCSGPGGRL GS*GCKHPECQWSQRGVRPLSVPLFQPP PGTGAGPTSWASASGSGAGACQPGS/PL GSVHTGSPSQAKSPSRVK*QECQHPTH VSSPVSRRPFGPKLP GGNRAGPAAPSPP RDTPAAPPPRPGPPSPGSLAQDAPGRSLP PPRTRRPAQSPRPRSASESEAARRGPVR RSRTGREEKSG |
| 1871 | 9922 | A | 2820 | 14 | 230 | FATLYPLKIFIFPKAFNPWREVGPLCPPPK /CKGPSKSPGW/CLNRPPIGKKLIPCKPR LTWAPPRIL*NGPP |
| 1872 | 9923 | A | 2821 | 170 | 303 | RPLRGTPC*CAAWASSWWGCCSACCSH CCLLGPCWHSGPCSA*WAFWCSGG |
| 1873 | 9924 | A | 2822 | 208 | 547 | AAPGAMGPWPDRLCGSALPSCRLPCYSS ASVSLRCAAENTFTQAGPCCWAWPHRA HQDFLQIPFRHLEAPRCSPPLSAWPPRH LLPAGDPLDQEQPPGIRGAP*RPLRGTPC CGSGVAAAGVRGCGPVWL*HPEPADSH TATAEPRI*AAPGAMGPWPDRLCGSALP SCRLPCYSSASVSLRCAAENTFTQAGPC CWA WPHRAHQDFLQIPFRHLEAPRCSP PLSAWPPRHLLPAGDPLDQEQPPGIRGAP LSLRRRLLL |
| 1874 | 9925 | C | 2823 | 48 | 173 | MVRKRMEMKMRKLSQLRASGQLKMM RMXMSIPRSRRPRGIX* |
| 1875 | 9926 | A | 2824 | 183 | 423 | |

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| 1876 | 9927 | A | 2825 | 147 | 588 | TLAFLIPICIGSPACPTMSDAAVDTSSSEIT TKDLKEKKEVVVEEAENG/REDRPCLTG NAENEVENGEQEA*QLR*DEE/EREGR LG REGGREGRKEG*LVEEEDGRLKIEEAES ATGKRATEDDEDDDCRYQSRRPDEDD LDSKKAKS |
| 1877 | 9928 | A | 2826 | 1 | 77 | SGRPFFFFFFFFFFFF*CKGFLIGYM |
| 1878 | 9929 | C | 2827 | 175 | 351 | MKLIQLSCQPFNSRHHVLKKKPLTFMILS HFQASLSSIFGFCSSLFRQSSFFSNILFF* |
| 1879 | 9930 | A | 2828 | 56 | 380 | KYLVDQHAGSPPVKNLAEAVQNIVQIL H*EIQKSVNHRMYL*KLDTDSL**FIQLQ VEPTILGIKVDVYKHEYKDKDGHSDFSNY SSHQVFFLLIFNKDNMAIN |
| 1880 | 9931 | A | 2829 | 3 | 129 | |
| 1881 | 9932 | A | 283 | 134 | 385 | CQIMDGM LAIQA WPTPQQVASNGTGLN PNAKVWQEIA PGNTDATPVTHGTESW HEIAATSGAHPEGNAEPQKIYVKNMK*C I |
| 1882 | 9933 | A | 2830 | 472 | 756 | SSADSKCTLTIGKPAKSRVQLCHKEETFP NQTNAYRTCVD*CLMSPTLLGTSIF*SQ MIIRVVPICMPNIFLIISC*VLCIRKPVSEL PHLLGF |
| 1883 | 9934 | A | 2831 | 1 | 170 | |
| 1884 | 9935 | A | 2832 | 1243 | 5595 | |
| 1885 | 9936 | B | 2833 | 2177 | 3174 | MGKTTPMIQSRPSFDTWELQVPPSTCGD YNSSFIKELRASQSNVIKPPGPVKLKESV VENHAYLSYAVEEEHAYLGPTVKPDDK AKTLSYEPLSSATVSTGSLLSYENTDLSL TDPESFSEHMDDSKQESTTSKEEETNIISS IVPSTQDIYQRQNSSDVHKSLLPAVDETT CGHTHFQQMIDKALYQSGKPETGHGIME EPELTLISTDTSIAEMDFANLTLEEKSEN EAKCFFQQSKTRLKRLKRVKHATFLPLA TEASDYPVAVSELSIEKPRTASTETPRRLTP VPGSLQEAFIKRKKSFMERSHQRQKEIR NKIHVSENSQIKTVKEKPSISSIL* |
| 1886 | 9937 | A | 2834 | 2268 | 2547 | KYLVDQHAGSPPGKSLCCLEKSQRMMM ISQNLDVVLRV*TADDAN*EKCVPIANL FFQVSNLLH*VLVYHLLKVCVTTCFSIH CRQQRFMNV |
| 1887 | 9938 | A | 2835 | 137 | 716 | TTTMSKKAKTKTKKRPQRATSNVFA MFDQSQIQGVQRGPFNMIDQNRDGFHS DK/EKVLHDLAISLGKNPH*WHYLD MMNEAPGPIQFSPCFLATLFG*GSLNGHQ IP*RCSFRKRLAFALDEEATGHPFREDYL /REELLTNPWGDRVYQIEEVG*TCTGEAP I*QKGGNSNYHRSFTRHPNWKAPKAQR |
| 1888 | 9939 | A | 2836 | 2 | 437 | LVIIESDLERAERAELSEGKSDSWKNN* E*WIRP*KH*WLQRISKCAELEELKTVT NNLKSLEAQAEKYSQKEDRYEEIKVLS DKLKEAETRAEFAERSVTKLEKSIDDLE DKFLCFTSPKTPSSSWMSHLSELCLFSS |
| 1889 | 9940 | A | 2837 | 1 | 834 | GSRVRRAAAGLSHCSPPARLP SGAMAGS SSLEAARRKIRSLQEQA DAAEERAGTLQ RELDHERKLRATAEADVASLNRRRIQAW EEEEFGFVPKERLATAFQKLAEAEKAA DESERGMKVIESRAQKDEEKMEIQEIQ KEAKHIAVEDADRKYEEVARKLVIIESDL ERAERAELSEGQVRQLEEQLRIMDSDL KALMAAEDKYQKEDRYEEIKVLSK LKEAETRAEFAERSVTKLEKSIDDLEEKV AHAKEENLSMHQMLDQTLELNNM |

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| 1890 | 9941 | A | 2838 | 9 | 1108 | PDRATRPRPRARPADPALVLGPLAAVMTM GAGKKKMRMLKLDKENALDRAEQAEA DKKAAEDRSKQLEDELVSQKKLKGTDR* TGQIL*RLSKMPKEETWNWQEKKATD AEADIVASLNRRIQLVEEELDRAQERLA TALQKLEEAKEKAADERSERGMKVIESRA QKDEEKMEIQEIPT*KRAKHIAEDADRK YEEVARKLVIIESDLEPCRGSGAELSEGK CAEA*KEEFENL*PNNFEVHLEGSRLRK YSQKERPDMEEEIKGFFPDKA*RRLETR AWSFAERSVT*NLEKSIDDLERAVTL QETEVQSHQRRSWDHALNGYDFHISFFA SLLPRLPRRSWMSHLSLSELHLSYSPADPG SLS |
| 1891 | 9942 | A | 2839 | 3 | 268 | |
| 1892 | 9943 | A | 284 | 305 | 1129 | DICKEYEVMYSSSCETTRNTTGIEESTDG MILRPEDLSYQIYDVSGESNSAVSTEDLK ECLKKQLEFCFSREKLSKDLYLISQRDSD QFIPIWTAANMEEIKLTTDPDLILEALRS SPMVQVDEKGEKVRPTHKRCIVILREIPE TPIEEVKGLFKSEYCPKVISCEFAHNSD WYITFQSDTDAQQAFKYLRKEIVKQFKA RPILAGIKAINFFC*EWSSNNGILESIVHP I*TAQYASPVFMQPVYNPHQQYSVYSI VPQSWVSKSYTLL |
| 1893 | 9944 | A | 2840 | 500 | 682 | |
| 1894 | 9945 | A | 2841 | 1617 | 2086 | GLAASSRKHQMVDADAVGGPGGPGM AGCDGLPGFGSDIRPRLWLWLGPRWL SS*RGTNILASVPKKLLM/DCYALARD RTATLGTDFDAISKATSNWIPDLWKETVF TKFPYQEFTHDL/VKTHTRVSKQKTQVP AVATTAARQTMEGQAPVEYI |
| 1895 | 9946 | A | 2842 | 55 | 665 | AMAEDHGLSNGDGPVEVTQGLELLVSA AAQDIVLLDGIQGLFLTQFDNIWVWDH FLGKLPHRVFKGGGEKQHLAVPGQHPL DADALILVALSGYHDSLIQNKHLDLFI NELDLEHQSSSTVPGVPMTICSLIFWPLSN LLPRTA*ASFSSG*NLPICSITFPV*SASSY VGERHRHWGYLSDGSTRLSMAKTKAA VLPVPD |
| 1896 | 9947 | A | 2843 | 43 | 548 | |
| 1897 | 9948 | A | 2844 | 1 | 876 | |
| 1898 | 9949 | A | 2845 | 222 | 482 | |
| 1899 | 9950 | A | 2846 | 3 | 218 | SLFQLKTTKTQSRVMGAIYDSSWFQEDR QAAERFTDRSTHLRLRNAEAAA*TKPAQ GPGSIPILPATPSSL |
| 1900 | 9951 | A | 2847 | 322 | 452 | LCCSI*IYLN/LLIC*QSFSVLK*DFRVD* KKKNPRMSHRVLNI |
| 1901 | 9952 | A | 2848 | 3578 | 5288 | TESREHFSPWYSVTAARRPQVASKAEEN LLMVLGTDMSDRRAAVIFADTLTLFEG IARIVETHQPIVETYYGPGRLYTLIKYLQ VECDRQVEKVVDKFIKQRDYHQQFRHV QNNLMRNSTTEKIEPRELDPILTEVTLMN ARSELYLRLFKKRISDFEVGDSMVS*E VKQEHQKCLDKLLN*LAFLSCYHGREL GLYVTMEEYFMRETVNKAVALDTYEKG QLTSSMVDDVFYIVKKCIGRALSSSSIDC LCAMINLATTELESDFRDVLCNKLRMGF PATTFQDIQRGVTSVAVNIMHSSLQQKGF DTKGIESTDEAKMSFLVTLNNVEVCSENI STLKKTLSDCTKLFSQIGGEVQAQAKF DSCLSDLAAVSNKFRDLLQEGLTENST AIKPQVQAWINSFFSVFHNIIEEEFNDE ANDPWVQQFILNLEQQMAEFKASLSPVI YDSLTLGLMTSLVAIVELEKVVVKSTFNR LGLQFDKELRSLIAYLTTVTWTIRDK FARLSQMATILNLERVTEILDYWGPN GPLTWRLTPAEVRQVLALRIDFRSEDIK |

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| | | | | | | KAALVS |
| 1902 | 9953 | A | 2849 | 233 | 801 | VVTLTGSNLYFYCSLFHFSVLPDQDVSLV *ICYLSLPLDIVCFCNVKIQFFFLSLESYY *FLTIFPHCFYLLKTPFKHRELFILVFGL LKIFQ/LC*FFYLILLRFFYFNFCLLDLF LFWIFIWYFVIFACSWFIGVSLKFLLVPL/ CSFFLRCRHSPLF*GAS*TDLYLGCIPFP* VCLLWEFCGGL |
| 1903 | 9954 | A | 285 | 1053 | 1403 | TFTQDSAGSLVVHSPMTSIWKTAESVDQ GHFPIIILFVYLLFETGSHSVTHATMQW CDHSSLQPQTP/SGSGDPPTLAC*VPGHIG MCHHTWLIFTPAETGSHHVPRLVSNP LA |
| 1904 | 9955 | A | 2850 | 170 | 494 | |
| 1905 | 9956 | A | 2851 | 70 | 1474 | RESGTWQPGKAGTQTGAKFWEVISDEH GIDPTGTYHGSDQLERINVYYNEATG GKYVPRAVLVDLEPGTMDSVRSGPFGQI FRPDNFVFGQSGAGNNWAKGHYTEGAE LVDFVLADV*RKEAES*DCLAQGFQLTHS LGGGTGSGMGTLLISKIREEYPDRIMNTF SVVPSPKVSDTVVEPYNAILSGHQLVEN TDETYCIDNEALYDICKTLKLATTPPFG DLNHLVSATMSGVTTCLRFPGQLNADL RKVAVNMVPPRLHFFMGGFAPTQDA GASQASTRALTVPRSSPKQMFDANKNM MAACDPRAWAAYLDGLPPCFRGPHVPL KEVDEQMLINVQKQKQPAIFVEWIPQQ CEKRAVCDIPHLRGLKNVRPPSFGKQAR PIPGAFSKPHLPKQFHGPCFRKALPSFIT GEGMDMEFHFPRPESNKNDLVSEYQ QYQDATAEEVEGEFEGRSLGRKVA |
| 1906 | 9957 | A | 2852 | 284 | 359 | QQEANPSAPLQHVSTSN/CVLTCCKGA EGLASCCYCHCLCNECCQGACGPDTHL AHCCRCQHSSKPPGGPRI/ASTQTCYY*C PCRLPGGSR*CLASCPYHWCPWTSPLG SPVPNKAPP |
| 1907 | 9958 | A | 2853 | 295 | 478 | |
| 1908 | 9959 | A | 2854 | 1 | 1167 | |

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| 1909 | 9960 | A | 2855 | 3 | 1328 | SGILGTTTSPFPVGVVLRVECLCPGPAP MSVPAFIDISEEDQAAELRAYLKSKGAE ISEENSEGLHVDLAQIEACDVCLKEDD KDVESVMNSVVSLLLILUEPDKQEAALIE SLC/EKLGPNFREGEPPRLRLQFVKATF STGMD*EILPVKIHVSICSLNKKVAASCG AIQYHPQLEPGIKFRKWDFLNWNLTG KKSTPLLKTTFMKALVDCKKSDAASKG MVELLSYPPGGQCFPRARVDAHRICIV RALKDPNAFPFDHLLTLKPRQVFWKGE LI/HIVPF*PNFVSA*MGHHMSRFYDP*LR TFH*IPLGPTMDPGIWPCKMRLFLWG MGQ*ENRISFWTTMPARNFRIGADDIV EAFVIDAGKELKMVYCNWSRPQRKVV VSHSTHRITFGKQQWQQTV/YDTLNAW KQNLNKIVKNSLLSPSGYLKFLCL |
| 1910 | 9961 | A | 2856 | 377 | 2393 | FSLECLGHENR*D*ITIYKITSGLTGKVFN KIQHPFTIKNKK*KTLNKLIEGNFLNLK GIYEPMVSIILNGEGLDYFPLRSETROG CLLWPFNFN/IVLDSQERAIROENKIKVI* VGKEEV*LNRMGDDMVVLCIVIQGKI* KIQRDLLINKFSKVTGYRI/NICRKLVI HI*YQLNKSQNDVKKT*FSTMVKGGL C/RVIPTLWESEAERLLEARRPAWETVRS HLYKNKQTKNNKQTKN/TLDVMTLICRL SYSEAEV*GWLEPQSSKLQ*AITGSLQSS LDRQS*TLTQKTKKKRKKLTASERVKY QYN*GSRNID/PHLSSN*LLENSA*GQFQ WGGKIVFFIK*CLETWISTWQNNGNWDS YLILHIKINSELT*DLNVRANIVSIFKEN/M GVNLSDFELGNDFLNK*/PLKTQATKEEN R*IKIKTICVSKDNKKAKIQPTE*DNFF*N HVLVKGIGICI*NM*RTVTIHKRHIIQFLKI QQGVWN*QFSKGGYTKGPLRHMEKVSQ PSLAIREMQMRSTMRYHLTPLE*IYNQS DNIKCW*GCREIGTLMHCWWYPRDIKT NVYTKTCAQMFLPALFI*AQK*NGP*FLS LTSALTKTWHIHT/MEYYSSQ*KKEMKV LIWPPTTMEKPLEKPYPSEECPRHERPTY YMISIMYKCPRTGEYI |
| 1911 | 9962 | A | 2857 | 3 | 445 | GEFADSF/SSMGSPVNAQDFCTDLAVSSA NFIPTVTAISTSPDLQWLVPALVSSVAP SQTRAPHFPGVPAPSSGAYSRAGVVKT TGGRASIGRRGKVEQETDQLEDEKSAL QTEIANLLKEKEKLEFILAAHRPACKNPD DLGFPE |
| 1912 | 9963 | A | 2858 | 295 | 1622 | DEMSVAGSFLTAACGTGNSPHLCPEHA RSRRLSPSVLF*DFCTDLAVSSANFIPTVT AISTSPDLQWLVPALVSSVAPSQTRAP HPFGVPAPSAGAYSRAGVVKTMTGGR QSIWQEGARWEQVRNF*RTLPGNVGAG WEAAPEMQEPSTEDEAT*WGLLAHP*LG ALAPSPFHPNSDSEFSP*EVLS*FLP*VSY RMLSDWALLCSLAEDLILNASHT*SATA GQKWFHSGVPGSREAAGASSTGVGEWR *WQTLNVLNGLFL*LF*LSPEEEKRRIRR ERNKMAAAKCRNRRELDTLQAGRYS VGCSFLKLKGKVGRLHKGK*VRLCLYA FPLSLCIQETDQLEDEKSALQTEIANLLK EKEKLEFILAAHRPCLARFPDGGPAPPE EMSVASLDLTGGLPEVA/TPESSEAF/TLP LLNDPEPKPSVEPVKASA |

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| 1913 | 9964 | A | 2859 | 3 | 1467 | PHLQRATEKPRLSRRPRRSEAVTVLLPS SASQRPPVSAPRPLARLCLTATMMFSGF NADYEASSSRCSASPARD\SLSYHSPA D\SFMSMGSPVNAQDFCTDLAVSSANFIP TVTAIST\SPDLQWLVQPALVS\SLWAPS QTRAPSTFSESPPPTAGAIYSRAGVVKT TGGRAQSIG\RRGKVEQLS\PEEEKRRIR R\ERNKMAAAKCRNR\RR\ELDTLQA\ ETDQLED\RKSA\QTEIANLLKEKEKLEF/ LSLAHR\PA\CKIPLIDLGLPRKEMSVGS \DLTGGLPEGS\TPESEEAFTL\PLNDPE AQGPQWEPVQGGISRHGS*KDRGPFDDF LFPSIHGPGSGFLRTARSVPDMGPILGPF YGRQIRGAFSHSGSLGMGAHGHRGWEP LCTPVVTC\TPSCNCLHVFRFHLPRG*LL PQLCSCPPQGGQQQ*AFL*LAQLTHAAG PVRGQGRGSRHPQVPLPELVHYREEKH IFPRGFL |
| 1914 | 9965 | A | 286 | 259 | 506 | PGYRRGHGGAAGRQEPAAARHNPAVRE DADGGD\RPRSAACPGTSTAPPGT*GS\G QAHRDGARPAPAPRPSHPSAGPAAGPSG |
| 1915 | 9966 | B | 2860 | 1 | 196 | MAEGNHRKKPLKVLES LGKDFLTGVLD NLVEQNVNLNWKEEEKKKYYDAKTEDK VRVMADSMQEKQX* |
| 1916 | 9967 | A | 2861 | 1 | 988 | MGSLEGNHRKKPLKVLES LGKDFLTGVLD DNLVEQNVNLNWKEEEKKKYYDAKTED KVRVMADSMQEKQRMAGQMLLQTFN IDQISPNKKAHPNMEAGPPESGESTDALK LCPHEEFLRLCKERAEEIPIKERNNRTR LALIICNTEFDHLPPRNGADFDITGMKEL LEGLDYSVDVEENLTARDMESALRAFAT RPEHKSSDSTFLVLSHGILEGICGTVDH EKKPDVLLYDTIFQIFNNRNCLSLKDKPK VIIVQACRGANRGELWVRDSPASLEVAS SQSSENLEEDAVYKTHVEKDFIAFCSTP KYSWCCHLEEVFRKHCSQ |
| 1917 | 9968 | A | 2862 | 12 | 914 | GSFQRCKKGQRLFPMAEGNHRKKPLKV LES LGKDFLTGVLDNLVEQNVNLNWKEE EKKKYYDAKTEDKVRVMADSMQEKQ MAGQMLLQTFNIDQISPNKKR*IGVTE AEITIYVLQYPAHPNMEAGPPESGRIL PDCLKLCPHEEFLRLCKERAEEIPIKER NNRTRLALIICNTEFDHLPPRNGADFDIT GMKELLEGLDYSVDVEENLTARDMES ALRAFATRPEHKSSDSTFLVLSHGILEG ICGTVDHEKKPDVLLYDTIFQIFNNRNCL SLKDKPKVIIVQACRGEC |
| 1918 | 9969 | A | 2863 | 12 | 1353 | GSFQRCKKGQRLFPMAEGNHRKKPLKV LES LGKDFLTGVLDNLVEQNVNLNWKEE EKKKYYDAKTEDKVRVMADSMQEKQ RMAGQMLLQTFNIDQISPNKKAHPIM EAGPPESGESTDALTLCPHEEFLRLC*RK ELKEIYPIKGRRKQPHTAGLFFI\CITEFDH LPPRNGADFDITGMKELLEGLWDYSV GVGRRFLTARGMDSALRAFATRPEHKS SDSTFLVLSHGILEGICGTVDHEKKPD VLLYDTIFQIFNNRNLPQV*RDKPQSSI VQACRGANPSGN*WVRDSPASLGKW PSSQSSGEPWRKDAV*QDPHV/ERRDFIG FPGSFKRPHNRAPWERPAQWGSIFITQ\LI TCLPRNIPWCC/HTLEEVFRKGTAHLETP R\AKAQMP\TIERTVR*QGYFLFPGEFE NWEGHKQPSPSLNPTFKEAPFFVTACIF |
| 1919 | 9970 | A | 2864 | 66 | 392 | |
| 1920 | 9971 | A | 2865 | 131 | 551 | KIRGVSCPSAPKSGEQTGQHNNINTGFHP LPLGAVTSPVPQGGDRLCPPSSPEPAQ PAQ/C*PCSDSGRSPGPGKAWTVAPC\ PEPSVFCLQSPGFEPWVLAHPSSERR ASSSGLDDDLPAQETGNGSGATRTCS |

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| 1921 | 9972 | A | 2866 | 943 | 1109 | LMVLSDFIFKLKI/WPGAVAHACNLSTLG GRGRWIT*GQFETSPASIVKPPSLLKI |
| 1922 | 9973 | A | 2867 | 112 | 1078 | ESSRQALLAKPLSACAEQPARAEVGAAT ALPVRWASGEMAPSGSLAGPLAALVLV LWGAPWTHGRRVTNVRVITDENWRELL EGDWMIEFYAPWCPACQNLQPEWESFA E/WGEDLEWNIKVDVTK/QPGL/SGRFII VTALPTIYHCKDGEF*AVIQGPRTKKDFI NFISDKEWKSIEPVSSWFGPGSVLMSSMS ALFQLSMWIRTCHNYFIEDLGLPVWGSY TVFALATLFSGLLLGLCMIFVADCLCPK RRRPQYPYPYPSKKLLSESAQPLKKVEEE QEADEEDVSEEEAESKEGTNKDFPQNAI RQRLGPSLATDKS |
| 1923 | 9974 | A | 2868 | 1 | 448 | |
| 1924 | 9975 | A | 2869 | 1 | 536 | |
| 1925 | 9976 | A | 287 | 1 | 2072 | FRRSPSPAASVSLGLGVAUVSSLVNGSTF VLQKKGIVRAKRRGTSYLTDIVWWAGTI AMAVGQIGNFLAYTAVPTVLVTPALGAL GVPPGSILASYLLKEKLNILGKVGCLLSC AGSVVLIHSPKSESVTTHAELEEKLDQS RVGGLPCASLLVMLAAHLLDPCRPMG PPTSWSTSASAPCWADTPCLPPRASGWR PKTSCITTRPVREPSACAWYSWPCSA SSSSSGTRNKALECFDSSVFGAIYVVF TLVLLASAILFREWSNVGLVDFLGMACG FTTVSVGIVLMRVFKEFNFLGEMNKS DTWRQSSPLIVAPRDHFHLERGVOFQNM NSVMGSHLMVVALSPGVDFIPQDDPAA LLVTELFANRLVSGYAPATGLQGTILQY GNTLMEVMPKICRLPRHECGSPGPV GSCAPPPSPHSTR/RRPPRSAD/CGPCKGT GTRRERAPGAG*AEAAGPEGGGVAGAA NAGAGAADAGAGGADAGAGGAGAGAGG AGAGAGGAGAGAGGAGAGAGGAGAGAG AGGAGAGAGGAGAGAGGAGAGAGAGGA GAGAGGAGAGAGGAGAGAGGAGAGAGA GGAGAGAGGAGAGAGGAGAGAGAGGAG AGAGGAGAGAGGAGAGAGGAGAGAGAG RAGAGAGGAGAGAGGACAGAGGAGAG AGGAGAGAGGAVAGAGGAVCSQTIFTR SHGGLHLWRPC |
| 1926 | 9977 | A | 2870 | 1 | 5193 | |
| 1927 | 9978 | A | 2871 | 1 | 356 | |
| 1928 | 9979 | A | 2872 | 1 | 401 | |
| 1929 | 9980 | A | 2873 | 151 | 5459 | AGARRRGGEAPLLPGLAAAEPPEAR PDGLAEPVRRGRRVSGPRGTMSAKVR LKKLEQLLDGPWRNESALSVELLDV LVCLYTECSHSALRRDKYVAEFLEWAK PFTQLVKEMQLHREDFEIIVIGRGAFGE VAVVKMKNTIRIYAMKILNKWEMLKR AETACFRENRDVLVNGDCQWITALHY AFQDENHLYLVMDYYVGGDLLTLLSKF EDKLPEDMARFYIGEMVLAIPIHQLHY VHRDIK |
| 1930 | 9981 | A | 2874 | 1 | 764 | MEKIPILRSLRAREQQAGKDVTLQGEHQ HLPPEGCCQTVPLSVGRRPPDTPGPETNS MEAAPGSPGEGCPACSRCLRWEPGPGR PCE*PEESPAGT/PAPCPGSPGPAQS LPPLPG/PLQPSPRSPASGPAPGHRHPEG GAGQAAEQIGPRGQPRSSLQTSPPRPL AAPVPMAPRGLAWQDVSEPPVGCGL NSSQKSPLSERPGPPVSGEAGP/DGSSHS AQLRQPPNRAGSGLESVSVSLEGQSRGA RD |

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| 1931 | 9982 | A | 2875 | 1 | 1641 | MKVCSSIAEVSDDTNPSPRTNSGHMTSV LKQALKDPCRTYRLVLTLETEVL DLFIERFCMTGGNSPICYLKAYHTNLYLS ADAQKVEAIDEGLAAATIFSPSRDVVVS QSQLRVAFDGDVLFSDSERIVKATLD RFFEHEKAHENKPLAQEQGSTSFDPKVE AFRSPSVPLPITGHSANVYQTPCARRRT TRPLVNWELIPRDNPPPPRQAFRDLGQS PAFSDAVATTSAVPPGGDCHLSEVRGAE TRQPAFAMKRPKEPSGSDGESDGPIDVG QEQQLRSSKLEKAEVLQMTVDHLKMLH ATGGTGFFDARALAVDFRSIGFRECLTE VIRTPTIWLLPGRSKAVESQSQFTGAHS TLGEPTAKK'A*SNPQVYMDIKIGNKPAG CIQTLRLSDVVPMTTENFLYMCTH/SKGL GFKGSSFHRIIPQFICQGSDFTNHGGTRG KSIYKKKFDDENFIFKHTGPGRLRRHGTK CPMAHLALMEASKGQDQHPLRRKERA QQVHDVVKLTRGRGRGISLKRIARSLCK DKETGLCTLTWH |
| 1932 | 9983 | A | 2876 | 1 | 949 | |
| 1933 | 9984 | A | 2877 | 185 | 339 | |
| 1934 | 9985 | A | 2878 | 673 | 1085 | GEPTAKK'A*SNPQVYMDIKIGNKPAGCI QTLRLSDVVPMTTENFLYMCTH/SKGLG FKGSSFHRIIPQFICQGSDFTNHGGHQS AQHGTCKCPMAQFGPHGGLKRAGPAPSS TGKERAQQKQGESAITSQPRSWKLT |
| 1935 | 9986 | A | 2879 | 141 | 1959 | PRPANLLKGGQITMSATVVDVANAAP LSGSKEMSLEPKKMTREDWRKKKELE EQQKLGNAEAEVDEEGKDINPHIPQYISS VPWYIDPSKRPTLKHQRPOPEKQKQFSS SGEWYKRGVKENSIITKYRKACENCNG AMTHKKKDCFERPRRVGAKFTGTNIAP DEHVQPQLMFDYDGRDRWNGYNPEE HMKIVEEYAKVDLAKRTLKAQKLQEEL ASGKLVEQANSKPHQWGEEEPNSQTEK DHNSEDEDEDKYADDIDMPGQNFDSKR RITVRNLRIREDIAKYLRNLDPIAAYDP KTRAMRENPYANAGKNPDEVSYAGDNF VRYTGDITSMGQTQVFAWEAYDKGSE VHLQADPTKLELLYKSFVKKEDFKE QKESILEKYGGQEHLDAPPAELLAQT EDYVEYSRHGTVIKQGERAVACSKYEED VKIHNHITHWGSYWKEGRRGNKCCHSF SKYSYCTGEAGKEIVNSECHINEITGEES VKKPQTLMEHLEKLEKKEKKKKKKKKK KHKSSSDSDDEKKHEKLLKALNA*EA RLHVKETMQIDERKRPVNSMY*TSR PUEEMEAYRMKVRQRPDDPMASFLGQ |
| 1936 | 9987 | A | 288 | 1 | 390 | ITLGPDSIIGIWSGNQHKQDPYIASMEHH TDWVNDIVLCCNGKTLISASDDTVKVW NAHKGFCMST/YKDT*ASSLSGNKDSIYS LAMNQLGTIIVSGSTEKVLRVWDPRCTA KLMKLIGHTDNVKAALL |
| 1937 | 9988 | A | 2880 | 711 | 1140 | GVGVCFPPVPSLRVLGRWAAFCALPGR SLRKSRLWGWGTGHTQS*EGELPWKAG/ WQRCFWRGGRQTLPLTCSPTRGCRRA AQEGAGCKARGAWWVRSPGRAGRPLR RGGSRVTLNSQMGSDATGETEWIKEMK PKKKKKMS |
| 1938 | 9989 | A | 2881 | 1 | 649 | MAGALVRKAADYVRSKDFRDYLMRVT QQPYKVFNSGPWAFSSSSYMSRPSAHISS LIVSRVSSSTSFQGGGLGAGMGVEPLDP HENLYVDFYRGFIHNCQNEANKMSFG RSQSEKAAAYLVPTTQRSGKGKIMELVE RSVVARVEHFWGPVANWGLPIAANDM KKSPEIISGRMTFVQPRNWLLFACHATN EVAQLIQGGRLIKHEMTKTASA |

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| 1939 | 9990 | A | 2882 | 1 | 389 | |
| 1940 | 9991 | A | 2883 | 27 | 554 | LAVGCRGVGLGVIGSGKRQQRQGPLGV SVSAQPCAGALVRKAADYVQSKIDFRD YLMSTHFWGPVANWGLPIAINDMKI KSPGDYSVGRMTFALCICYSLTFMEILP YKVQI*PLNWL/LCFACHGTNEVRPSFIQ GEGRLIPNTRMDLKRASGINQWGKGKN KVFEGLSLCPGCC |
| 1941 | 9992 | A | 2884 | 1 | 162 | QCAEKIASNPKIVVAMAKESVNAAFKIT LPEGADDRKEGMPFVEKRKANFKDQ |
| 1942 | 9993 | A | 2885 | 1 | 196 | |
| 1943 | 9994 | A | 2886 | 148 | 427 | CLLGFTTHSASHDQPLPAGAGGTQRLTR AVGKSLAMEMVLTGDRISAQDAKQAGL VSMICAVETL*CLLGFTTHSASHDQPLPA GAGGTQRLTRAVGKSLAMEMVLTGDRI SAQDAKQAGLVSMICAVETLVGGAIQC AEKIASNSKIVVAMAKESVNA |
| 1944 | 9995 | A | 2887 | 1 | 1484 | EATLTRPRPAGGPAAGWYCPSAKTSGQL GAGFTFSPLERHCPLSPSHLAVHPAGAGP VQANREAPASPIFGLACCSGPVPDLNA AGTPRIFTSPTLRPLARGANFEYIIAEKR GKNNTVGLIQLNRPKALNALCDGLIDEL NQALKTFEEDPAVGAIVLTGGDKAFAAG ADIKEMQNLSFQDCYSSKFLKHWDHLT QVKKPVIAAVNGYAFGGGCELAMMCD IYAGEKAQFAQPEILIGTIPGAGGTQRLT RAVGKSLAMEMVLTGDRISAQDAKQA GLVSKI*CPF*DTGWKEAIFAEKIASNS KIVVAMAKESVNAGRSPNLSECIYLEGV AVPRACRWLEAGYSEESILKERRLSPE VFGKVVLPPERMLAPALEPQRLPPSAHL DLLCLASCKERA WNEQSQRSSWCRPRP ALALVLSFLVFILGYFSLFAAPLPPHSLSS RAQFAISPFQFLSLLGAVGYRSVTFGGH SRAVGSARSPLGQCL |
| 1945 | 9996 | A | 2888 | 1 | 946 | GRGVQRAMAALRVLLSCARGPLRPPVR CPAWRPFASGANFEYIIAEKRGNNTVG LIQLNRPLPVNWLCDCLND*LNQGLKIF EEDPAVGAIVLTGGDKAFAAGADIQK LQNLFSRDCYSSKFFGRHWGPPSPRVK KPVIAAVNGYAFGGGCELC*CVDIIL/ YAGEKAQFAQPEILIGNLPRVRGGTQED SPVPVGSKSLAMEMVLTGDPDPQPD QASRVLSKICPVETLVEEANQCAEKIA SNSKIVVAMAKESVNAAFEMTLTEGSKL VEKKLFYFNLWPLDDRERRG*PRFVGKE KGPTFKDQ |
| 1946 | 9997 | A | 2889 | 1 | 384 | VRDYNLTEEQKAIKAKYPPVNRKYEYL DHTADV/QWIVLHRA*YFFRLHAWGDT LEEAFEQCAMAMFGYMTDTGTVEPLQT VEVETQ/GWGEEFSLSKHPQGTEVKAITY SAMQVYNEENPEVFVIID |
| 1947 | 9998 | A | 289 | 1 | 1050 | FRVNMQDGGPSPAEHKAESAGMEAR FLGLPDAAGSSGPTPARRCPAPRPAGVS YVIRDEVEKYNRNGVNALQLDPALNRLF TARRDSIIRIWRVNQHKQDPYIASMEHH TDWVNDIVLCCNGKTLISASSDTTVKVV NAHKGFCMSTLRTHKDYVKALAYAKG* VELVASAGLDRQIFLWDVNTLTALTASN NTVTTSSLGKDSIYSLAMNQLGTHIVS GSTKVLRVWDPRCTAKLMKLKGTNDN VKALLNRDGTQCLSGSSDGTIRLWSLG QQRCIATYRVHDEGVWALQVNDAFTHV YSGGRDRKIYCTDLRNPDIRVLICEEKAP VLKMELDRSADPPPAI |

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| 1948 | 9999 | A | 2890 | 1 | 332 | RDYNLTTEEQKAIKAKYPPVNRKYE*DDL QSLLFHFLDEWLYKFSADFFIPREVKVL SIDQRNFKLRSIGWGEEFSLSKHPQGTEV KAITYSAMQVYNEENPEVFVIIDI |
| 1949 | 10000 | A | 2891 | 3 | 425 | SFMAQEEEDVRDYNLTTEEQKAIKAKYPP VNRKYEYLDHTADVQLHAWGDTLEEAF EQCAMAMFGYMTDTGTVEPLQTVEVET QVHADEFFIPREVKVL SIDQRNFKLRSIG WGEEFSLSKHPQGTEVKAITYSAMQVY NE |
| 1950 | 10001 | A | 2892 | 91 | 598 | LKNRRRSRPSIRQSIGSTSVSRWLTSLFTY LDHTADVQ*V*REFIPLKPRQ*ED*MFQS WLHAWGDTLEEAFEQCAMAMFGYMTD TGTVEPLQTVEVETQGDDLQSLLFHFLD EWLYKFSADFFIPGWGEEFSLSKHPQG TEVKAITYSAMQVYNEENPEVFVIIDI |
| 1951 | 10002 | A | 2893 | 359 | 938 | IYFFRLHAWGDTLEEAFEQCAMAMFGY MTDTGTVEPLQTVEVETQQK*LQVLLF HFWDEWLYKFSADFFIPGKLCAIVF*K RL*RPGAVAYACNPSTLGSRRGRWIT*GQ EFETSLTNKEVKVLSIDQRNFKLRFNGW GEEFSLSKHPQGTEVKAITYSAMQVYNE ENPGSFCDHWTFTTQKIKRLPTGKK |
| 1952 | 10003 | A | 2894 | 220 | 345 | LKKEKSLMEKHFF*QTDSSVSNEKNHE PSDIVNSLQWAMVS |
| 1953 | 10004 | A | 2895 | 1 | 281 | |
| 1954 | 10005 | A | 2896 | 83 | 425 | |
| 1955 | 10006 | A | 2897 | 1 | 3600 | |
| 1956 | 10007 | A | 2898 | 1 | 197 | |
| 1957 | 10008 | A | 2899 | 1 | 963 | |
| 1958 | 10009 | A | 29 | 376 | 610 | FPAFWESQVRWIASASGVQDQPDQYGEI LFLKLQKLGGHGG/IR*EDHLSLGGQGC KEPRLYHCTPAWVTEHYLVSKK |
| 1959 | 10010 | A | 290 | 1 | 366 | FPNSSRLIWPECNRIKEESLVASPGSFC PHLDLALGLGL/GVGLMVELGLKLGLFL GLGFDLGVGLGIGL/GVKLGLSDGY/GLG FRLGLGL*AGLVGLGIRVGLKPGLGLEI FVGLILCICI |
| 1960 | 10011 | A | 2900 | 49 | 247 | DLTRNHSPLQTVHDVRWFMIFFQV*YRR IKFVKRNASPSGI*NII*TINTFVCIYK*IFR YKNMHI |
| 1961 | 10012 | A | 2901 | 1066 | 1768 | NPQSSSSEGS*DFPRLTVTNRLLVQRSE VTQAPGQYTVDVEGHGCTFIQATLKYN VLLPKKASGFSLSLEISKELDFCF*P/RQ VNLQYTGIRNKSSMVIDVKMLSGFTPN PCHPIELENKGQSD*SKNDPCSFY LENVFGQPDSPFFC*AEQPLCSTFQPGP SHGLTDYEEKEEYALAFYQHRTVVPVSE *DKAITRRVGEAISCNKLILLYQTWKKIM NHLTS |
| 1962 | 10013 | A | 2902 | 620 | 1124 | ETPAPCLQAWVPQACREGPLAFRELLGG VLALSTPGERCSVSSEFETRARCTQ/PC WGSPKFLSPPHAKPAITLRPELKEAPWP APSLGPPGGLSTPPSGIPCPPQCCQGHVA LCRGLRPSPW*TE*PVCWKMPRCPEKLP PGIFGNETYLVPIVNWPTGTSFLSTY |
| 1963 | 10014 | A | 2903 | 2 | 399 | WKESQGRCEW*VARGL*ADLT*GFHWH LPGAPPWGLLTGGGQGRGHGRGGWA LSGRPPRGFHWHLPGAPPWGLLTGGG QGRGHGRGGWALSGIPRLQSFQVWA ESPLQLPWGCVAGISVHTGVSWLP |

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| 1964 | 10015 | A | 2904 | 73 | 867 | GRAEQTS DTHFFASTSACSHNLTMSCPN YCSGNSNSGSLRTSRHIPLTSDLCPTSVS CGDVL YLPTSSQDHTWVTDNCQETCGE PTSCQPVHCETGNLETS CGS/SHC/CTTCP GPCQGSFLPASFFSSSCLPVSCRTTEVC/ RPAAVRPLRAVVQ*FTSP*GDCVAQCLAR PQFCLSKSCQPQNLLTSGCQPSSCLAYRP QSLHVVS S L RPLGPLFSGCQPLTHVFST VSSHLALEHGSPNICFLQSSILLHRSSSRA VCSSALF |
| 1965 | 10016 | A | 2905 | 1 | 478 | |
| 1966 | 10017 | A | 2906 | 800 | 1209 | LFSSGAVPQRTSPHQAPKNMQTSGRLS NVAPPICILRKNPPSARNGGWET*CPNSL NSNQQLVDLKLTV DGLEKERDFYFSKL RDIELICQEHESNSPVISGII GILYATEEG FAPPEDDEIEEHQ QEDQDEY |
| 1967 | 10018 | A | 2907 | 1 | 3961 | MSSKHLKSEQIKDQIRVPVISLIPKIHSAQ EEQLSSTAVCSCPARVFCVTKVAVVQ MWMLHDLVQMVPRLQWLPHFTLFSN PLILYHSHELAPSAEQRECKLAYMPVS SASAHLLQLAFDFNLSVLSLARNML ANSASVRILKGGKV VND DCTHEADVYI ENGIIQQVGRELMIWRGQGLVIPGGIDT STHFHQTFMNATCVDDFYHGTKVMLLF AKGGFLGFFILLGLLQTRLMASLAKS D |
| 1968 | 10019 | A | 2908 | 48 | 308 | NPRCGPGSRFVSSWCSVFPEAGGG*RK EPGMRGAGYKQRMGS*SKGPF AFIMPF PRPRPGFVLP PPPHLPDLNKGPHFSQKKK KK |
| 1969 | 10020 | A | 2909 | 3 | 214 | |
| 1970 | 10021 | A | 291 | 49 | 418 | FMINPPNQVGRYRNINLTNIYQKPLAP VIL/HGEIFKIFLTGIGVTQRYPLSPLPFKV FLAALDRK*REGAGEEVNGIENKRIKLSF VSDMIVYVENSKEKNGQLLELMRGICKT ATKLQKL |
| 1971 | 10022 | A | 2910 | 312 | 387 | |
| 1972 | 10023 | A | 2911 | 3 | 216 | NCLLRPKNKSVRWGP GAGAALLRPSA ALGAGSRACSVPPAAPQT PRPQVSAPA WGPGR AARGSGRMERRMKAGYLDQOV PYTFSSKSPGNRLAR\TLIGPLGLMDP GSLPPLDSEDLFQDL SHFQETWLAEAQV PDSDEQFVPDFHSENLA FHSPTRIKKEP QSPRTDPALSCSRKPPLPYHHGEQCLYSS AYDPPRQIANQVPCPWCLDSRPYSFPFG QSNGIS*DPLAPPSP T LAMGTSGNIAPSSS SPWDICHSFTSQGG/APG/HPSQAPYQH LSEPCPPYPQSFKEHYHPLYGTGGAS QAVGTRGGSGMGAQ/RYPGAGVVIKQE QTDFA YSDVTGCASMYLHTEGFGSPSP GDGAMGYGYEKPLRPFDDVCVVP EKF EGDIKQEGVGAFREGPPYQRRGALQLW QFLVALLDDPTNAHFIAWTGRGMEFKLI EPEEVARLWGIQKNRPAMNYDKLSRSL RYYYEKGIMQKVAGERYVYKFVCEPEA LFLAFPDNQRPAKAEFDRPVSEEDTV LSHL\DES PA*PPYSGLAPRPSVRAPGHA RYPRLQPRRPLRSRPLGAPAVRREG AAGWSSG |
| 1973 | 10024 | A | 2912 | 119 | 444 | GFGVGTTPALTCPVTPSYSPKARPS*T/EL EPSPRCQPQCQTLGPQAEQNQMSSAPSL ASPPSKQPPLMANRCCCVPRSRHLCGIQ NRLGFWDSREERGGDATWVSVD |

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| 1974 | 10025 | A | 2915 | 1 | 574 | GADGGGAFRLSGPGP*APPGSSALMMP SSCPWRTGALGPSPAGSRALGRCTSSVG PGSRWLTRTSSPGCAYQNLNEDDGAQ ASPEPDGGVGTRLGPGIPAE/PSIRSFVV LQHHSAAAPSAPTPAAAGPNTL*SRRT AEWCWPPSCCCLGPGADPGRRGNWRR PPLPRCLORQSSSCRAFLLLVPGV |
| 1975 | 10026 | A | 2916 | 355 | 511 | LFLETESCFVAQAGARWAVITHCSLKL/L GPCNPISAL*VARTTGMSHHTP |
| 1976 | 10027 | A | 2917 | 1815 | 2152 | INKEMSGQARWLTPVIPALWEVKVVDH LRPGVRDWHQPGQOSETPVSTTIQK*ARY GGMCL*S*LLRRLTQQNHLNQGGRCSE LRSRYCTPAWARQSKTSSQEKKEKEM PW |
| 1977 | 10028 | A | 2918 | 315 | 480 | |
| 1978 | 10029 | A | 2919 | 1 | 1845 | |
| 1979 | 10030 | A | 292 | 5 | 377 | FMINPPNQVGRYRNINLTNISQKPLAP VIL/HGEIFKIFLTGIGVTQRYPLSPFKV FLAALDRK*REGAGEEVNGIENKRIKLSF VSDMIVYVENSKEKNGPILLEMRGLSK NATKLQKLI |
| 1980 | 10031 | A | 2920 | 407 | 802 | |
| 1981 | 10032 | A | 2921 | 914 | 1134 | QESLLLQFTKSSSCPSETTSARTLLSILLS AFWAKPFNKSLGSSKLSHIFLSSDSPSK/A VPTSAYYPVPKSLPH |
| 1982 | 10033 | A | 2922 | 1 | 447 | |
| 1983 | 10034 | A | 2923 | 218 | 544 | SGFSLSLRGSSISFSL/CFKVGMCVTYPRCY C*SPVP*KPLIKPGWVSELPKPMNWASC SRTLASFLLQAARSHPWTPMKMETMEQ SKLRSQPCPKAAGAVDPRAVVHGT |
| 1984 | 10035 | A | 2924 | 3 | 260 | |
| 1985 | 10036 | A | 2925 | 1 | 534 | |
| 1986 | 10037 | A | 2926 | 198 | 562 | LKCGKQWSDPITSPQTESQLLGSSQQQL HQQRHLQGP*K*NRDSPLCFSLSSCPIPK TYTNRHILLP/SSSKSLCKFL*PA*ISPQKM GFSLSQSVCKFSKLLCSASLIKLKAFNSI QVTS |
| 1987 | 10038 | A | 2927 | 72 | 270 | |
| 1988 | 10039 | A | 2928 | 325 | 535 | |
| 1989 | 10040 | A | 2929 | 492 | 696 | |
| 1990 | 10041 | A | 293 | 346 | 489 | QLQAMAIFEYLKKTFLRPGTVPHSCNPS TLAGGRGGWIT*GQELEASP |
| 1991 | 10042 | A | 2930 | 822 | 1759 | SSAEPSPSPAPSQQTAAGAPPLCAVS PMASASGAMAKHEQILVLDPPDCLKFKG DG*VFIRPEQYYTV*KWCKRSKRHGPF PVFTDVVTNLKLRNPSPDRKVCVKVTT VPS/RRYCVRPNSGNDPGSTVTVSVML QPFDDYDPNERSKHKFMVQTIFAPPNTSD MEAVV/WKEAKPDELMDSKLRVCFEMP NENDKLNDMEPSKAVPLNASKQDGP PKPHSVSLNDTETRKLMECKRLQGM MKLSEENRHLRDEGLRLKVAHSDKPG STSTASFRDNVTSPPLSLVAVIAAIFIGFF LGKFI |
| 1992 | 10043 | A | 2931 | 2 | 417 | FVAQQLQGDSLHFMQALYGQHFPIEVR HYLSQWIESQA/WNTYDRCPMELVRCIR HILYNEQRLVREANNNGSSPAGSLADAMS QKHLQINQTFEELRLVTQDTENELKKLQ QTQEYFIIQYQESLRIQAQFGPLAQLSPQ |
| 1993 | 10044 | A | 2932 | 1 | 855 | |
| 1994 | 10045 | A | 2933 | 1 | 810 | |

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| 1995 | 10046 | A | 2934 | 224 | 2606 | TMAVWIIQAQQLQGEALHQMQUALYGGQH FPIEVRHYLSQWIESQAWDSVDLDNPQE NIKATQLLEGLVQELQKKAHQVGEDGF LLKIKLGHYATQLQNTYDRCPMELVRCI RHILYNEQRLVREANNSSPAGSLADAM SQKHLQINQTFEELRLVTQDTENELKKL QQTQEYFIIQYQESLRIOAQFGPLAQLSP QERLSRETALQKQVSLEAWLQREAQT LQQYRVELPEKHQKTLQLLRKQQTILDL DELIQWKRRQQLAGNGGPPGSLDVLQS WCEKLAELIHWQNRQQIRRAEHLCCQLPIP GPVEEMLAEVNATITDIISALVTSTFIEK QPPQVLKTQTKFAATVRLLVGGKLNH MNPPQVKATIIEQQAKSLLKNENTRND YSGEILNNCCVMEYHQATGTLAHSFRN MSLKRIKRSRRGAESVTEEFKTLFESQ FSVGGNELVFQVKTLSPVVVIVHGSQ DNNATATVLWD\NAFLQEPGRVPFAVP DKVLWPQLCEALNMKFAEVQSNRGLT KENLVFLAQKLFNNSSSHLEDYSGLSVS WSQFNRENLPGRNYTFWQWFDGVMVEV LKKHLKPHWNDGPILGFVTKQQAHDLLI NKPDTGTFLLRFSDEIGGIIAWKFDSE RMFWNLMPFTTRDFSIRSLADRLGDLNY LIYVFPDRPKDVVYSKYTPVPCESATA KS/VLDGYVKPQIKQVPEFVNASADAG GGSATYMDQAPSPAVC/PPQAHYNMYP QNPD*VLDTDGDFDLEDTMDVARRVEE LALGRPMDSQWIPHAQS |
| 1996 | 10047 | B | 2935 | 123 | 219 | XPPTGMTMDKSELVQKAKLAQAERYD DMAAA* |
| 1997 | 10048 | A | 2936 | 1 | 1815 | |
| 1998 | 10049 | A | 2937 | 1 | 510 | |
| 1999 | 10050 | A | 2938 | 107 | 961 | VVGLGRKRSSRSGASLGRVFPVPCSPPTG MTMDKSELVQKAKLAQAERYDDMAC SSERHVTEQGHRELQPKRNLLSVAYK NVVVGARRFLPGRVISSIEHENREGMKKK QQMGKVEYP*EDRRQNLQDICK*CFWEL LDKYLIPN/AVTQES*GVLL*KLKGGYF RYLSEVAS*DNKQTTVSNSQPGFTREHF EISKKEMQPTHPIRLGLALNFSVFYIEIL NSPEKACSLAKTAFDEAIAELDTLNEESY KDSTLIMQLLRDNLTLWTSENQGDGEGD AGEGEN |
| 2000 | 10051 | A | 2939 | 208 | 1178 | EGRGHLARSFARKGLCSLQPSHGRVSRD LGRYKKCILPRLWIEKQEEHWTWSQGM TMDKSELVQKAKLAQAERYDDMAAA MKAVTEQGHELSNEERNLLSVAYKNVV GARRSSWRVVISSEQKTERNEKKQQMG KEYREKIEAELQDQNDVFELLEQISLFP NATQPRKVKVFLLEK*KGDFRYLF*K WQS*RQQTQPTCVETPQQLPRKQFEISK KEMQPTHPIRLGLAPKFPQSFYIEPKL PLKKA*AWAKTALCFRHF*SNLLNL DTLEWKSLLKSDSTSDSWQLLRDNLTLW DIRKTRGDEGDAGEGEN |
| 2001 | 10052 | C | 294 | 140 | 172 | |
| 2002 | 10053 | A | 2940 | 1 | 459 | IEIHIKCGGIPAVLAAPAMGLEFLDLVS QPSRAVYIFAKNGIPELRTVDLVKGQ HKSKEFLQINSLGKLPTLKDGDFFILTE/SA NRSVYLQGGCWHITEMRFSKCKAEGPA KRSAILIYLSCKYQTPDHWYPSDLQAR ARVHEYLGWHAD |
| 2003 | 10054 | A | 2941 | 2 | 310 | |
| 2004 | 10055 | A | 2942 | 205 | 454 | |

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| 2005 | 10056 | A | 2943 | 5 | 437 | AQESRDCGDHDRATALQPGQQSEILLQ RLPPENAVD*VALEGSQPL*TLACLLSCK YQTPDHWYPSDLQARARVHEYLGWHA DCIRGTFGIPLWVQVRRANLPFLSFPLAP VPSQLHVKLCTDKTLSVLGSASILRCSI HTS |
| 2006 | 10057 | B | 2944 | 307 | 447 | XSAILIYLSCKYQTPDHWYPSDLQARAR VHEYLGWHADCIRGTFGIPL* |
| 2007 | 10058 | A | 2945 | 2 | 384 | |
| 2008 | 10059 | A | 2946 | 1 | 1278 | MPGLGFREKKGGSRTVIPASRGCGLPAPI LCTKWELPLSGSSRCLAAAAALQGTVWT AESSSLTPAFQSRGWGLIPYFPARRDPAT AAAHOTALSAFTAIPAVLAAPAMGLELFLA DLVSQPSRAVYIFAKKNGIPELRTVDLV KGQHKSKFELQINSLGKLPTLKDGFILT ESLAILIYLSCKYQTADHWYPSDLQGF GARVHEVPWAWHADLHPVGTFWYYP WGVQGVWGHSLGVQVPEEKVGTQTRT AMDQALQWLEDKFLGDRPFLAGQQVTL ADLMALEGS*CKPVALGYELFEGRPRI AAWRRRVEAFLGAELCQEA/HTSILSIL EQAARKKTLPTSP*EAYQAMLLRNRPGS PEGSGMGAKEISNKDSFCYLLAPFYLSLL PQSLLSKLQCEALHRQRHSSVLWQVLLL LRCKHT |
| 2009 | 10060 | A | 2947 | 298 | 456 | NIYQLE*K*FKNGQVWLGAVVRACNPST LGGR/WIPWGQEFGTSLANMVKPRLY |
| 2010 | 10061 | A | 2948 | 59 | 190 | ARSFHSDAPQGHLECHWCPCGVLEL*GHR NPDTCPHLEQGISSK |
| 2011 | 10062 | A | 2949 | 319 | 460 | HFSYIHWFYTEKYKIKITHQDYLQKFIIY/ CTEEKHAYH*PNKILFIT |
| 2012 | 10063 | A | 295 | 2008 | 2438 | WSLHRPRGPLLWHMPRVPPPLTGL*SSP HDSVGPQWKSPPPTTSFNSPDPENVQN HPGKPVAKSPFVPQRNGH/PPKR/PTWGS STCWGEVIRSGSPPTKPVWPTSCEFGS VLPEDETVFPHPFVSLILFAISFALVCG D |
| 2013 | 10064 | A | 2950 | 78 | 3703 | FQELGAREPFGNMYDADEDMQYDEDD DEITPDLWQACWIVISSYFDEKGLVRQ QLDSFDEFIQMSVQRIVEDAPPIDQAEA QHASGEVEEPPRYLLKFEQIYLSKPTHW ERDGA SPMPMPNEARLRNLTYSAPLYV DITKTVIKEGEEQLQTQHKTFIGKIPIML RSTYCLLNGLTRDLCLENECPSPDGR YFIINGSEKVLIAQRKMATNTSFCRLQK TDSKYAYTGECRSCLNSSRPTSTIWWVS |
| 2014 | 10065 | C | 2951 | 162 | 293 | MGNLLKVLCTCTDLEQGNFFLDFENAQP TESEKEIYNQVNVAL* |
| 2015 | 10066 | A | 2952 | 286 | 1327 | AGAKFFP*F*KVADAQPTSESEKEIYNQV NVVLKDAEGILEDLSYRGAGHEIREAI QHPADEKVAKKAWGAVVPLVVGKLKK FYEFQRLEAALRGLLGALTSTPYSPTQH LEREQALAKQFAELHFTLRFDELKMTN PAIQNDFSYYRRTL SRMRINNYPAEGEN EVANELANRMSLFYAEATPMLKTLSDA TTKFVSENKNLPIENTTDCLSTMASVCR VMAGNTIYRSQILQNEETVSFLSWRAM VGCS*YSYDHRSTSSGEAFCLKLPKFDK GCIKVLKDQPPNSVEGLLKSRLRYTTKH LEWMRLPPSKLKSMLPITILGIKHPAVDR ROYSAMTENAVF |
| 2016 | 10067 | A | 2953 | 75 | 478 | AVKMCDF*DTA*FKEAFQLFDRGTGDG KILYSQCGDPKSDEMNVKVLDFEHLPL MLQTVAKNKDQGT*DYVEGLRVFDKE NGGTVMGAEIRHVLVTLGEKMTTEEVQ MLVAGHEDSNGCINYEELVRMVLNG |
| 2017 | 10068 | A | 2954 | 2 | 343 | |

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| 2018 | 10069 | A | 2955 | 34 | 353 | |
| 2019 | 10070 | A | 2956 | 2 | 303 | |
| 2020 | 10071 | A | 2957 | 1 | 999 | |
| 2021 | 10072 | A | 2958 | 255 | 528 | ARYKIHTGKGTDSGETGKVLSSHAPCGR CSRPFWARHPDRSMPHKRFIVDTNQLLS CPATSISTSSSVNVLPRCD/FPEDQTAEFK EAFQLFDRTGDGKILYSQICGDVMRALG QNPTHAENVLKVGNPKSDEMNVKVL FEHFLPMLQTVAKNQDPGSPMGFMSKE LRVFKYKIEGNGTVMGAEIRHVLVTPG* KLTEEEVEMLVAGHEDSMGICINYEAFV RHTPVGVTPGWAGASSAWC |
| 2022 | 10073 | A | 2959 | 26 | 518 | AVKMCDFTEQDTAEFKAEFQLFD/RKPG DGKIPCTAQCGDVMRALGQNPPLNAEV LKAPGEPPRSDDMSVKEHDCHEFLHIL QTV AQNQGQIGTYAEDYVEDFRVFDKEG NGTVMGAEIRHVLVTLGEED*QRKKV EMLVAGP*RTANGLVSNEYELVRMVLN G |
| 2023 | 10074 | C | 296 | 165 | 290 | MCHRAGPASLSAGQFIHIFLVTPMAAPRI SAVCGPESRHQ* |
| 2024 | 10075 | A | 2960 | 453 | 744 | |
| 2025 | 10076 | A | 2961 | 736 | 1062 | |
| 2026 | 10077 | A | 2962 | 295 | 782 | PLLCNPDPGWYWWVKQSEISKESQEM DARPKLDLGFKEGQTIKLCIGNITNKKGG ASKPRTARGGGLSLLPPP*GKVTIPPPSS /VKLPSTNHVTPPSIPKSNHGGSDADILLA DLDSPAPVTTPTPTVSVSNDLAWGDFS TASSSVPNQAPQPSNWWVQF |
| 2027 | 10078 | A | 2963 | 192 | 324 | |
| 2028 | 10079 | A | 2964 | 1 | 1044 | |
| 2029 | 10080 | A | 2965 | 1 | 811 | |
| 2030 | 10081 | A | 2966 | 1 | 750 | |
| 2031 | 10082 | A | 2967 | 493 | 1946 | |
| 2032 | 10083 | A | 2968 | 539 | 1215 | |
| 2033 | 10084 | A | 2969 | 414 | 1762 | |
| 2034 | 10085 | A | 297 | 883 | 1095 | GSQV*DQPGQHGKPPSL*QNLAEERG GHL*SQLLRRLRQENHLNPGGRCC*SELR SRHCTPAWATRAKL |
| 2035 | 10086 | A | 2970 | 449 | 1305 | SKSRMSAEVIHQVEEALDTDEKEMLLFL CRDVAIDVTPPNVRDLDLNRERGLS VGDLAELLYRVRFRDLLKRLKMDRKA VETHLLRNPHLVSDYRVLMAEIGEDLDK SDVSSLIFLMKDYMGRIKISKEKSFLLD VVELEKLNLVAPDQLDLEKCLKNHRI DLKTKIQKYKQSVQAGTSYRNVLAQAI QKSLKDPSNNFRLHNGRSKEQRLKEQLG AQQEPVKKSIQSEAFLPQSIPEERYKMK SKPLGNLPLIDWHWALRTELSFEDTFTS LGY |
| 2036 | 10087 | A | 2971 | 473 | 1164 | SKSRMSAEVIHQVEEALDTDEKEMLLFL CRDVAIDVVPNVDRDLDLNRERGLS VGDLAELLYRVRFRDLLKRLKMDRKA VETPLFKDPPLVSDYGVLMAEIGEDLDK SDVSSLIFLMKDYMGRIKISKEKSFLLD VVELEKLNLV/APPDQLDLLEKCLKNIP QK*P*RQSQKYKQSVQAGTSYRNVLA QAAIQKSLKDPSNNFRMITPYAHCPDL KILGNCSM |
| 2037 | 10088 | A | 2972 | 482 | 692 | EKPL*SYLSSFFHFLEMGSHSIPRLVCSGV IVAHCSLQLLGSSDVPTS/ASR*LGLTGSH TTIPSLGLFLN |
| 2038 | 10089 | A | 2973 | 1 | 358 | AQLVEFGEHSMAPPAHFRALLYHPGTAT LVPHPAISQHSPPWGNA/RG*PV*RQR HLTAPRSPPHPRFRHKPGKDPRENPSRW PEVPSLPQTHVVPQAAWDTVNTTVCK NRSTKPD |

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| 2039 | 10090 | A | 2978 | 136 | 500 | GTLPNSSLCESNNGHPQRGRGSCPSRY TGVPSPPRLSRIQSWIR/HLHPPSPTRPSY SSPQASASPVGLRGHPAQWTTCRSRVP SPVRFSSGSDGEKRLGQSCPHGNDPGAA CISRPPYA |
| 2040 | 10091 | A | 2979 | 242 | 9991 | FKLELHQESDMEFNNTTQEDVQERLAY AEQLVVELKDIHQKDVQLQQKDEALQE ERKAADNKIKKLHAKAKLTSLNKYIE EMKAQGGTVLPTEPQSEEQLSKHDKSST EEEMEIEKIKHKLQEKEELISTLQAQLTQ AQAEQPAQSSTEMEEFVMMKQQLQEKE EFISTLQAQLSQTQAEQAAQLSSMQQVV REKDARFETQVRLHEDELLQLVTQADVE TEMQQKLRVLQRKLEEHEESLVGRAQV VDLLQ |
| 2041 | 10092 | B | 298 | 191 | 494 | MKLKRGAGSCKKPGSSGWGPAVGEFHS VQNICARREYQRQDYMADAMAQKQLD AEFQKRLEKNKIAAEEQTAKRRKKRQKL KEKKLLAKMKLEQKKQEGPX* |
| 2042 | 10093 | A | 2980 | 3 | 211 | |
| 2043 | 10094 | A | 2981 | 1 | 519 | |
| 2044 | 10095 | A | 2982 | 291 | 686 | GLGTAYISQDVWKSLEYVQAEVCCRGR VFLVCSCGSCWSKSSRCEPPYAVLSIQVE AAHMHEIWCRRSDRDLPWESSCSLLLE KDPP/SGPQTDQPKKHLTNFKSDKGDTF YPWTQNSGAGHGLGRQPSLGV |
| 2045 | 10096 | A | 2983 | 1 | 639 | |
| 2046 | 10097 | A | 2984 | 2 | 423 | GFLVLLTSRMKLRTLAKQRRHILSVDPK LRRRSRTGKAAPWCLIIAGTPLIIHPRFK GVRPCRDACLGPSPLAASPAFLGEGQEL ATSARNLTTRPRNACSPGFLLSRVHLCG TPLEI*PPGQGMFAAQDSS*AVSICAGPH WKSDCSTHLAGTPRAPGILAQGSL |
| 2047 | 10098 | C | 2985 | 80 | 106 | MRMKFGLD* |
| 2048 | 10099 | C | 2986 | 259 | 531 | MSPAHKNFQTPEPQRPGIPPEPPPGACY KCQKSGHQAKECLQPRIPPKRPICAGPH WKLDCTHLASTPRAPGTLAGGSLTASQ IFLA* |
| 2049 | 10100 | A | 2987 | 3 | 505 | |
| 2050 | 10101 | A | 2988 | 1 | 1056 | |
| 2051 | 10102 | A | 2989 | 1 | 1482 | |
| 2052 | 10103 | A | 299 | 2 | 478 | SGRLPWLAQPPPRCDHRGPRKSRRRSSS PRMRREEQKLKLERLMKNPDKAVPIPEK MSEWAPRPPPEFVRDVMGSSAGAGSGE FHVYRHLRRREYQRQDYMADAMAQKQK LDAEFQKRLEKNKIAAEEQTAKRRKK/R PQS**KKNLLAKMKLEQKKQEG |
| 2053 | 10104 | A | 2990 | 399 | 567 | ACYKCWKSGRVKECLQPRIPPKPCPIC AGPH*RSDCSTHLAATPRAPGTLAGGSL |
| 2054 | 10105 | A | 2991 | 1 | 468 | |
| 2055 | 10106 | A | 2992 | 1 | 984 | |
| 2056 | 10107 | A | 2993 | 1 | 900 | |
| 2057 | 10108 | A | 2994 | 1 | 522 | |
| 2058 | 10109 | A | 2995 | 3 | 1150 | |
| 2059 | 10110 | A | 2996 | 3 | 500 | LEGASYGETKADVAEGKSQKKATEWRS QGQRRKGEETSQLKDCRRTNQLSVKRT NQLSVIWTNQDVGSYANPLMAAEP AQ AVKLGWRPSPKPHIGDKSVSFWLLWMG SVQQGQKIGP/PSQGNACRPRNSS*SHVP CGGGPHWKLDCTHLAATPRAPGTLAG GSL |

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| 2060 | 10111 | A | 2997 | 3 | 603 | GHSRPRNWSQWSPRFLWLEAHRPSGSP DSAE LRSQVSDCLGTSRHTGALFLALG IYAASCYVARFIRVRPHRDAYS LQGRLS DHSPTFQGCQTTQGRLPWSFTLSGKSRF SGEGATTSPA HKNFQTPEPQWPGIPPEPP PTGACYTCRKSGHWAKECPQARIPPKPH PICVGP H*KSDCSTHLAATPRAPGTLAQG SL |
| 2061 | 10112 | A | 2998 | 1 | 669 | |
| 2062 | 10113 | A | 2999 | 1 | 762 | |
| 2063 | 10114 | A | 3 | 32 | 474 | LYALRNQIKPPPHVTGGQ*QKQERTKPA WRPPRP/GPPPFIALIGFCSSVPVAVVEL RVEPPGGHWPLSPLGEVRGEWRRPLSGL AS/VGQWLVP RSPEGGGGGWAGSPQVS GGWPPSAHLRNPPLSLGDILPAQHPALS PGGPKLCG |
| 2064 | 10115 | A | 30 | 147 | 766 | GALHLIRKGSPLHGQA HKHVAQQGRGIL SRVHRPTHVHTQGRKATRLGLCSAHGR APHP SFLPLVPVCCS/WHHCETPRPCPLL PCPPSSGASTRTASSPVLSLTD*PYLSE TEEQVSPGLTHKASLEPRSDSDAKTSSH PRDWPHPMVDCAAALSWTQPLWMFCG SRLAFHDAPAPAHMRAIWASRAIPAARP GPHLGLAAASC |
| 2065 | 10116 | A | 300 | 72 | 409 | VCSETGFILYCRN/DCKWDAPILETVWFF VRS*TLDMNCTPAIPFLFIYPLEMYGHA Y*MTCTRIFMAALFIATNQKSPKCSINSI HATKYI IAMKLIQLYPYVATWINKVF |
| 2066 | 10117 | A | 3000 | 1 | 519 | |
| 2067 | 10118 | A | 3001 | 1202 | 1315 | |
| 2068 | 10119 | A | 3002 | 1 | 930 | |
| 2069 | 10120 | A | 3003 | 132 | 248 | |
| 2070 | 10121 | A | 3004 | 3 | 439 | |
| 2071 | 10122 | A | 3005 | 1 | 357 | |
| 2072 | 10123 | A | 3006 | 1 | 765 | |
| 2073 | 10124 | A | 3007 | 1 | 1434 | SVAFVFACPAVDYLVKISWELQGDEEQD GLRNMWQTLQKTKDYEDVRIQNAINI AQGASEAIGQRQSSAAKPRRSGKESVRE PWARVPGALGVAARKYQKMKGIEIKRR ERLKC GAKIERRKRLKDREVGEEKKRP LTGFEIEPPKVTVM PKNQSFTGGSEVSIM CSATGYPKPKIAWTVNDMFIVGSHRYR MTSDGTLFIKNAAPKDAGIYGCLAKAPK LMVVQSELLVALGDITVMECKTSGIPPP QVKWFKGDLELRPST/CFLLSILAP/PLQS LPSLNFNSFHFLADFLAATPRAPGTLAQG SLTDSFPDLLGLAAED |
| 2074 | 10125 | A | 3008 | 166 | 421 | RPRSERLLWGTSPLS/CALTL*GDPPTTSG PQTNQLKEHLTNFKSGPHWKMDCPHP AATPRAPGTLAQGSLTDSFPDLLGSAAE D |
| 2075 | 10126 | A | 3009 | 1 | 434 | |
| 2076 | 10127 | A | 301 | 92 | 617 | DRVLSLLPRLECSG SILAHCNVCLP/GFK RFS\CLSLPSSWDYRHTPPCP/V*LVFLVE MGFRHFSQAKSRTL/TGDPPASASQKCW NYRRDNLA WLASALNKVINLLKSEIPSF FLVQLSGFSRTLLLQGFNFNYHTLVYS NNLPIMQFTFTQDFGRISGKPFPGIMILCN REILYIM |

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| 2077 | 10128 | A | 3010 | 1478 | 2240 | WQVPLSWGRGKYPSTPSPSPLAASPTFL GQGQVPLNPFSTLSGKSRFPAGASTPQ PLLLHPQRQVPLSWGRGKYPSTPSPSPA ASPAFLGQGQVPLNPFSTLSKSRFPRG QETPNRLFHPNLLSLHPNLPFHPDLLS LCPNLPCLNPFSAFLEGKNPPPLLRVST LFSGLASFTMGACYTCQKSGHWAKECP QPGIPPKPCPISVGPH*KSDCSTHLAATPG APGTLAQ/GLTDSFPDLLGLAAED |
| 2078 | 10129 | A | 3011 | 1 | 624 | |
| 2079 | 10130 | A | 3012 | 321 | 512 | |
| 2080 | 10131 | A | 3013 | 1005 | 1251 | KGGWSQRHSQGACYTCRKSGHWAKEC PQP GIPKPRPICVGP H*KSDCSTHLAANP RAPGTLAQGLTDSFPDLLGLAAED |
| 2081 | 10132 | C | 3014 | 18 | 56 | MAINSIRSLQLM* |
| 2082 | 10133 | A | 3015 | 188 | 364 | |
| 2083 | 10134 | A | 3016 | 602 | 2459 | FWGEGEKATAFLICNLAGCLRCPVDMN SVQGSDSNEEDYDPNCEEKEEEEEEDVPA GDIEDYVVGVASDVEQQAADAFDPVEE YQFTCLTYKESEGVALNEHMTSLSLSL KVSHSSWLNLYLVNFHWQVSEILDRIK SNSAQLLVEARVQPNP/SQKHVPTSHPPH HVCAGCGMQVCAKRENLL/SLWACQL*F CRSCWEQHCSVLVKDGVGVGVVSCMA\ QDCPLARNTSGTFVFP LLPNEEFEEKY RRYLFRDYVESHYQLQLCPGADCPMV IRVQEPRA/RARVQCNRCNEVFCFKCR QMYHAPTD/CATIRKWLTKLQDDSETA NYISAHTKDCPKCNICNEKDGGINNHM QCSKCKHDFCWMCLGDWKTGHSEYYE CSRYKENPDIVNQSQAQA/RREALKKY LFYFERWENHNKSLQEAQTYQRNHEKI QERVMNNLGTWIDWQYLQNAAKFFGQ GSFSSLLQCRYTLQYTYPYAYMESG PRKKLFYQQAQLEAEIENLSWKVERA DSYDARGDLENPDIIITEPTGGTNPCKD FHDTLSWDVDVPGVRKISLARSRAAH TACLAGSAFHDPQATAQGPTPERHWQH LLVDFCFLFSLFVSTQGRRPC |
| 2084 | 10135 | A | 3017 | 103 | 769 | GPCCIPHIQQLILFQCFKHFSGLCFQLCK LMMPSKSLVMEYLAHPSTLAGLVGVAC GMCLGWSLRVCFGMLPKSKTSKTHTD TESEASILGRQPGSPG*FLVVRN*L*RWG KGERGCPSASHAAVSSPTKQISKKKSPE MAQNNGEYWWASPKVGGSKVPDEETLI ALLAHAKMLGLTVSLIQDAGRTQVAPG SQTVLGIGPGPADLIDKVTGHLKLY |
| 2085 | 10136 | A | 3018 | 99 | 478 | |
| 2086 | 10137 | A | 3019 | 2 | 87 | |
| 2087 | 10138 | A | 302 | 367 | 619 | ETRCRGHPPRDREPPPS*PGIQSSPGVP/PS RPSNKA YPRLPIRPQPPGLSFRISTPPRPSP KPPCPPHIGRHVQPTKTS AVSILS |
| 2088 | 10139 | A | 3020 | 1 | 921 | |

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| 2089 | 10140 | A | 3021 | 1 | 2203 | MGGASARPAAPSGRWGVPLPGRPFWEV MSPSARPPRLGGVPNSSLRTHGDDGG FVEQRRGKGDSEGLRLIKLVVFSW QLVMAFDKAELPSSPKVLVLTTRATG GVGLQTLRRLQERPGIGQLGALCLICTVR LCGHEEMTSTFNPCKLSKQEGQNYGF FLRIEKDTEGHLVRVVEKCSAEKAGLQ DGDRVLRINGVFVDKEEHMQVVDLVRK SGNSVTLLVLDGDSYEKAVKTRVDLCEL GQSKEQGLSDNILSPVMNGGVQWTQ PRLCYLVKEGGSYGFSKTVQGGKGVY MTDITPQGVAMRAGVLADHLEVNGE NVEDASHEEVVEKVREGPRRVGYGDR QQMAAALQKRGLTVKNKQTESNNINK KRPHKNPIQSAASKIEELEKNYFKIQYG SKKEPVQVKTTVSKKNKAGGITLPDFKL YYKVTVTKTACSRYPFWKMNLCVILLIL /VFPMPVFLQLAYFIVSNIRLLAHKQRLIF SCLLWLTMYFFWKLGDPPILSPKHGIL SIEQLISRVGVIGVTLMALLSGFGAVNCP YTYMSYFLRNVTDTDILALERRLLQTM MIISKKRLRGPGVVGFLIYSPVQIAE DLTIQQEVDALIELSRQLFLETADLYAT KERIEYSKTFKGKYFNFLGYFFSIYCVW KIFMVKFWSQHISFILVGIIIVTSIRGLLITL TKFFYAISSSKSSNVIVLLLAQIMGMFYV SS |
| 2090 | 10141 | A | 3022 | 2 | 215 | |
| 2091 | 10142 | A | 3023 | 50 | 1598 | GGLWPQRAVASGSGKWRQEPSLHFAMS FLIDSSIMITSILFFGFWLFFMRQLFKD YEIRQYVVQVIFSVTFASFCTMFELIIFEIL GVLNSSSRYPFWKMNLCVILLIVFMV PFYIGYFIVSNIRLLLSPLSQVA*TTDWL FSCLLGLTFMYFFGKLGDPFPLSPKHGI LSIEQLISRVGVIGVTLMALLSGFGAVNC PYTYMSYFLRNVTDTDILALERRLLQTM DMIISKKRMAMARRTMFQKGEVHNKP SGFWGMIKSVTTSASGSENLTIQQEVD ALEELSRQLFLETADLYATKERIEYSKTF KGKYFNFLGYFFSIYCVWKIFMATINIVF DRVGKTDVPVTRGIEITVNYLGIQFDVKF WSQHISFILVGIIIVTSIRGLLITLTKFFYAI SSSKSSNVIVLLLAQIMGMFYVSSVLLIR MSMPLEYRTIITEVL/GEELQFNF/YIHRW FDVIFLVRRLGILFPLFGLHKQAPEKQ MAPLNLKPYLQTDKRPSGFQKFRI |
| 2092 | 10143 | A | 3024 | 1 | 158 | |
| 2093 | 10144 | A | 3025 | 2 | 1067 | AAELGTFAQTQSGAWRAERSWHNRGP MMWRPSVLLLLLLLRHGAQKPSPDAG PHGTGRVHQAPLSDAPHDDAHGNFQY DHEAFL*REVAKEFDQLTPQESQARLGRI VDRMDRAGDGDGWVSLAELRAWIAHT HQRHILDSVSAAWDTYDTRDGRVWE ELRNATYGHYAPGEEFHDVEDAETYKK MLARDERRFRVADQGDSDMATREELTA FLHPEEFPHMRDIVIAETLEDLDRNKDGY VQVEEYIADLYSAEPGEEPAWVQTERQ QFRDFRDLNKDGHLDGSEVGHVWLPPA QDQPLVEANHLLHESDTDKDGRUTKAE ILGNWNMFVGSQATNYGEDLTRHHDEL |
| 2094 | 10145 | A | 3026 | 2 | 860 | |

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| 2095 | 10146 | A | 3027 | 2 | 1681 | FGTLGSAPFESCPFQKEDGMIKFQIQGHI VQERVTFKDVAVVFTKV*LALLDKAQI NLYQDVMLENFMNLMWIPLPVSFQLG SANGESQOEIQGRDKSEVRIFIPPFSLEV AVEWLYSISIDORDAHPKTDPKLRPEEA QRKSLSRNVKMHC FVKPRAAPQTEPTLE PTLFPSYPGVRPVPWRMRKEAYGLQSPE SPARSSGHSQGYPGEDLHRAEQRPERFA GSAWTSWLQRLATWKRIQRTGQNTWLE ALANLLANMTQLPGHFSTFLVSAPHPAA EKPLLHSILTHRPVHLLATVTLPAEEAP LMADITAQAILTPQLCSGTLALLAHVAAR AHADTNLQHVGPAGDTTGDMASMTLL PGSDTVDLKDTAPCIVAAPVPAMAKKG QGIAQAIASEGANPRPWQLPRTVGPVVN GEGKCGVGAPRVPTALPSGAVRRGPPS SRPQTHQQLPPCAWKRCRHSTPAHENSQ VGYTLQSHRGRDAQGLGSSSLASACLD VRHGVKGDYFRTLRFNDPCAGFQTGMG PAAPLFCCLISPFQNGGIYPKAVAPLYLGS N |
| 2096 | 10147 | A | 3028 | 51 | 569 | SLRTVPPHYLQSGPGTPIPPSSLGPASGTR RVES/CVAAPNEQEGSSKGGARPVTICDS QNRPCPPPPSPALPQADPSLKTWLLN HIRWDTDSMICMEDSS**GFK/PNKDSIK VQVRLRGVQGVGHCMGGAALPSTSLSS CLTPFPAPLNSRHTTLAPPLQPENPAQR TTP |
| 2097 | 10148 | A | 3029 | 2 | 395 | |
| 2098 | 10149 | A | 303 | 2 | 519 | FPLFLFLLLLLAFVVALTTTRIQGVPTL VLQAKRVNTSRPHPD/GS/QPPTSASFNQ LNPTTNTSPQLRSHVASGYVG*KQMOPY H/PPQHAPAPPQPCPWQVDTFLPAPTRPL LGSFGSPSRRSPGGVPPAGKGPAPGPE CPPTAQRPTT/RQYLGPLFKGDPRNSPRE KPRS |
| 2099 | 10150 | A | 3030 | 2 | 1038 | GLLEPFSKLLSFVIQNAVFTLAYLVELCG LCYRAFTKERDKFYLSRSGCSKSFCRRL KLKSPLPDTNLLLLVQFALPDAGTKLD*V NNPEQADDLSCTWDVGTAVAMECVRQY INEVLDFMADMHTLTKLKSMMKTCQA SDEDTFGGHLKVGLAQIAAMDISRGNH RDNKAVIRYLPWLYHPPSAMQQGPKEFI ECVSHIRLLSWLLGSLTHNAVCPNASSP CLPIPLDAGSHVADHLVILIGFPEQSKTS VLHMC SLFHAFIFAQLWTVYCEQSAVAT NLQNQNEFSFTAILTALEFWSRVTPAIL QLMG/HINKVMGRKWVLLSMWISLMGG NLPGNAIWT |
| 2100 | 10151 | A | 3031 | 3615 | 5322 | EVPPNPACYQHQA*SVCLCLHLKSSLTSS RR*/CTDKCHDCGAILEEYDEETLGLAIV VLSTFIHLSPDLAAPLLLDIMQSVGRLAS STTFNSQAESWPPTASSRSCSKARSKVIH PLRIQAPQICLIPDTQTLNPIVDFPDGTF RTLASSLMDFNELSSIAALSQLEGLNNK KNLPAGGAMIRCLENIATFMEALPMDSP SSLWTTISNQFTFFAKLPCVLPLKSLE PFSKLLSFVIQNAVFTLAYLVELCGLCYR AFTKERDKFYLSRSVVLELLQALKLKS LPDTNLLLLVQYENKMNEKAERLVKL LNSAQQQFQFICADAGTKLAESTILSKQ MIASVPGCGTAAMECVRQYINEVLDFM ADMHTLTKLKTSLHMC SLFHAFIFAQL WTVYCEQSAVATNLQNQNEFSFTAILTA LEFWSRVTPSILQMAHNKVLIPMWLPM IQSNIKHLASAGLQRLQAIQNHVNHSLR TLPGSGQSSAGLAALRWLQCTQFKMA QVENPVLGKQPLNFILYEWTPSAPQCQH SGLAIMGLKTNNDLPQAGWGNHIGLY |

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| | | | | | | NPLS |
| 2101 | 10152 | A | 3032 | 3 | 1078 | FFSSVFPAAIEPGERASARRRVSRAGCLA LTLPALLLVTHQVPAEAAVSRAMAEALT ALESLEMGFPRGRAEKALALTGNQGIE AAMDWLMEHEDDPDVDEPLETPLGHILA GREPTFSEQGGLKDLVLAAGEGKPALS */EEERQEQTKRMFGAWLAQKGSREIRE EREGREVALERERQRRVRQGEVLSAARQ RLQED\KMRR\AAAEEERRREKAEELAAR QVREKIERDKAERAKKYGGSVGSQPPQ VVAPEPGVPSPSPQEPPTKGEDDKCRI QVRLPRWDPH*PQTFRAREQLAAVRLAY VELHRGEELAGGGARDPVQIASVAFPRR AFLRSLTMERPLQELGMAAKTRNQD |
| 2102 | 10153 | A | 3033 | 2 | 565 | IHFQQEHWPSQLLLRESLEDMMHLSALG LCLLLVTVSSNLAIAIKKEKRPPQLSRG WGDDITGVQTYEEGSLCCK*GSH*WV IHHLGDCQYSQALKKVFAQNEEQEMA QNKFIMLNLMHETTDKNLSPDGQYVPR MFVDPSLTVRADIAGRYSNRLTYEPRD LPLLIENMKKALRLIQSEL |
| 2103 | 10154 | A | 3034 | 73 | 262 | |
| 2104 | 10155 | A | 3035 | 29 | 867 | PLEGIADNRPHGETSTLPATFCSPSAPEL ASMSVVPNRSQTGWPRGVTFQGNKYI QQTKPLATLAERTINLYPLTNYTFGTRAP LTRRTSSVAARFQRIEGKNFDKIGMRRT VEGVLIIVHEHRLTPWCYLLQLGTNPL NYLGWLNLTGGEDEVIEGLKTA**PEIPG SVQDGV\QD\WGPLTDCHWVTWWRP KFLNPPSVSHIFPAHITKPKH/IRKLFP SSLQEKALVLQFPKKFTSW*PATPLFELY DNA\PGYGPISSLPQLLSRFNFYIN |
| 2105 | 10156 | A | 3036 | 2 | 817 | RARIPKMAAVKDSCG*GEMATGNRRRL HLGIPEAVFVYYSY*RKMYHYFMKOP GNETADTVLKKLDEQYQKYKFMELNL AQKKRRLKGQIPEIKQTLKILKYMQKKK EISTNFNGRPRFFAGRLTLYLQKLSVPPT R*RG/CLGLGANVMLEYDIDEAQVALLGK DLASTATKILDSRGGRTLFLARDQFTTTE VNMARGLLIGDVKKEGNKD\STKNKA LMLGQFKNVGLVFPNMFIFKYPIFYRFD INFGMFNQPRNFKEKINTILFIY |
| 2106 | 10157 | A | 3037 | 3 | 468 | ERJMEWHRHTMTECSAQEPKSHDIYLR LVKLYRFLARRTNSTFNQVVLKRLFMSR TNRPLSLSRMIRKMKLPGRENKTAVVV GTITDDVRVQEVPKLVKALRVTSRARS RILRAGGKILTFDQLALD/SPYVRSKGRK FERARCRRARRGYKN |
| 2107 | 10158 | A | 3038 | 1 | 693 | |

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| 2108 | 10159 | A | 3039 | 105 | 756 | VDHPPYKRTEKVRAQRSPKSQYIYLSLL LKLYRFSGPPEEPSNIQTRVVLKRLFMSP HQTGPPLSLSRMIRKMKLSWPGKQRRRA VVC/VGPITD/DVRGSRYPKLKVCCTAP *PSRAPQAAILKAGGKULTFDQLALGLP LKG\CGTVLLSGP\SKGRKVYRHRFRQP QEPHPKPHQNPTRFSKGRKFERARGRR ASRGYKKLTLDPTLLYKKIFA |
| 2109 | 10160 | A | 304 | 444 | 920 | NPSLRCWLGLSPGKLAGARGRGTVHVHVG GPEGPCHTSTSTKRMAGRHEVSTGGGG KAP*/SQGIRGQAGQG\GARS\GVAGNG GGGARSRLRLSPAASATA/SGPEGS\GP GSGGRSRVPVEAAPP\CP\SDV\VP\AARGA AAAGPGGTWLPASQVGPSPGWG |
| 2110 | 10161 | A | 3040 | 301 | 390 | |
| 2111 | 10162 | A | 3041 | 1 | 737 | MWFAYSPTFCHDWKLPEASAEAKRMP ALCFLYSLQHPLCEDGVCAHEAGVWGI GGLIAYVKGYEEVSQKFTSIRRVRGDNY CALRATLFQAMSQAVGLPPWLQDPELM LVVFAILLHSHLECREPLLPILSLYMGA LVRCTTLCGYYKNIHDIIPDRSGPELGG DATIRKMLSFWWPLALILATQIRSRPIVN LFVSRDLGGSSAATEAVAILTATYPVGH MPYGWLTEIRAVYPAFDKNPNPSNKLVT SNTVTAHIKKFTFVCMALSLTLKDSVQ KPDISLTGRLVQTLPTMRHQRGESKDV APLASWLSEPTSSSEASQTSSKLTINSQG EGKAKQKLECGTSLIVLRSCENQERIK AAEKRNRSWTLGGLGAWRPLLFELPVI VQTPDQTNRFQFRYP\AKTQSGLC\SFHFS FDLLTLEAFVKVWFGCLLILLCFVMFW TPNVSEKILIDIIGVDFAFELCVVPLRIFS FFPVPTVTRAHLTGWL/QGPGAHAGCFC SHFASQSPGMPGAP\HPDPLL\HGR\TCA LHHPVPGLLQEHSRHP*QKWPGAGGR CNNKKDAELLVAFGSNSGHTENQSAYC QPLCFPGPW\WQFC\SHRGS\GDFD\SHIPCG SHAIRLVDGNPCCVSCFRQE |
| 2112 | 10163 | A | 3042 | 889 | 1577 | RGKKNVTLKKIRSQFTIRESFDLRYKEHI PLPKLEFPLDTKVFGLLGEDMVCTGPTG VALKGPHWKYIGIIDEKGDLVNFSYQKL VFRTSWSTWLPGRPVLLRDCSLKTPKP AAQAQEP\TVHLR\PRRQ\GFGSMRSLID WVSLTHSDGDVIVPIVLSNERYHWP\VL GWVGGVDCDEFFRVVLGEARLHLDGV AHQH*GKKEPFTCSKTTSVSHLVEVVP QKLSWVI |
| 2113 | 10164 | A | 3044 | 2188 | 2706 | RESIDQGF\SNFFFLRRSLDSVTQAGVQ WHDLSSLQPPPPGFK*K*FSCSLSS*DY RSPATMPGLIFLYFFFLVETGGFTVLAR\I MVSIS*PQ/CDPPASASQ\SAGIQKNSFFFL ETRVSAFVAQAGVQWCDLGSPQPPPG V\QPF\SCLSLPSSWDYRRTPPGPANFAVC N |
| 2114 | 10165 | A | 3045 | 33 | 198 | |
| 2115 | 10166 | B | 3046 | 6 | 125 | MAGQFRIYLWDPLLILSQIVLMQTVYYG SLGLWLALVDGL* |
| 2116 | 10167 | A | 3047 | 1 | 110 | |
| 2117 | 10168 | A | 3048 | 260 | 798 | RPGHAQTLGSPSLALGMAGQFRSYVWD PLLILSQIVLMQTVYYGSLGLWLAIVVD GLLRISPSLDQMFDAEILGFS/TPFQGRLS MMSFILNTLNSA\LGLLYFIRRGKIQCLDF TVTVHFFHLLGLLGSNSPSPSGG*TLV GLGPKPVVALHSLAVIGEYLCMRTELKE IPLNSAPKSNV |

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| 2118 | 10169 | B | 3049 | 1 | 528 | MRRQDCPNPMKKIRSSSPVQQERVSSLY FQSARGGLGVDVSALGTVTHVSPSSSAR VAMAMSAERGCSMGHIMGYRGVGRFT RGNGDHARVGYKGNPPEVSISGYDDNW YLGRDATLSCDVRNPEPTGYDWSTTS GTFPTSAPVPRAPSWSTQWTVCSIHRL HITNAVDGPR* |
| 2119 | 10170 | A | 305 | 504 | 935 | AYLQSSMIAQSRATRTGLATWHQHKL DRHFPRLSSRHPLFETCSSPPCKRWGEKS HFRACKEGRESAPCGIPRPFKVHTPRG KLRMARPVPRRFGGSRLGPRSRRKRRTK QPR*PAAPRDSFGAPAAPPTPRPSAARNG GG |
| 2120 | 10171 | A | 3050 | 31 | 206 | GSSCRSRSLVVLSIVLEGPAPAPGDPQT SPSALDKLKEFGNTLEDKARELISRIKQS ELSAKMRVPLRPRHEALPVAPGPGGSV DRLGRPSPSRPGPPDVSQLG*AEGVWK HTGGQGSQTHQPHQTE |
| 2121 | 10172 | A | 3051 | 21 | 353 | SAAGTGPEPEPEPHRHLLNRPADRPQSG PRASGRAQSPGPSMARAAALLPSRSPPT PLLWPLLLLLLLETGAQDVRVQVLPEVR GQLGGTVELPCHLLPPVPGLYISLVTWQ RPDAPANHQNVAAFHPKMGPSFSPKPG SERLSFVSAKQSTGQDTEAELQDATAL HGLTVEDEGNYTCEFATFPKGSVRGMT WLRVIAPKPNQAEAQKVTFSDPTTVAL CISKEGRPPARISWLSSLDWEAKETQVSG TLAGTVTVTSRFTLVPSGRADGVTVTCK VEHESFEAPALIPVTLVRYPPPEVSISGYD DNWYLGRTDATLSCDVRNPEPTGYDW STTSGTFPTSAVAQGSQLVHIAVDSLAFN TTFVCTSQPNPWALARAQVIFVRETPQ ALAPRCGPAGVGGRGGDTAGAAASGW GVLGLHPCMRVRRRRKSPGGAGGGASG DGGFYDPKASGVGKWGPRLLDTSSPWS HGTRWQG*GGGGGGREGREPRHVA STSRMTWSPSWTAPSSHGG/PVYV*PGPP WPGPLPSCRRDRRRRRCCGRCCCCSW KPEPRMCEFKCYPRCEASSGAPWSCRAT CCHFLDCTSPW |
| 2122 | 10173 | A | 3052 | 1 | 1620 | MARAAALLPSRSPPTPLLWPLLLLLLLET GAQDVRVQVLPEVRGQLGGTVELPCHL LPPVPGLYISLVTWQRPDAPANHQNVAA FHPKMGPSFSPKPGSERLSFVSAKQSTG QDTEAELQDATALHGLTVEDEGNYTC EFATFPKGSVRGMTWLRVIAPKPNQAE AQKVTFSDPTTVALCISKEGRPPARISW LSSLDWEAKETQVSGTLAGTVTVTSRFT LVPSGRADGVTVTCKVEHESFKEPALIP VTLVRYPPPEVAISGYDDNWDLGRDAT LSCDVRNPEPTGYDWSTTSGTFPTSAPV AQGSQLVHIAVDSLFTTFVCTVTVNAV MGRAEQVICVRETPNTAGAGPTGGIIGGI IAAIIATAVAATGILICRQQRKEQTLQGA EEDLEDGPPSYKPPTPKAKLEAQEMPS HLFTLGA*EHSPLKTPYFDAGASCTEQE MPRYHELPTLEERSGPLHPGATSLGSP VPPGPPAVEDVSLDLEDEEGEEEEYLD INPIYDALSYSSPSDSYQKGFMVSRAM YV |

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| 2123 | 10174 | A | 3053 | 408 | 2708 | DPSSGHWLHWSIRPPAAGWSPRSGRAA ARAQSPRRREHGAPGRTGPGGGPRLLLL AVLLAAHPGAQDVRVQVLPEVRGQLGG TVELPCHLLPPVPGLYISLVTWQRPDAPA NHQNVAAFHPKMGSPFSPKPGSERLSF VSAKQSTGQDTEAELQDATLALHGLTVE DEGNYTCEFATFPKGSVRGMTWLRVIA KPKNQAEAQKVTFSQDPTTVALCISKEG RPPARISWLSSLDWEAKETQVSGTLAGT VTVTSRFTLVPSGRADGVTVTCKVEHES FEEPALIPVTLVRYPPPEVVISGYDDNW YLGRTDAT/L*ACDVRSNPEPTGYDWS TTSGTFTSAVAQGSQ/LVIHAVN/SVLFN TTFVCTVTNA/VGIGAGAE/QVIFVRET RASPRDVGPLVWGAVGGTLLVLLLAG GSLAFILLRVRRRRKSPGGAGGGASGDG GFYDPKAQVLGNGDPVFWTPVVPGPME PDGKDEEEEEEEKAEGKGLMLPPPPALE DDMESQLDGLISRRAYTPSPVPVPSA GAAAVACTDPVPSSGVHGHNDHKNSSS MFRMKALAQSPYKTPNTAGAGATGGII GGHAAIIATAVAATGILICRQQRKEQTLQ GAEDEDELEGPPSYKPTPKAKLEAQEM PSQLFTLGASEHSPLKTPYFDAGASCTEQ VGAHGKTKEMPRYHELPTLEERSGPLHP GATSLGSPVPPGPPAVEDVSLDLEDEE GEEEEYLDKINPIYDALSYSSPSDSYQG KGFVMSRAMYV |
| 2124 | 10175 | A | 3054 | 115 | 467 | |
| 2125 | 10176 | A | 3055 | 315 | 431 | |
| 2126 | 10177 | A | 3056 | 53 | 442 | PRVMAM/ATKGGTVKAASGFNAME DA QTLRKAMKGLGTDEDAIISVLAYRN TAQ RQEIRTAYKSTIGRDLIDDLKSEL SGNFE QGAGTDEGCLIEILASRTPEEIRISQTYQ QQYGRSLVEDDIRSDTSF |
| 2127 | 10178 | A | 3057 | 186 | 1268 | PRDMAMATIGGTVKAASGFNAME DAHT LRKAMKGLGTDENAIISVLAYRN TAQRL EIRTAYKSTIGRDLIDDLKSEL SGNFEQ VIVGMKMPT*RDDVQELRRAMKGAGT DEGCLIEILASRTPEEIRISQTYQQYQ RSLEDDIRS DTSFMFKRVLVSL SAGGR DEGNYLDDALVRQDAQDLYEAGEKKW GTDEVKFLATVLCSEPKITLLHVFDEYQ KDIHRRHIEPEVLNSETSGIFWKIALLGLA VKCMRNKSAYFAEKLAYKSMKGLGTD DNTALIRVMVSSSQKMDMLDIPAHTSKR LLWKSPLYSEFIKNRVATSGDYRKIVLLV LCGREMIKIPGRDREGSSTLLNFF |
| 2128 | 10179 | A | 3058 | 1 | 4608 | |
| 2129 | 10180 | A | 3059 | 1 | 465 | |
| 2130 | 10181 | A | 306 | 163 | 387 | IRQKKAIFVIVAFKRRGLRKT D/YYYAR GG*FVKNKYRGFIHEL GTTCGKYFLCTL AIDPSDSNIIISMPEQT |
| 2131 | 10182 | B | 3060 | 109 | 192 | GSSSNEYLYERFGLLAVPSIRSLVQSK* |
| 2132 | 10183 | A | 3061 | 1 | 1542 | |
| 2133 | 10184 | A | 3062 | 1 | 4226 | EAVLCSSRGRPDSSMPDCCRNAALEARS CQSM TSLFSNTVSP TQDGTSSLPRRQSSF AKPPLRALYD LLIAPMEGGVVESTEPLG TSRSGFASGTALFWLGDNGKAASPPGVS VSSLENDNTQCNRL EQGYREAAVPD WTQDLALCLLPTLQSLKARTAPHLCVPS SCYKAWYTLAVSKVSGMVEGKAWIILL LLAASTHALLQRPQEGDITPLAGSRAAA VSCQARPFSTFGLMHSSGPVGRHRQLIL VLE |

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| 2134 | 10185 | A | 3063 | 2 | 4195 | ALDFPGRFRPTASFIWASVLFETIRHEA EVSTDYKLSLFDLQTSSYQALQRVLVSL GHHDEALAVAERGRTRAFADLLVERQT GQQSDPYSPVTIDQILEMVNGQRLVL YYSLAAGYLYSWLLAPGAGIVKFHEHY LGENTVENSSDFQASSSVTLPTATGSALE QHIASVREALGVESHYSRACASSETESEA GDIMDQQFEEMNNKLSVTDPTGFLRM VRRNNLFNRSCQSMSTLSFNTVSPTQDG TSS |
| 2135 | 10186 | A | 3064 | 8 | 665 | SAQMAVTTADPRVRPRVRTQLCSLATSN RHAWCILSPEEKSAVTALWGKVNVDEN VGGKALGRLLVVLPLVPDRFFESFGDL STPADAVNGQIPKVKVSWSRKCLGAIFS DGPGETWDNLQGSPLTLK*ACTC*QAC TWDP*RTFRLPGGNVAGFVVAWAHSL GKEFQPHQCKLA*SRKLVGLVLAKCPW PHKYHLKLAFLAVQFLFKGFLWSLKT NY |
| 2136 | 10187 | A | 3065 | 8 | 531 | SAQMAVTTADPRVRPRVRTQLCSLASLI QTRMVHLTPVEKSAVTALWGKVNVDEN VGGKALGRLLVVPWTPQRFESFGDL SVP*SLLRANP*GERLHGKKSASVPFSDG LAHLADNLKGTFAHTEVSLHCDKHLHRG SLKNFRLGQRAWSVAGPIHFWEKNF NPTSCRLA |
| 2137 | 10188 | A | 3066 | 91 | 951 | TPHFHQGTGKRAAWPTWFNPAGPGIFLR R*GPGKAQRRRSIAPRPVAVGFPSPGIVRC PHGFGYPHERLRAGPRLPALRKLVRAGI HKEGWPGPIGNSVDPRKPDQVPRSPLOA NVQRLKKYASNFILFPQSRPRAPKKGDR SVAELKLGHPSLTGPVMPVRNVYKKAE KARVITEEEKNFKAFAFLMARANAPAL RHTGQKEPREAAEQGC*KAHNKALPGD LESVGGQSCWVSTWCVSWEQLGLGWGFT AVTSSCQGIWGLERQSKPWIMLNLVL KPCWLF |
| 2138 | 10189 | A | 3067 | 1 | 1603 | MKLLKSILLTILLDFSLHTCASLVPALQW JLLLLITVLVVEGIAVAQKTQDQGNIGIK HIPATQCGIWWRTSNGGHFASPNYPDSY PPNKECIYILEAAPRQRIELTFDEHYIIEP SFECRFDHLEVRDGPFGFSPIDRYCGVK SPPLIRSTGRFMWIKFSSDEELEGLGISEQ IIPFIPDPDFTYLGRYFKFPS/HDCQFE/HL RELDGDSAAALVR*NKRRKQNGQAFD IWDL*/MPFQKLIYLRFLDYQMEHSNEC KRNFVAVYDGSSSIENLKAFCSTVAND VMLKTGIGVIRMWADEGSRLSRFRMLFT SFGGASPAQAALSFCHSNMCMNSLVCN GVQNCAYPWDEHNCKEKKKAGVFEQIT KTHGTIIGITSGIVLVLLIISILVQVKQPRK KVMACKTAFNKTGFQEVFDPHYELFSL RDKEISADLADLSELDNYQKMRRSSTA SRCIHDHHCQSQAASSVKQSRNLSSMEL PFRNDAQPMKTFNSTFKKSSYTFKQ GHECPEQGGPKDRVMGGRFPC |
| 2139 | 10190 | A | 3068 | 163 | 392 | HQELLFLLSSRRLSRSPSEGRPTM/AL GEKKIGFPSLLWCFPPSAAGASSQIKWQ PCGSGAPPLPGCSGKRRA |
| 2140 | 10191 | A | 3069 | 190 | 352 | HQELLFLLSSRRLSRSPSEGRPTMVL EKRK*GFHPHSCRAWRLKVCEGKS |
| 2141 | 10192 | A | 307 | 131 | 395 | LWAARAAVLTSLPTGSPSAALSGCCRP GGQGRYSVAACRGRAAGGVAPVPAHT* AAAPLGHFSFLLGIVSPAPEPHFELGHYY SGLS |

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| 2142 | 10193 | A | 3070 | 1 | 794 | MSRERPPGTDIPRNLFSIAAL/DGARLLP* PAAQPRGGAGGGARRGRDAVRGPPIRSR TESGP/SGPDLHQPEAAGGRP/CSRSPDT RKRVRFADALGLELAVVRRFRPGELPRV PRHVQIQQLQDALRHFAPCQPRARGLQE ARAALPASEPGFAARLLTORICLERAEA GPLGVAGSARVVDLAYEKRAPAAYAGP APPPPRADRFAFRLPAPPIGGALLFALRY RVTGHEFWDNNGGRDYALRGPEHPGSG GAPEPQGWIFI |
| 2143 | 10194 | A | 3071 | 133 | 1079 | ARRILQNFSLYPSGEDLKGYKVIQAQTA FSANPANPAILTEA/SAPIPHDGNLYPRLY PELSQYMGSLSLNEETRANVAVVSGAP LQQQLVAPRSSINYMGGLLLTG*LMLGI RRSR/II*GKGFREVILCKDQDGKVLGRL KSIDNGVIFVQLVQANSSSLGLV*EFGDQ VLQINGENCAGWSSDKAPRWSNRPF*E KITMTIRDRPFERTITMHKSTGHVGFIF KNGKITSIVKDSAAARNGLLTGPNLCGN SMGQNVIGLKDSQIADILSTSGTVGTITI MPAFIFEHIKRMAPSIMKSLMDHTIPEV |
| 2144 | 10195 | A | 3072 | 242 | 512 | AWVPCLLRHCDREPAPRGRTSPSLWPQE GT/P/GQDRGGGPWLQGPSLQ*QRSHGG HLPAPQGPLGGPHDNSSFRPGRGGAGRG QGIEQGSK |
| 2145 | 10196 | A | 3079 | 184 | 561 | QQRGRGLRKGSGASGAGMMEHTHTEA HPHTWVCTSTHTCTHTLGDYDMLHVL CVSIHMYV/CPHT/MSLALGMSAHTLHM FSHTKLLSR*HAGRHPMPKQVTCTYVP TPSPTHVLGHACGCRPHAS |
| 2146 | 10197 | A | 308 | 327 | 598 | GPARNPAQCRWAGTAGGPSTLSAAAGP GAKPLMPGAA/GAGQAGWLL*VQGPSP RPPGTLAGPQARHTALVPARASPTPPC KLRGGLRP |
| 2147 | 10198 | A | 3080 | 63 | 426 | GLLFPQHCPAHRPRCLRPSSAGRGS PALSRPSALCHLCLPRSSLAPRSVSPAA TPHH*ALQGLVEPWGPLHSAPLHR*APA SGPAGNVRAWPACRGWCLSRPLPGTV GEGAASRAF |
| 2148 | 10199 | A | 3081 | 1 | 588 | |
| 2149 | 10200 | A | 3082 | 81 | 289 | |
| 2150 | 10201 | A | 3083 | 3 | 387 | |
| 2151 | 10202 | A | 3084 | 2 | 290 | RPPGPSRSPAPPSSRRPLPKMACCACC ARVTAGVPGLGWGVGGPGQSPVTRR ARPPSGLLGFEARPLVPWTSRSPRCQCT ACGHLVEFVL |
| 2152 | 10203 | A | 3085 | 2099 | 5383 | VIQTSLSPPATNDRGHFSLDNWTGKP VHSMVAHLDAVTCLAVDPNGAFLMSG HDCSLRLWSLDNKTVCQEITAHKKHEE AIHAVACHPSKALIASAGADALAKAHKE QGGKRLHLPVEDDGFGAQAAPCWEEVP QGTNAQFLGCKGLCPSPAGPSEHTRKD GGRCLDTQDMAAFCWDSHLPFRKKGAE LQSPPLLPQIPAGSGVSFHIQIGLTREF VLLPAASELAHVKQLACSIQDQKRPRVQ VPRP |
| 2153 | 10204 | A | 3086 | 2 | 426 | EDGSLATFLGRRQFAFAEMRHSKRTHCP DWDSRESWGHEYSRGSHKRKRSHSST QENRHCRPHHQFKESD/CCSMCIPLEASH SVEEDTHPSHYLEARSLNERDYDRDRYV DEYRNDYCEGYVPRHYHRDIESGYRIHC SRS |

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| 2154 | 10205 | A | 3087 | 39 | 1514 | GDGAAAILWGVCRSGRGGKTAVWRHFS AEGPFAFAEMRHSKRTHCPDWGSIESW GHESYRGSHKRTRISHSRSENHRCKPH HQFKESDCHYLEARSLNERDYDRRYV DEYRNDYCEGYVPRHYHRDIESGYRIHC SKSSVRSRRSSPKRKRNRHCSSHQSRSM KSVDTLGEGAFGKVVECIDHGMGMHV AVKIVKNVGRYREARSEIQVLEHLNST DPNSVFRVCVQMLEWFDHGHVCI VFEL LGLITYDFIKENSFLPFQIDHIRQMAYQIC QSINFLHHNKLTHDLKPENILFVKSDYV VKYNSKMKRDERTLKNTDIKVVDFGSA TYDDEHSTLVSTRHYRAPEVILALGWS QPCDVWSIGCILIELYPWGSQFFRLQ**K EHLAMMERNIRTPYPQHMQKTRKRY FHP*PSLDWDEHSSC/AGRYVRRRCKPL KEFMLCHDEEHEKLFDLVRRMLEYDPT QRITLDEALQHPFFDLLKKK |
| 2155 | 10206 | A | 3088 | 2 | 175 | |
| 2156 | 10207 | A | 3089 | 1 | 534 | |
| 2157 | 10208 | A | 309 | 1 | 630 | |
| 2158 | 10209 | A | 3090 | 1 | 325 | LEKERDFY/FGKLR/NIELICQENEGENAP VLQRIVDILYATDEGFVIPDEGGPQEEQE EYYSLGPAEQHGYSSLQIMCLTVKYSL LSLEDSLVSFHKQKVPLLVFVF |
| 2159 | 10210 | A | 3091 | 3 | 930 | SSRGRAGGVWRFERDEDTGAGCGQW TRFCREPKMAVNVYSTSVTSDNLSRHD MLAWINESLQLNLTKIEQLCSGAAYCQ FMDMLFPGSIALKKVKFQAKLEHNEYIQ NFKILQAGFKIRMGVDKIISVDKLLKGK FQDNFEFVQWFKKFFDANYDGKDYDPV AVARIQGGQETAVAPSLVAPALNPKVKPL TSSSAAPQRPVISTORTAAAPKGWALGV VRKNPGVGWNGDDEAAELMQQGQRI*NL LFEDLGGERDFYFGKLRNIELICQENEG ENDPVLQRIVDILYATDEGFVILDEGGPQ EEQEEY |
| 2160 | 10211 | A | 3093 | 337 | 903 | CNRNTSTLTRCTNVCINTPRPAPLLAP/ QATLHFQFP*/PPLPL**QPQALSATRLSL/ VCHGSGRLRLPLQAAPGWLPGLPLSL FSCRGRVLLC*PGWSCYLGLKLSSHGL PKCWDDRPKPPSPASFEWAPTRPNPLPQ HGTQSQCFLSVGEAPRPHSGSAYYTNQC LQCSRPCSERTRRLGVLLPK |
| 2161 | 10212 | C | 3094 | 821 | 1051 | MAMELINNKHWPSVRALCWNTVLAYVI GEGVNSGRSCLAQTLVTFPRKGSFRD WVLGPAPGGNGALRLFRKILFC* |
| 2162 | 10213 | A | 3095 | 1 | 594 | |
| 2163 | 10214 | A | 3096 | 3 | 761 | TSRGRVGTQAGEPRDLRPPPCSSPLRV/ AVVACLEQPERGAWEAHNIPQNGDSAV RSFGITGTHVKLPGPAPDINPNVYDFKTT YDQMYNDLLRKDK\ELFTQNGILHIAGR NKRIKPGPERFQNCDFDLILTCEERV YDRVGWKI*ISREQGDLPSPVHVVNLDI QDNHEEATLG/ARFLICEVCQCIQHTED MENEIDELLQEFEEKSGRTFLHTVCFIL FSFLDICF |
| 2164 | 10215 | C | 3097 | 129 | 314 | |
| 2165 | 10216 | A | 3098 | 1 | 1434 | |
| 2166 | 10217 | A | 3099 | 1 | 831 | |
| 2167 | 10218 | A | 31 | 1 | 365 | FFFLLLILFLLLIQYHYIFYTFLWLRLLV LTGSI*CCKITMNST*IE/TVFKDYEH LYVCKLKNLEKTDKVLTIHNFRLNQ*E PEVLTRAKMYKIYNDIE |

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| 2168 | 10219 | A | 310 | 101 | 520 | RRLQKPGCLIWTRGST*CPLTLLPSRGA GLGTC/KPAMPEPPTHSMGTCAARASPT STTPCST/CAQSHRPGRNKQPKG*GMRA HGAGLAGSSTCSPGVGSTG*SQGL |
| 2169 | 10220 | A | 3100 | 1 | 1251 | |
| 2170 | 10221 | A | 3101 | 1 | 5355 | MAGWLRWLWDGWLTDGWLACMSEW MMDGWMDGWIDGWMDGWNPIVPETQ VLHEEIELPGSNVKLRYLSSRTAGYKSL KITMTQSTVPLNLRVHLMVAVEGHFQ KSFQASPNLAYTFIWDKTDAYGQRVY LSDAVVSVGFYETCPSLILWEKRTALL QGFELDPSNLGGWSLDKHHILNVKSGIL HKGTGENQFLTQQPAIITSIMGNRRRSI SCPSCNGLAEGNKLLAPVALAVGIDGSL YVGDFNYIR |
| 2171 | 10222 | A | 3102 | 205 | 393 | |
| 2172 | 10223 | A | 3103 | 2 | 158 | |
| 2173 | 10224 | A | 3104 | 1 | 1923 | MRPPPALALAGLCLLAPAAAAASYFGRQ SRLMPSRDPHAGALSAAILASGEPSLPR TPSPPSAFALRSGDREGWVDGWDLFPV SGQRIVRVQGEWGKPRTSFAFDYNTKCF GILIREYANIRRAGNIYVFGPLMNDCPQQ MASSLQAKTWAFAHQCSAAKGQLHTE LLHEDALKKWTSPAMGWERSRSHDKPR RLSRPLVPPRPFPRAPCAGSSRVRRGLAD QKGGQFPTQRSLLPTGSASFTPDRCAES WCLRPRALIGCSLTSSNPAAPRWAREGG GCGWRCASDKPESHFQSQVDFVPTIGGV APPLHGRGQTSSAPLLMEPHLLGLLG LLGGTRVLAGYPIWWCWAQGCVAVNI FADIYLWVRAILLHLYIHVILYAGKWSQ WAMGAGEKVLRLSEATRFVSVRQPVPR EHSGYPRQVHEIQSCMGRLEADTKQSG HIVENEIQASIDQIFSRLEILSSKEPPN KRQNGR/LFRVNSLKYDVQHLQTLALRN FQHRRHAREQQERQERAFRC/RSKPFTT *TLDTTITNWDRIHLQF*LPSLPRKFHN GHGIDLILDGHNLDGLRTQRLTLKGT QKKILDIANMLGLSNTVMRLIEKRAFQD KYFMIGGMILLTCVVMFLVVQYLT |
| 2174 | 10225 | A | 3105 | 1 | 566 | FSGRPTPRPGAVACRAGDMDPLFQQTH KQVHEIQSCMGRLEADTKQSVHIVENEI QASIDQIFSRLEILSSKEPPNKRQNAK LRVDQLKYDVQHLQTLALRNFOHRRHAR EQRRRQRIEELLSRTFTTNGTQKKDPLTL PNMLGLSNTVMRLIEKR/AFQDKYFMI GGHPA*PLWALFLWFQYRT |
| 2175 | 10226 | A | 3106 | 53 | 151 | |
| 2176 | 10227 | A | 3107 | 432 | 649 | GSHPPAQAGVQWVCSTLQF/LNS*SSNL SLHSCWDYKFKLVCICKGDGKEFLHMH LKKDVTLEKLIPRYV |
| 2177 | 10228 | A | 3108 | 2 | 677 | PPSFQPSDGRGDASGRNAAMAAQGE QLVLVGDGGTGKTTFVKRHLTGEFEKK YVATLGVEVHPLVFHTNRRPIKFNVD TARQEKFGGLRDGYIQAQCAIIMFDVT SRVTYKNVPNWHRDLVRVCENIPIVLCG NKVDIKDRKVKAKSIVFHRKKNLQYYHI CAKSNYNFEKPFLWLARKLIGDPNLEF/V AMPALAPPEVVMDFASTYEHDLEVA QTTAL |
| 2178 | 10229 | A | 3109 | 1 | 549 | |

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| 2179 | 10230 | A | 311 | 411 | 640 | ADIDSRGPKMSLQSSS*SRGSWMSGN*W SFSSDPTYSGSGGSAPSPNPTQGAEECGR TAPGLAGSSTCSPGVGSTR*SHFRPTHPS LENLEDIALTNVLQNRFRVRAEPASLKSPV IALLCMSDLTVGTTVTQLQHLNMTMGVIG SQDGRDQVAALNHQKQGDLPFPRVTV LWRKGIDQTFWGLLNTGSELTLPIDPK CRCSPPVKVEAHGCQVINGVLAQIQLTV GLVGPRPVPSTTQGAEECGRTAPGLAGS STCSPGVGSTR |
| 2180 | 10231 | A | 3110 | 2 | 822 | APALAPASAASPAFEFTLPPSFQPSDGR GDASGRNAAMAAQGEQVQFKLVLVG DGGTGKTTFVKRHLTGEFEKKYVATLG VEVHPLVFHTNARGPIKFNWDTAWPWR NSGGLARDGLYIPSPRVPIIMFDVTSRVT YKWNVPNWALGDLVTSV/CENIPHLCCEVA NKVDIKDRKVKAKSIVFHRKENFQYY DISAQKVPTNLKKPFLWALLGSLMGDP* LWNLLPMPLLSPPPR/EVVMPEQLWPAT SMKHDLLEVASDNCLPPDEDDDPVKK |
| 2181 | 10232 | A | 3111 | 116 | 599 | PQVISLPKCCDCRCEPLHLAAEKSLEPTVR ETTKVPGEAKSEPHKNKMDGRGGKPMG GCEGPDAMYVKLISSDGHEFIVKRDHG LTSGET*KPMLSGPGQFAGGKTHEVN FREIPSHIAIRKVCNVFFTYKV/RATPNS SHPRFPEFPNLAAGNLHWELA |
| 2182 | 10233 | A | 3112 | 84 | 348 | KYTIKTKTVLKKSGIFSTCPKPKSCYDFV PLNAGPIPPKSILGTNGPTHLEMLD*RL NKPTPISQRSPLTQVGHR*TRPTRRRPR T |
| 2183 | 10234 | A | 3113 | 122 | 518 | KSLEFFPPALSPSPALILCHLMQAPYHLK VSWPTDPT/ALEMLD*RLPLPHA*HKG ETHTCGPLSDHTFKAPDPLQICLLSHQG PASPSQQTHPYQPSEVTADSGGTQVDKA NQEEATNTKHHEQEEEQD |
| 2184 | 10235 | A | 3114 | 1 | 1452 | MSAYCLQLGGLQALLALTQTPGHRDSL DAQPAAVLVCGWPWLASFSERTIVGHK EWTIKDKLKNKFKDEFDIVSLPCTLGSH QPQDPMKLKLPWSITYGRCLAPGDHTVSL VIKLVESASLSLAVSNMMLSDMIRWMPAG CGRCLLGLQSESRVCGQCVGMEQVCR VSGPHIRWIPQQLHSCFFLYPSYPLEP SSNTSFICPHSRTYNGSLLSCIPNSAAAAA PPTPQATSFSPCSPKQRLPTGRVVEGSD HRVHEARLPGNHSRSGVDSAPPTLAHA GLLLTEETLKENGRRAEALRVGVHWR HGTSQGPGRTLWAEKVKPHFRTRGQVY DASSAPVTEHTATELPAGNQSQPGLQE GGLEGTVVTLVSWKVT/MVSRRC*CRY GQRPH/HHLKVLGNQRPTHLEMLD*RL PLPQRLTPKGKHTPVVPPLL/QPFKAPPD PLQICLLSHQGPASPSQQTHPYQPSEVTA DSRWDTR |
| 2185 | 10236 | A | 3115 | 1 | 414 | |

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| 2186 | 10237 | A | 3116 | 112 | 1655 | QEHLQRASPRLLQLLPPLPPPPPPAFGGSLSSLGSRMSRQVVRSSKFRHVFGQPAKADQICYEDVRVSQTTWDSGFWC/SVNP*VLWALICEASGGGAFLVPLGKTGRVDKNAPTIVRR*HS/APVLDIAWCPHNDNVIA/SGSEDICTVMVWEIPDGGMLPLREPVV TLEGHTKRVGIVAWHTTAQNVLLSAGC DNVIMVWDVGPAGAAMLTLGPEGPPDA NYRGDWEPDGGICTSCRDKRVRIEPR KGTVVAEKDRPHEGTRPVRAVFVSEGKI LTTGFSRMSEKQVALWDTKHLEESPV/S LRKLHTRNGVPVAFGPDNTNIVYLRGK GISGPIRVFENTSEAPFLHYLSMFS/SKES QRGHGLHGPNRGLEVNKICEIAGFYKLH DGR/CVSPMPKPVPRKSDLAFOEDLGPTQ PQGPDPC LHGLKEWLGGRDAGPLPSSPL KDGYVPPKSRELARVNRGLDPGRRRAA PEASGTPSSDAVSRLEEEMRKLQATVQE LQKRLDRLEETVQAKL |
| 2187 | 10238 | A | 312 | 375 | 519 | GMLFPKQITPQSI*VETNAKNV*GGDIAS FMGSTHALFEFPDSSHSA |
| 2188 | 10239 | A | 3122 | 200 | 469 | RGGGAGPLTGHVHVLGLGIAHAAADQFD RLAAGICGHSHPHPLGPHCCAPLWS GPQQN*PTADVAESLQLVTVHQSETEDG EFTECNN |
| 2189 | 10240 | A | 3123 | 1 | 2520 | |
| 2190 | 10241 | A | 3124 | 1 | 1950 | |
| 2191 | 10242 | A | 3125 | 1249 | 2166 | |
| 2192 | 10243 | A | 3126 | 1 | 2424 | MVAIHSALESSLLFQEQSQLLYLVTVHE NLNFMAGFTDGSVTLNKGDITRDRHSK TQILHKGNYPTGLAFRQAGKTTHLFVV TTEENVQDLQFIVAGDECYLYQPPERDC RDDHVFSLYFMIPFFFTTL/VIALPQLVPIT GVCGRYLLLLCWQTFVAVGILGHFSKT MLLFFMPQVFNFYSLPQLLHIIICPRHRI PRLNIKTGKLEMSYSKFKTKSLSLGTFI LKVAESLQLVTVHQSETEDGEFTECNM TLINLLL/QSPWAHT*EKPHIAPAAAAAFS FLCDHWHPGRFLPSADY*LDFTYGFLQL ATLSLSPSLQPIGTIGKLEPSYVIRKFLD AQRIHNLTAYLQTLHRQSLANADHTLL LNCYTCLKDSSKLEEFIKKKSESEVHFDV ETAIKVLRQAGYYSHALYLAENHAHHE WYLKIQLEDIKNYQEALRYIGKLPEQA ESNMKRYGKILMHIIPEQTTQLLKGLCT DYRPSLEGRSDREAPGCRANSEEFPIFA NNPRELKAFLEHMSEVQDPSQGIYDTL LELRLQNWAHEKDPQVKEKLHAEAISLL KSGRFCDVFDKAWFQQIMHYHMQHEQ YRQVISVCERHGEQDPSLWEQALSYFAR KEEDCKEYVAAVLKHIENKNLMPPLLV VQTLAHNSTATLSVIRDYLVQKLQKQSQ QIAQDELVRVRYREETTRIRQEIQELKAS PKIFQKTKCSICNSALELPSVHFLCGHSF HQHCFESYSESDADCPTCLPENRKVMD MIRAQEQKRDLDQFQHLKCSNDSFS VIADYFGRASPNFIFYV |
| 2193 | 10244 | A | 3127 | 1 | 411 | |
| 2194 | 10245 | A | 3128 | 2 | 243 | |
| 2195 | 10246 | A | 3129 | 1 | 1176 | |
| 2196 | 10247 | A | 313 | 640 | 975 | VPWEAGGSMISICFYPRQSEQSHNIVKSK RPVTFQQNRCQKGGGHSADVSTCQCF QCSHREQGFAKPQFSYL*NGGSNSFYLT GCFDNLITSVFCSVRFIHGPKAIKGYH |
| 2197 | 10248 | A | 3130 | 2 | 496 | |
| 2198 | 10249 | A | 3131 | 2211 | 2568 | |

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| 2199 | 10250 | A | 3132 | 100 | 2726 | AMMGPIPGPHLLLDPLLPSSFCPLPPGITV CDSCRGSLVFGDMEGQIWFLPRSLQLTG FQAYKLRVTHLYQLKQHNILASVGEDEE GINPLVKIWNLEKRDGGNPLCTRIFPAIP GTEPTVVSCSLTVHENLNFMAIGFTDGSV TLNKGDIRDRHSKTQILHKGNYPTVGL AFRQAGKTTHLFVVTTENVQSYIVSGKD YPRVELDTHGCGLRCSALSDPSQDLQFI VAGDECVYLYQPDERGPCFAFEGHKLIA HWFRGYLIIVSRDRKVSPKSEFTSRDSQS SDKQILNIYDLCKNFIAYSTVFEDVVDVL AEWGSLYVLTRDGRVHALQEKDTQTKL EMLFKKNLFEMAINLAKSQHLDSDGLA QIFMQYGDHLYSKGNHGDGAVQQYIRTIG KLEPSYVIRKFLDAQRIHNLTAYLQTLHR QSLANADHTLLNLCYTKLKDSSKLEEF IKKKSESEVHFDVETAIKVLQRAGYYASH ALDLAENHAHHEWYKIQLEDIKNYQE ALRYIGKLPFEQAESNMKRYGKILMHHI PEQTTQLLKGLCT*LSAQPRRPQR*GGPR LAGPTLRSFIFIFANK/HPRDLKAFLEHMS EVQPDSPQGIYDTLLELRLQNWAHEKDP QVKEKLHAEAISLLKSGRFCDFDKALD LCQMHDQDGGGLYLEQGGKLFQQIMHY HMQHEQYPAGQSA/CCERHGEQDPSLW EQALSIFARK/KEDCKEYVA AVLKHIE GNLMPPLL VVQTLAHNSTATLSVIRDYL VQKLQKQSQIAQDELVRVRYREETTRI RQEIQELKASPKIFQKTKCSICNSALELPS VHFLCGHSFHQCFESYSESADACPTCL PENRKVMDMIRAQGTEPRFMSINSQHQL QVLQ |
| 2200 | 10251 | A | 3133 | 11 | 707 | AKMGAYKYIQELWRKKQSDVMRFLLR VRCWQYRQLSALHRGSRPHR/RPDKVH RLGYKQAKQGYVIYRIRVRRYI*DSCSR DRRGGRKRPVSKGATFGKPVVHHGVNQ AKVWFYPTSVAEERPGRHICGALRVL NSYWVGEDSHLPNFLGVIPHGSHSHKAI R/RNP*PPQWITQTQSHKHREMRGLTSA RPERAVGLGKGHKFHHHTIGVSRRAAW RRRNTLQAPPLPLI |
| 2201 | 10252 | A | 3134 | 1 | 333 | |
| 2202 | 10253 | A | 3135 | 1 | 1530 | |
| 2203 | 10254 | A | 3136 | 1 | 554 | ILSQVRCQAQLAQAAGGGLSFRAASSL PVSPSLAVSMKAFSPVRSIRKN/SALSDH SLGNSRSK/TPVD/DPDGALLYNMKDCYS \KLKEL\VPSPPEQRR*ARWEIL\QH\IRL TSWDLADSPWDLAFPLIVQPGIHQRTRG RNQ\RSRTPLGPPSTRDISILSFAGLLEFPS ELMSNDSK\ALCG |
| 2204 | 10255 | A | 3138 | 3 | 251 | |
| 2205 | 10256 | A | 3139 | 1 | 1674 | |
| 2206 | 10257 | A | 314 | 22 | 297 | GKEKLSHSAWAPKSQNSNSSASSWSN QSQAQPRFKGEDI/ESHLLMGREALS*IQS /GRLVYLQSLs*T*RFSTASPEQLDTECRL VHSQTLs |
| 2207 | 10258 | A | 3140 | 1 | 648 | MSLRKLTIMVEGKGPNIPHACGCRQRS SIKVSLPAVTSKSESPKEPEQLRKLFIGG LSFETTDESLSRSHFEQRRTLTDCAVMRD PNTKCSKGFGVITYATMEEKYHTVNGH SCEARKALSKQEVASASSSQ/GRSGSGN FGGGHGGGFGGNDNFHGENFRGHSSF GGSHGGSGYGGSGDDYSGFGNDGSGNFG GGGSYNDFGNYSNQSSNFGPM |

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| 2208 | 10259 | A | 3141 | 579 | 2102 | SPKEPEQLRKLFIGGLSFETTDSELSRSHFE QWGTLTDCVVRFGDKAVKQPISLAYL GAVFSECL*K*LIAL*LELCWQRNVLL*F *KLTS*I*G*WETGRTFYKRLV*SFLLPYS KLK*QKLLRSDFVLHKLTLFSGMRDPNT KRSRGFGFVTYATVEEVDAAMNARPHK VDGRVVEPKRAVSREVSFFFFFLNLL GYVLL*T*DSGVF*TYQNFLFEYRLC*SK PMVFLLLDSQRPGAHLTVKKIYVGGIK EDTEHHLRDYFEQYKNEVVEIH*LDR GQWPRKRGFVTFDDHDSVDKIVSKY QIVAFSGSTICMAF*TLIPCCIIYVFFLVQ KYHTVNGHNCEVRKALSKQEMASASS QR/GYACCLIKP*R*L*VTPV*MI*CLNFM S*GRSGSGNFGGGRGGGFGGNDNFGRG GNFSGR/GYVWFIYM*F*LLTIFAMKILQ YGNCIQNVTLSPSHT*NLKFLTGGFGGS RGGGGYGGSGDGYNGFGNDGKFFRNK |
| 2209 | 10260 | C | 3142 | 42 | 152 | MIXXXXXXXXXXXXXXXXXXXVSPSAFA PXXXXKSLG* |
| 2210 | 10261 | A | 3143 | 3164 | 3255 | |
| 2211 | 10262 | A | 3144 | 12 | 336 | SPVQL*F*LFLVFC*LWSWSAVVYLGPL GTPSADAHT/AGLSKTPPHWAARARLDD VFSLRTFSSHSLNMELVQDLTASAPMYS STSRDPP/CLGLPKCWDYKREPPRAH |
| 2212 | 10263 | A | 3145 | 602 | 744 | TPASLKIPVE**NTLLAKMVSIS*PRDLPA SASQSAGITGVSHRARC |
| 2213 | 10264 | A | 3146 | 269 | 483 | |
| 2214 | 10265 | A | 3147 | 2 | 988 | KYPPPAVLWFFGFFVLRRSLALSPRLECS GMISAHCKLCLPGSRHSPASASRVAGTT DVHHHAQLI/LYVFLVETGFHRVSDGL NLLTRLHLPKCWDYR/R*ATTPGLCFVF* KKRNAREGGROPDPHKS*FL/VFFFLFFL KWSL/DSVSKAGVQWHGLSSLQAPPRGF TPFSCSLPSSWDYRRPLPRANFFVFL** VDGGFTVLARMVLIS*PRDLPASASQRAG UTGLSHCAWSEFF/CFKGTGSHSVTHARV QRHNLDSLEA*TPGLN*SSRLSLPSSWD YRSTPPSPANFCSFSRDGVSPC*PGWSRS SDLVIRPPRPKVPGLQA |
| 2215 | 10266 | A | 3148 | 2 | 608 | RDSPPRSLDSGARRDAPPHSPAECRAH AATWRLKPRPHRPHSLTAPLPVHWAGT TEPLSPRPATGTREPRPLHFPATPRSHS/ WRLARPCRPQGPS*DRLFSAGAGPGVVS CLDREKNAGHWLSSAFALVWLWLTEH WLLLVGFIGYVKAGSVYPGCRACFFW AVLAGLGCLPAVSGIPRERFWVPRLHL VPWLALWE |
| 2216 | 10267 | A | 3149 | 131 | 453 | |
| 2217 | 10268 | A | 315 | 152 | 437 | GLRLCLSRPLTRPGDDSVGGSAMASGAG GVGGGGGKIR/TRCHQGPQKPYQQGR QQHQVWDPDAAVAWRVGKLGWRGRA VRGPGAPRGADRR |
| 2218 | 10269 | A | 3150 | 403 | 787 | MGRIFLDHIGGTRLFSCANCDTILTNRSE LISTRFTGATGRAFLFNKVVNLYSEVQ DRVMLTGRHMRDVSICKNCNSKLGW IYGVWPLKDSQRF*GKGRR*SGERIVLVS EELRALEEHVPPDNS |
| 2219 | 10270 | A | 3151 | 171 | 382 | KNSYKCEECGKIFNEYSHLIARK/RIYT*E KLYQYKDCEKAINVCSHLTQHQRV/H*K KYYKFNYCQKVQKI |
| 2220 | 10271 | A | 3152 | 76 | 195 | VHLLNPQHMLPSTHKQRRTTL*KGHAE HLQYYLNNQKLS |

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| 2221 | 10272 | A | 3153 | 2 | 634 | VVWESLNREDLWPCFLRRILGGSSYSTA EMVSGQTLQRAHLREAASISLNSQGVW RKSARFSQLERGTEEQQLQIPDLGQHP SKAPVFPQVQAHPRFQTPHGHKLQRN QDPGQLQ*IPMLGQTPWTQATGPTI*TQP SGRSPCSHYSGMSTDGFMALHSLTQVS SQPTCRLLEACPWTSSGGLPRISGWT RQVFGSVDRDLISP |
| 2222 | 10273 | A | 3154 | 275 | 463 | GKFFSLCETLFPVSGVGSFFSSCTMDSSRS LGVGSKNSHFLA*NTDLRLSLCPFPGW KEDIKF |
| 2223 | 10274 | A | 3155 | 5904 | 7919 | FMFINMSVCRLITTKYLLLLFLHESLILS ENLRKDVEAVTGSPASQTSICIGILLRSA ELALLHPVDQANTLKSPVSESVPVVP DYLPTENGDFLSSKRKQISRDIRRSVT VNHMSDNRSMSVDLSHIPKDPPLFKSA SDTNLAKRAFPMDYLSDKHLGKISEDE SSGLVYKSGSGEIGSETSDKKDSFYTDSS SILNYREGFRIYLSFG*VMGNQNILSSTL TSKGNETVIESIFKAEDLLPEAASLSENAD ISKEETPPVRITLKISQSSLGESLRERLPH PNLGFPLVFSYKNMKRSSSQMSFEATIS LDSMILEEQLLSDGSDSHMFLEKGNRK NSTTNYRGTAESVNAGANLQNYGETSP DAISTNSEGAQENHDDVLSMVVFKITGV NGEIDIRGEDTEICLQVNVQVTPDQLGNIS LRHYLCNRPVGSDQKAVIHSKSSPEISLR FESGPGAVIHSLLAEKNGFLQCHNENFS TGFLTSSLMNIQHFEDETVATVMPMKI QVSNTKINLKDDSPRSSTVSLEPAPVT NDHLVVERSDDGSHIRDSHMLNTGND LKENVKSDSVLLTSGKYDLKKQRSVATQ ATQTSPPGVWPQSQANFPAEFSGLHLGE QLMEENESLKQELAKAKMALAEAHLE KDALLHHIKKMTVE |
| 2224 | 10275 | A | 3156 | 149 | 382 | ARHCGSCP*SQHFGRSR*AEHLRTGV*D QPAQRGETPSLWKNTKIRRAQWWCPPVI PATSGGLRQENYLNPRQRQLQ |
| 2225 | 10276 | A | 3157 | 162 | 342 | |
| 2226 | 10277 | A | 3158 | 1 | 1995 | FRLVTPGVPAFSGCGRRHGRGTRGRAM ASCVGSRTLSKDDVNYKMHFRMINEQQ VEDITIDFFYPHTITLLSFTUDSLMYFAF TTDDSV*DNWIRGILSGILLFLIKV*AFP NGPLTRHPALWRMVFLSELYFLFLVF LLFPEFEQAKSLMDWLDPNLRYATREA NVMEYAVNCHVITWERIISHFDIFAFGHF WGWAMKALLIRRYGLCWITISITWELTEL FFMHLLPNFAECWWDQVILDILLCNGGG IWLGMVACRFLERRTDHWASFKDIHTTT GKIKRAVLQFTPASWTYVRWFDPKSSFQ RVAGVYLFMIHWQLTELNTFFLKHIFVF QASHPLSWGRILFUGGUNSFPQLRQYYA YLTDTQCKR/L*GTQCWVFGVIGFLAVI VCIKFGQDLFSKTQILYVVLWLLCVAF TFLACLYGMIWYAEHYGHPKRKPTPECE DGTYSPEISWDHRKGTGSEDSPPKHA GNNESHSSRRNRHHSKSKVTNGRWER NEKPWVNSKMFPECLGTEEGKWELHLG TPRGGGSRAHRGKPGRGEGTLGVILRSL SLCFPTDLGRVQADHRLGGPFANVGSLL TSALDMRSPVAARCVERETVAISFHSCQ EQLRAMLDRCGSVNIFPSDEALTPWLMD WSPVFNFIYESTFPID |
| 2227 | 10278 | C | 3159 | 410 | 538 | |
| 2228 | 10279 | A | 316 | 3 | 609 | |
| 2229 | 10280 | A | 3160 | 4 | 334 | FFPKALIFCREVGPIPPPKIRFP/SPKFPGN RFSPPRVVKKPPGP/SPFKRPPIRKKILPCQ PP*TLAPRIL*KGPP/PSSSSG*NPYYLFIQ QKTEYLLWSRPCWHCEQR |

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| 2230 | 10281 | A | 3161 | 1 | 1130 | PLLPTSLSVEDAAILLQQVMRAFASKQAST VVFSDTVVVSEKFINDCTELFRELHMQK AEKEMKNNPVHLITEEDLKQISTLESVST SKKDKKDERRRKATEGSGSMRGGGGGN AREYKIKKVKKKGRKDDSDDESQSSH TENEESGYDKKDENILEDVKWGKTSQFL EIFQDIEKARDKTLEADSELESVFMSTT SASGTGRKRTIKDLQEEVSNLYNNIRLFE KGMKFFADDTQAALTKHLLKSVCTDITN LIFNFLASDLMMAVDDPAITSEIRKKIL SKLSEETKVALTKLHNSLNEKDQHALLV KYQGLVVKQLVSQSKKTGGDYPLNNE LDKEQEDVASTTRKELQELSSSIKDLVLK SRKSSVTEE |
| 2231 | 10282 | A | 3162 | 20 | 2478 | RVCSSASTASQAVMADAWEEIRLAA DFQRAQFAEATQRLSERNCIEIVNRLIAQ KQLEVVHTLDGKEYITPAQISKEMRDEL HVRGGRVNIVDLQQVINVDLIHIENRIGD IHKSEKHVQLVLGQLAIDENYLDRVGQEV NDKLQESGQVTISELCKTYDLPGNFLTQ ALTQRLAIIHGHIDLDNRGVIFTEAFVAR HRARIRGLFSAITRPTAVNSLISKYGFQE QLLYSVLDELVNSGRLRGTVVGGQRDK AVFVPDIYSRTQSTWVDSFFRQNGYLEF DALSRGIPDAVSYIKKRYKTQLLFLKA ACVGQGLVDQVEASVEEAISSTWVDIA PLLPTSLSVEDAAILLQQVMRAFASKQAST VVFSDTVVVSEKFINDCTELFRELHMQK AEKEMKNNPVHLITEEDLKQISTLESVST SKKDKKDERRRKATEGSGSMRGGGGGN AREYKIKKVKKKGRKDDSDDESQSSH TGKKKPEISFMFQDEIEDFLRKHIQDAPE EFISELAELYIKPLNKTYLEVVRVFMSS TTSASGTGRKRTIKDLQEEVSNLYNNIR LFGKRGWKFFADDTQGWLLPKHLEEV QCVLISLNLINFLGFGILMDGQ*DDPG RPFTSELKELSKLSEETKVALTKLHN SLNEKSIEDFIFCLDSAAEACDIMVKRG DKKREERQILFQHRQALAEQLKVTEDPAL ILHLTSVLLFQFSTHSMHLHAPGRCVPQII AFLNSKIPEDQHALLVKYQGLVVKQLV SPSKKTGGDYPLNNELDKEQEDVAST TRKELQELSSSIKDLVLKSRKSSVTEE |
| 2232 | 10283 | A | 3163 | 1 | 389 | IPSEISRSVAFSL/LPLLSVSGLEAIQRTPK NQVYSRHPPENGKSKFLNCYVSGFHPSD IVGDLLMNGERIE*A*HSDLAFRKDWAF YLLDYTEFTPT/EKDEYACRVNHVTLSQP KICKWDRDMLSASMEA |
| 2233 | 10284 | A | 3164 | 2 | 409 | RPRVRPRVRSIRAEMSRVALAVLALLS LSGLEAIQRTPKIQVYSRHPAENGKSNFL NCYVSGFHPSDIEVDLLKNGERIEKVEH SDLSFSKDWAFYLLYYTEFTPT/DEY ACRVNHVTLSQPKIVKWDRDM |
| 2234 | 10285 | A | 3165 | 26 | 299 | |
| 2235 | 10286 | A | 3166 | 11 | 486 | |
| 2236 | 10287 | B | 3167 | 198 | 282 | XPSLEDLSNSIQKLHLAENAEPEEQSAA* |
| 2237 | 10288 | A | 3168 | 80 | 827 | AQQAVLARSKLESCLRELHGHNRSLKEE GVQRAREEEERKEVTSHFQVTLNIDQL QMEQHNERNSKLQENMELAERLKKLI EQYELREEHIDKVFKHKDLQQQLVDAK LQQAQEMLKEAEERHQREKDFLLKEAV ESQRMCELMKQOETHLKQQLALYTEKF EEFQNTLSKSSEVFTTFKQEMEKMTKKI KKLEKETTMYSRWESSNKALLEMAEE KTVRD/ERTGGPAGKNPTAGEAVPGTAD RAQ |
| 2238 | 10289 | A | 3169 | 1 | 2511 | |

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| 2239 | 10290 | A | 317 | 1 | 949 | MGSCAARASLTSTTPCSTAPSPINHPKAE ECERTTAQDWQAAPPAAPVRDPLGEPS WAPESGGDVESLYIYLRDCKYTNQHPVF SSRFVNPIDTLYLAALVGPWKTFMSSS GIVNTPIGTLYLAQVTVPPPLHTRFFALSP RQPRSFKNGLLFQTGTTLNPLSGYSSDY KGFRFRNHPQTGFSPAGANQRGPLVAT LSGPGGEGQSAVVPVSLVKKRTTLAPNT QTASPRALADSLMQLARQVSPGKRAV SATAINLKVCKHTSQHPVFSSRFVSAPID TLYLAALVRTWRVFMSSSGIVNTPIGTL YLAQGL |
| 2240 | 10291 | A | 3170 | 93 | 517 | GRGHLGG/VWC*RSQERAQQIKEASAEIT /CSWLQMKQNRKPSQEKTRDTTRMENP DRGFVPGKECSFEQLEHVREMQEKLARL HFSLDVCGEEDDEEEEDGVTEGLPEEQ KKTMAADRNLQDQLSNVGSCLGALVPGG MRGGE |
| 2241 | 10292 | A | 3171 | 3 | 348 | FFAFFLGLIPFNAPLPHSTWGAAEHPPES VKSHSLKRMRGAVW/CLRGTPQR/HCS SGSAFSARCSFWIELLRSSRLSSWSRLR SAIVFFCSSGKPLSDPNPLPHRPPPHTH PG |
| 2242 | 10293 | A | 3172 | 2618 | 5946 | PGCNFSLDVCREEDDEEEEDGVTEGLP EEQKKTMAADRNLQDQLSNARGRAWQL APMEPELLVRKVSALQACVRGFLVRRQF QSLRAEYEAIVREVEGDLGTLQWTEGRI PRPRFLPEKAKSHQTKAGDRVANPEQ GLWNHFPCEESEGEATWEEMVLKKSGE SSANQGS�CRDHSSWLQMKQNRKPSQE KTRDTTRMENPEATDQRLPHSQPQLQEL QYHRSHLAMELLWLQQAINSRKEYLLL KQTLRSPEA |
| 2243 | 10294 | A | 3174 | 16 | 319 | LGTRPAHRSSQ*GKGSPPLPGAPLISRGA GKEGGPGDRAAHADFLPAEEGAHHGM/R GSHGSPLIAPLPTYPHPPSGLFPLGALPLA RPRHQGAALGSVHEIQ |
| 2244 | 10295 | A | 318 | 1 | 4425 | |
| 2245 | 10296 | A | 3180 | 417 | 736 | YGLGAVAHACNPSTLGGQAGQITRLAV QDQPDQHCETPSLIKMQKN/LPGHGGVC LQSQLLRGLRQGNCLNQGGGSCSEPRSH QCTPAWAIE*ESVSKKKKKKKLVV |
| 2246 | 10297 | A | 3181 | 1 | 2061 | MGA VRDELHSLVVPPLMGRGAQTMA AAALRDPAGCVTFEDVTIYFSQEEWVL LDEAQRLLYCDVMLENFALIASLGLISFR SHIVSQLEMGKEPWPDSVDMTSAMAR GAYGRPGSDFCHGTEGKDLPEHNVSVE GVAQDRSPEATLCPQKTCPCDICGLRLK DILHLAEHQTTTHPRQKPFVCEAYVKGE FSANLPRKQVQONVHNPIRTEEQASPV KTCRDHTSDQLSTCREGGKDFVATAGFL QCEVTPSDGEPHEATEGVVDFHIALRHN KCCESGDAFNKSTLVQHQRHSRERPY ECSKCGIFTYAADLTQHQKVHNKENP YECFEGGKFFKPAALSLVKHRRVHTGES HVC GDCGKFFSRSSNLQHKRVHTGEKP YECSDCGKFFSQRSSNLHHKRVHTGRSA HECSECGKSFNCNSSLIKHWVHTGERP YKCNECGKFFSHIASLIQHQIVHTGERPH GCGECGKA FSRSSDLMKHQRVHTGERP YECNECGKLFSSSSLSNHRRLHTGERP YQCSECGKFFNQSSSLNNHRLHTGERP YECSECGKTFRQRSNLRQHLKVHKPDRP YECSECGKAFNRPTLIRHQKIHIRERSM ENVLLPCSQHTPEISLRTDLIRALSSTML NLVHPSTHTGEVP*EC*LCWKLSGDKLH SLTVEFISVFSLLGL |

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| 2247 | 10298 | A | 3182 | 441 | 1074 | QVRVQSLKK*CWG/FNWGHSGGKI*KQI GPYLNTG/TRLKSKWIVPQNCIISRRQQG KRVVHLGLGKDFLNPTPKAQSM/RGKIDK LYFIKIENFSLKGTIRRTKRQAVEWQK/IV LQNISDK*VASRLHKEVSKLNKVKPIVDL MRCF/RPELAASGPCSLSFSCFQH*IQNV LLEIQVRSHQPSSELSNRRPWHKSVHNSL QCWAKHEAPLFSLL |
| 2248 | 10299 | A | 3184 | 178 | 488 | VSSTVFGNTVRNKTEDDSGGNWEPRTI LQASGKLKNPKARLASECLSPFDSTGKAI HLCQVCGRASRSHYSLGHH/MRHSVHG E*S*KCPGCGKGFSTKLDLRW |
| 2249 | 10300 | A | 3185 | 7 | 310 | KKRSHCAQAGLELLSGQLG*TSSVQKIR KLAGCGGVHPWSQLLERLRWEDSLPQG GQGCSEP*SHHCTPAWATE*DPVSNNNK QKQPKESNLSRATSRP |
| 2250 | 10301 | A | 3186 | 65 | 203 | KGDFQGHQGPWDAPP*PAFWWQREAR GEGEAMSSQSPCRGRGNAEMYRPSAQPE TGPASG**TEAARGSSGWAEPWPRG*KP PEFPMRLGWPFPTPGAFSLPILCDEERP* GQRSSGCESQQLRSPRETELQVTSPTCF SAGPRRPGPAPGGPQAARAYCCHLKTSS EPTFHQAPTQAEVSWEFSPA/PPADKEMT SMATPEKCPSTQVAPAIRKAALPHPERGN YFLSAAWPQGAPFPLWGSASPFVALPWS PRAGAAPLCPGKAPPSKTRLGRAVTFP* AEGGTGRGRGHVAVPLPWERQGRNV |
| 2251 | 10302 | A | 3188 | 1 | 2559 | |
| 2252 | 10303 | A | 3189 | 259 | 3222 | |
| 2253 | 10304 | A | 319 | 160 | 747 | VLNGSGRPSQSKKHFPKPGTFGGASVH QMFIMSLPA/GPDLSGFDEDDKGWPNQ LDMSDYSSSYQDVACYGTLPRDSPRRN KEGCTSKTPHALTVSPFKGIFSSATKVQ APNACKRGA*GKG*PWEKGASSKPGRD FLREGRKMSWKLFRNKLISQPYVPVGV CLTSVFTIASLGEQGMVFLKVDLFKLT G |
| 2254 | 10305 | B | 3190 | 114 | 2876 | MDKFLDTYTLPRLNQEEVESLNRPTGSE IEAIINSLPTKKSPGPDGFTSEFYQRYKET VVCRLSPPSFNGGLPLGSDLVIFYAPGPQ KIIWVMVHV GALALKDGFSPLDVGVHG FCRFRNHHQTGFSPAGANQRDPLAATLS GPGGEGQSAVARLTGEKKNHPGAQYAN RLSPRVGRFINAAGTTGFPTGKRAVSAT QLMVKDDVTYAIKLSWCWPLDIIPSCLA LHRIETELMGKFDKGRLPHTPHMLRLA IE |

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| 2255 | 10306 | B | 3191 | 1 | 2640 | MEIRGRVEQRVGYTIEQINHMRDVFGR LRRRAEDVFPPVIGVAAHKGGVYKTSVSV HLAQDLALKGLRVLLVEGNPDQGTASM YHGWVVDLHIHAEDTLLPFYLGKDDVT YAIKPTCWPGLDIIPSCALHRIETELMG KFDEGKLPTDPLMLRLAIETVAHDYDV IVIDSAPNLGIGTINVCAADVLPVTPAE LFDYPSALQFFHMLCDLVKNVDLKGFEF GELAPLYGCWGLRTGIACAPHHASL NLHGLNQIRNVKKQSVYLMNLRKSGTL GHPGSVDETTYERLAEESLDSLAEFFEDL ADKPYTFEDYDVSFGSGVLTKLGRDL ATYVINKQTPNKQIWLSSPSSGLKRYDW TEKNWVYSHDCVSLHDLAAELTKALK TKLDLSSLAYSGKELDAQPGYYMLHAQ YMLRPPLSSPMQHRAPETGPTSRNSVLN AVTPPAPTTPPSPLFDSRGSRRKTYQNV QQFIDEGNYTSGDNHTLRDPHYVEDKG HKYLVFEANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACKRDAELA NGALGIIELNNDYTLKKVMKPLITSNTVT DEIERANVFKMNGKWYLFDSRGSKMT IDXGSPXKIRLFYTDYSGKHYGKQSLTT AQVNVSKSDDTLKINGVEDHKTIFDGDG KTYQNVQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENGYQGEES LFNKAYYGGGTNFFRKESQKLQQSACK RDAELANGALGIIELNNDYTLKKVMKPL ITSNTAAANQESSHVQQALALEQQFLE RTQALEAQIVALERMRADQTTAKQGM CTQVHLTNTSRHAGRPSKCQFCSTRQR HRLSDPKQDLGNRRFSPPP* |
| 2256 | 10307 | A | 3192 | 1 | 454 | MERRNRRTGRTEKARIWEVTDRTVRTW IGEAVAAAAADGVTFSPVTPHTFRHSY AMHMLYAGIPLKVLSLMGHKSISSTEY YTKVFALDVAARHRAIRVPRQQGDYRT RIWKFEGLSNVLVIQLNKLIICVMCLVR DCDVLKTYFHL |
| 2257 | 10308 | A | 3193 | 2758 | 2946 | |
| 2258 | 10309 | A | 3194 | 2372 | 3570 | EALLPGDQDSQSGKVAAREVWFLPSSF APVLLRLVGNHHVGDNSIDSWKNAGR/V FKDSKFDANDPILKDQTQEWSGSATFT SDGKIRLFYTDYSGKHYGKQSLTTAQVN VSKSDDTLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGEESLFNK AAYGGGTNFFRKESQKLQQSACKRDAE LANGALGIIELNNDYTLKKVMKPLITSNT VTDEI |

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| 2259 | 10310 | B | 3195 | 1 | 2232 | MKLMETLNQCINAGHEMTKAIAIAQFND DSPEARKITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQRVGYTIE QINHMRDVFGLRLRAEDVFPVIGVAA HKGGVYKTSVSVHLAQDLALKGLRVLL VEGNDPQGTASMYHGWVVDLHIHAEDT LLPFYLGKDDVTYAIKPTCWPGLDIIPS CLALHRIETEFMGKFDENNAGMVRVL QPFTSDEKKSISTLTTFPGKHLRRDKSLT TAQGCCKINNKTSPETSPDLALKGLRV LLVEGNDPQGTASMYHGWVVDLHIHAE DTLLPFYLGKDDVTYAIKPTCWPGLDII PSCLALHRIETELMGKFDGKLPTDPHL MLRLAIETVAHDYDVIVIDSAPNLGIGTI NVVCAADVLIVPTAELFDYTSALQFFD MLRDLLKNVDLKGFEVDVRIITKYSNS NGSQSPWMEEQIRDAWGSMVLKNVEPE NGEVGKXGSPQLINQEKMFIRNRSYI DRDSEYLLQENEPDGTLDQKLLLEDLQKK KNDLRYIEMQPFPLVSSSRVWVKRGELT AYVEDTVLFSRRTSKQQVYFFLFNDVLI TKKKRRSDSSLREGDNQKAYKETYGVS HITRHDMLQIPKQQQNEKYQVPQFDQST IKNIESAKGLDVSDAGMVPVLQPLHLTE KSGYSTLTIPVNLRTSLTQRKVMCQNL VTHLKSTEWEKHKTIVDGERKTYQKRS AVFRMGILHSATTIR* |
| 2260 | 10311 | A | 3196 | 1260 | 1340 | LPMALAVGFCFRFNHHQTGFSPAGANQ RGPLAATLSGPGGEGQSAVARLTGEKK NHPGAQYANRLSPRVGRFINAAGTTGFP TGKRAFGFCFRFNHHQTGFSPAGANQRG PLAATLSGPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINAAGTTGFPTGK RAGFCFRFNHHQTGFSPAGANQRGPLA ATLSGPGGEGQSAVARLTGEKKNHPGA QYANRLSPRVGRFINAAGTTGFPTGKRA QAQAK*WHYREPLLLRAQLTNPPSGQQL KSVDQWPVQKQFSSGSDLYQLHPFHVQ HFLEPCFPRHPEFAPPSTGTESHYYCWIW |
| 2261 | 10312 | B | 3197 | 200 | 2602 | MQLARQVSRLESQVKHEGQHTKMSQ VLWRSQEENPATLGNNIQLFDWIPQNDL LGHPKTKAFITHGGTNGIYEAIYHGVP VGVPMFADQPDNIAHMKAKAAVEVN LNTMTTRPGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTGFPTGKR AVSATQLMDFADFGTTIKQDFRLLGQTS VDRLLQLSQQAQVKGQQLLPVSLVKRK TTLAPNTQTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLGQTSVDR LLQLSQQAQVKGQQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQVSRLESG QILPDFGPHHQTEFSPAGANQRGPLAAT LSGPGGEGQSAVARLTGEKKNHPGAQY ANRLSPRVGRFINAAGTTGFPTGKRAVS ATQLIPKVDKTTKIGKKQSRKTGNSKNQ SASPPPKESSSSHATEQNWTFENDELRE EGFKRSNCSELQEEVQTHGKEVKNEKK LDEWLTRITNEEKPLKDLMEKTKAQEL RDKCTSLSRFNQLEERVSVMEDQMNE MKREEKFREKRIKRNEQSLQEIWDYVVKR PNLRLIGVPESDGENGTKLENTLQDIIQD FADFGTTIKQDFRLLGQTSVDRLLQLSQ QQAVKGQQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLESGHQAPC MKSNNALIVILGTVTLDVAVGIGLVMPVL PGLLRDIVHSDSIASHYGVLLALYALMQ FLCAPVLAALSDRFGRRTVLLASLLGATI DYAIMATTPLVWIYPLVNSPSC* |

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| 2262 | 10313 | B | 3198 | 1 | 3198 | MKLMETLNQCINAGHEMTKAIAIAQFND DSPEARKITRRWRIGEADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQVRVGYTIE QINHMIRDVFGTRLRRAEDVFPVIGVAA HKXSPVIGVAAHKGGVYKTSVSVHQAQ DLALKGLRVLLVEGNDPQGTASMYHG WVPDLHIHAEDTLLPFYLGEKDDVTYAI KPTCWPGLDIIPSCALHRIETELMGKFD EGKLPTDPHMLRLAIETVAHDYDVIVID SAP |
| 2263 | 10314 | A | 3199 | 1 | 2259 | |
| 2264 | 10315 | A | 32 | 603 | 855 | GGWIMRSGVRDQPDQHGETLSLLKLQK LAGHGGACL*SQLVRRLRQEYHLNPGG GGCSEPRFGHCAPAWATE*DSVSGKKK KKK |
| 2265 | 10316 | A | 320 | 1812 | 5065 | PNKTGGKTVSDGLHHPSQLHSLKLENDQ GFYNVDSSTGFHNKTNPVGPFRKSPFLV MGVDWAETRSMQMMQMRAPMSDDIL ARDGRSRLSRGNRRNGGGCRDDDDG GGAGAVRTGEGATEELPPVGGRRVPQH RGELFVLSSAGDLHRDRDTHRGAGSG GGSAMASGAGGVGGGGGKIRTRCHQ GPIKPYQQGRQQHQVSSSRPDLSGFDED DKGWPEQLDMSDYSSSYQDVACYGTL PRDSPRRNKEG |
| 2266 | 10317 | A | 3200 | 1 | 2418 | |
| 2267 | 10318 | A | 3201 | 1907 | 5097 | TSKKIVKQAPVLTFTTA/LLAGGAIAQFA KENNHKAYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHVVFALAGS PKDADDTSIYMFYQKVGDNDSIDSWKNA GRVFKDSDKFDANDPILKDQTQEWSSG ATFTSDGKIRLFYTDYSGKHYGKQSLTT AQVNVKSDDTLKINGVEDHKTIFDGDG KTYQNVQQFIDEQNEGILPISEPPKQDFR LLG |
| 2268 | 10319 | A | 3202 | 891 | 2136 | GATQAFAKENNQKAYKETYESAKGLD VWDSWPLQNADGTVAEYNGYHVVFAL AGSPKDADDTSIYMFYQKVGDNDSIDSW KNAGRKFVKSDFDANDPILKDQTQEW SGSATFTSDGKIRLFYTDYSGKHYGKQS LTTAQVNVKSDDTLKINGVEDHKTIFD GDGKTYQNVQQFIDEQNYTSGDNHTLR DPHYVEDKGHKYLVFEANTGTENGYQG EESLFNKAYYGGGTNFRKESQKLQSA KKRDAELANGALGIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLGYVNSL TGPYKPLNKTGLVLQMGDPNDVTFTY SHFAVPQAKGNVVTISYMTNRGFFEDK KATFAPSFLMNIKGNKTSVVKNSILEQG QLTVN |
| 2269 | 10320 | A | 3203 | 1 | 3987 | |
| 2270 | 10321 | A | 3204 | 2 | 247 | QGAGFSSSLRMASIFSIHVGTRDLSRLS TILSPLYNTVAPGAN*CRELKLVLDAAD VLSTEVKRVITSSASNITPAFFCS |
| 2271 | 10322 | A | 3205 | 1099 | 2224 | DGQQIALHRLALRELQQAHVHAGLPQQ AKILFDGGSE/TRQNPLQLVHMGPRPL DKKNFQEP |
| 2272 | 10323 | A | 3206 | 1366 | 2673 | |
| 2273 | 10324 | A | 3207 | 1 | 7035 | |
| 2274 | 10325 | A | 3208 | 1 | 2328 | |
| 2275 | 10326 | A | 3209 | 1 | 2328 | |

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| 2276 | 10327 | A | 321 | 819 | 1242 | KAYASLSLWQAPSGESRPAPAAADLRGS SG/RPP*TFPNPPCGPHTGCPAGSFISFQ PRCLLVAKSKPGMPVSDEAAYESPWKG GAGAPALGLLGALSSEVADRALQAAPA WAPRDAGRDLPGQDRPQGPAGASLGP SRS |
| 2277 | 10328 | B | 3210 | 1 | 2541 | MPRQVSGSGPGLLVAGQAAGVTGGKK SLCQYRKPDGSGIVSLKIDWIERYQLPQ SYQHRKAGECLLHEYEDLVPIRDTLRLF PGGRYLPRAKHVAPSEPDEQDEQKLRD FADFGTTIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLESGQDFA DFGTTIKQDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGQDFADFG TTIKQDFRLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQTASPRAL ADSLMQLARQVSRLESGQDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQAVKGNQ LLPVSLVKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVKGNQLLP VSLVKRKTTLAPNTQTASPRALADSLMQ LARQVSRLESGQDFADFGTTIKQDFRLL GQTSVDRLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADSLMQLA RQVSRLESGQDFADFGTTIKQDFRLLGQ TSVDRLLQLSQGQAVKGNQLLPVSLDD VTYAIKPTCWPLAIIPSCALHRIETELM GKFDEGKLPTDPHMLRLAIETVAHDYD VIVIDSAENLGIGTINVVCAADVLIPTPA ELFDYTSALQFFDMLRDLKKNVDLKGFE PDVRILLTKYSNSNGSQSPWMEEQIRDA WGSMLVKNVRETDEVGKGQIRMRTVF EQAIDQRSSTGAWRNALSIWEPVCNEIFD RLIKPRWEIR* |
| 2278 | 10329 | A | 3211 | 1 | 3849 | |
| 2279 | 10330 | B | 3212 | 1 | 6724 | MDNFFAPVFTMGKYYTQGDKVLMLPLAI QVHHAVCDGFHVGRLNELQQYCDWE QGGADFADFGTTIKQDFRLLGQTSVDR LQLSQGQAVKGNQLLPVSLRKQNTSRPP SMHVDVDFVAAESKEVVPQDGIPPKRPL KVSQKISSRVENLNTLNLKELMLCHHQ EEGAGEDLDRVYDLMIFFVRENRTQVD HHLCMWMTLLLLKVKKWLKMEYLHQ NGHSKYHRRFLPVVGFQAEEDGVLSTV RIGFSHLL |
| 2280 | 10331 | A | 3213 | 532 | 1232 | |
| 2281 | 10332 | A | 3214 | 8749 | 11698 | CSWHDRFPDWKAGRILPISEPPSNRIFAC WGKPAWTGLLQLSQGQAVKGNQLLPVS LGFRGPPASNPGGAPGSASVAAAAVA AKAAAAAAPVDNAAPHSAKLEERRK PDPRRDFADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKTTLAPNT QTASPR |
| 2282 | 10333 | A | 3215 | 3 | 452 | |
| 2283 | 10334 | A | 3216 | 24 | 609 | GIPQTQREPTMVLSPADKTNVKAAGWK VGAHAGVEYGAEALERMFLSFPTTKTYF PHFDLSHGFCPLRATGKKVADALINA VAHVDDMPNALSALASDLHAHLRVGP GSTFKLLSHLPCW*TLGRPPSPAEFQPLA VARLPWEKFPGLFVEAPLLDLQITFKVG SFGWPLFFCFPGPPSPSPFLHPYRGL |

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| 2284 | 10335 | A | 3217 | 3 | 583 | EPRLRKAGLLSRSRQNDQEGREGAQQG WPAYGPARGVVPQPVVQTGTWQGNTG QRVPQLPPHPPPIHLVSRHRGKLRHGFLR PMPEPRGLESKGT/GQCSGSCSMYVTMR AKRPWEGGHDTLTQQGGCRSSVCGRRA HEALRPRVWCGEGPQWTWCAVCPNRS APGAGLADRQHPGESRAWGETRLGEAG GAE |
| 2285 | 10336 | A | 3218 | 3 | 398 | |
| 2286 | 10337 | A | 3219 | 1766 | 3896 | NTKLDQAQQAPEDHYPISLLPSHMAIG LLMAQEGHCKDSSAMGEEAHHPLTPAT PPFPPLSPDWGHMQPDDFFVPVAVPAVFR GPPQLQCHGRRFLNNSPCAQKSSSGLVV EPGLSRTLLEMVKLTSMRGQFLEAQIPT GISLTLQYQLYQKQTNKNMSYSFVFLK WVALGQGRRAGYPSLEDADSRFRNGSR SFLITVIGITLTVEIVTSGMMKGTRVRWS GAGNEGMMGLEEGRNERSVKEAPPRRA VEAQPKDRTWDVGKGGQTEGEGRGLEV EGQQHQGSEPGTIPFSVSWGVLLAGLC CLVPSSLVEDPQEDAAQKTDTSHHQDQ DWEDLACQKISYNVTDLAFDLYK\SWLI YHNQ\HVLVTPTSVAMAFAMLSLGTKA DTRTEILEGLNVNLTETPEAKIHECFQOV LQALSRPDTRLQLTTGSSLFVNKSMKLV DTFLEDTKKLYHSEASSINFRDTEEAKEQ INNYVEKRTGRKVVDLVKHLKKDTSLA LVDYISFHGKWKDKFAERIMVEGFHV DDKTIIRVPMINHLGRFDIHRDRELSSWV LAQHYVGNATAFFILPDPKMWQLEEK LTYSHLENIQRAFDIRSINLHFPKLSISGT YKLRVPRLNGITKIFSNEADLSGVSQEA PLKLSKAVHVAULTIDEKGTEATGAPHL EKAWSKYQTMFNRPFVVIKEYITNFP LFIGKVVNPTQK |
| 2287 | 10338 | A | 322 | 2 | 373 | PRVRVRVDLVSGWGGKMVDLFVLVTV KRVIDYAVKILVKPDWTGVVSDGVKHS LNPFCDIADVDEAVLLKEKLVKEGIACV CGPAQCQETNRTALGMGAHRGIHVEVS P**AQRCLPQVARG |
| 2288 | 10339 | A | 3220 | 3 | 1226 | MRRNKPRQRGVREARPAGGAGPGWGRG ARCSGAGEGGGGERRGSPPAALALAPAS GPRRNFPDARCLYQIHHQGAFLLAGSA SLSAVTGVPEGEARFTEDYCPEEKMGF HKPKMYRSIEGCISGAKSSSRFTDSKR YEKIDFQ\SCFGLHETRSGDNCNACVLLV KRWKKLPAGSKKNWNHVV DARAGPSI LKTTFEPKVKVKTLSGWNRIKSTQISKLOK EFK\RSNSDAHSTTSASPAQSPCYSNQS DDGSDTEMASGSNRTPVFSFLDLTYWK RQKICCGIYKGRFGEVLIDTHLFKPCS NKKAAAEKPEEQGPEPLPISTQEWTECP DLSLVVSWRPPLSSLPAGCSLHGLAADW TTDMITVTTSKREPSCQEGSFQRRKA FPKRLPKMAEVQVLLL |
| 2289 | 10340 | A | 3221 | 1 | 269 | |
| 2290 | 10341 | A | 3222 | 240 | 377 | SNTHRVPTFTDAWEVEMVTSLSLQSFL LPHIHCLKLQ*DPLHSP |
| 2291 | 10342 | A | 3223 | 47 | 263 | |
| 2292 | 10343 | A | 3224 | 416 | 498 | KRLSLQSFLLLPHIHCLKLQ*DPLHSP |
| 2293 | 10344 | A | 3225 | 1 | 305 | RTRGRTRGGDGGGHLGSGRNGGSMN APPAFESFLPLRG/QRRITINKDTKVPNAC LFTMNKEDHTLGNIIKSRACFPFAFCRD CQFPEASATLPVQPAEL |

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| 2294 | 10345 | A | 3226 | 74 | 562 | GSGGGGGHLSGRNGGSMNAPPFE SFLLEGEKK/ISDAGCGGPRITINKTKV PNACFLTINKEDHTLGNIKSQRDLKDPQ ALFAGYKVPHPLEHKIIIRVQTTDPDYSQ VRAFTNRQSPDLISELSLLGSAFRGGHK KTSQERNLSRGARGGLCSGL |
| 2295 | 10346 | A | 3229 | 1 | 2661 | |
| 2296 | 10347 | C | 323 | 303 | 395 | |
| 2297 | 10348 | A | 3230 | 1 | 1454 | |
| 2298 | 10349 | A | 3231 | 1 | 2364 | |
| 2299 | 10350 | A | 3232 | 1 | 1368 | |
| 2300 | 10351 | A | 3233 | 114 | 1473 | VKGDRFGALRFNDPCAGIKLPMTFFTEL EKTTLKFIWNQKRARIAKSILSQKNKAG GSTLPDFKLYYKATVTKTAWYQYQNR DIDQWNRTPSEITPHTYNYLIFDKPEKN KQWGNDSLFNKWCWENWLAICRKLKL DPFLTPYTRINSRWIKDLNVRPKTIKLE ENLGITIQDIGMGKDFMSKTPKAMATKD KIDKWDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAAKRH MKKCSSSLAIREMQIKTTMRYHLTPVRM AIKKSGNNRCWRGCGEIGTLHCWWD WKLVPQPLWKSVMRFLRDLELEIPFDPAL PLLGIYPNDYKSCCYKDTCTRMFIVALFT IAKTWNQPKCPTMIDWIKKMWHIYTME YYAAIKNDEFM/SFVGTWMKLEIILSKL LQEQKTK |
| 2301 | 10352 | B | 3234 | 1 | 1890 | MDKFLDITYLPRLNQEEVESLNRPIITGSE IVAIINSLPTKKSPGPDGFTAIFYQRYKEE LVPFLKLFQSIEKEGILPNSFYEASILIP KPGRDITKJENFRPISLMNIDAKILNKILA NRIQQHIKKLIHHDQVGFTPGMQGWFNI CKSINIQHINRTKDKNHMISIDAFAFD KIQQHFMKLTNLKLGIDGTYLKMIRTIY DKPTANIILNGQKLEAFPLKTGTRQGCP SPLLFNIVMELLARAIRQEKEIKGIQLGKE EVKLSLFADDMIRIKYLGILIRDMKDLF KENYKPLLNEIKEDTNKWKNIPCSWVGR INIVKMAILPKVIYRFNAIPKLPMTFFTE LEKTTLNFIWNQKRARTAKSILSQKNKA RGIMLPDFKLYYKATVTKTAWCWYQNR DIDQWNRTEPSEITPHIYNYLIFDKPDKN KQWGKDSL FNKWCWENWLAICRKLKL HPFLTPYTTINSRWIKDLNVRPKTIKLEE NLGNTIQDIGMGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTISVNRQPTK WEKIFATYSSDTGLISRIYNELKQIYKKK TNNPINKWAKDMNRHFSKEDIYAAQKH MKNAHHHPSEKCKSKHNEIPSHTS* |

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| 2302 | 10353 | A | 3235 | 1 | 2676 | MKAEIKMFFEINENKDTTYQNLWDAFK AVCRGKFIALNAHNRKQERPKIDTLTSQ LKELEKQEQTSHKASRRQEMTKIRAEK EIEIQKTLQKINESRSWFFERINKIDRPLA RLIKKKREKNQIDAINKDKGDIITDPTEI QTTIREYYKHLYANKLENLEEMDKFLDT YTLPRLNQEEVESLNRPIITGPEIVAIINSLP TKRSPGPDGFTAIFYQRYKEELVPFLK LFQSIEKEGILPNSFYEAIIIPKPGRDIT KKENFRPISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIRKSINVV QHINRTKHKNHMIIISIDAFAFKIQQPF MLKTLNKLSDGTYLKIIIRATYDKPTANII LNGQNLEAFPLKTGTQGHPLSPLLFNIV LEVLARAIQKEKEKAQNLLKLISNFRKV SVYKINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWNIPCSWIGRINIVK MAILPKVIYRFNAIPIKLPTTFFTELEKTIL KFIWNQKRAHIAKTIQSQKNKAGGIMLP DFKLYYKATVTKTAWYQYQKRDIDQW NRJELSEIIPHIYNHLIFDKPDKNKKWGK DSVFNKRCWENWLAICRKLKLDITLTPY TKINSRWIKDLHVRPKAIKTLEENLGITQ DIGMGKDFTSKTPKAMATKAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKIFAIY SSDKGLISRIYKELKQIYKKKTNNPIKKW AKDMNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRKAIKKSGNN RCWRGCGEIGTLLHCWWDCKLVPVW KTVWQFLRDLEIIPFYPAIPLGIYPKD Y |
| 2303 | 10354 | A | 3236 | 1 | 3045 | MDKFLNTYTLPRLKQEEVESLNRPIITGS DIEAIINSLPTKKSPGPDGFTAIFCQRYK EE/LEKEGILPNSFYEAIIIPKASDITK KENFRPISLMNINAKILNKILAKIIRQHIK KLIHHDQVGFIPGMHGLFNICKSVNIIQHI NRTNDKNHMIISIDAFAFKIQQHFML KTLNKLAKQNLLKLIGNFSKVSQYKINVQ KSQAFLYTNNRQTESQIMNEFPFTIASKR IKYLGILTRDVKDLFKENYK |
| 2304 | 10355 | A | 3237 | 1 | 2142 | |
| 2305 | 10356 | A | 3238 | 1 | 1551 | MRFKEKIHLENIKEPSEAAADGGAVAS YPLAKIVDEGRYKAEVMQLRCGWRAP ASDCVHSVAVVGVDVSVLEVLARAIQKE KEIKGIQLGKEEVKLSLFADDIMIVYLENP TVSAQNLLKLISNFSRVSGYKINVQKSQ AFLYTNNKQTESQIMSELPFTIASKTIKYL GIQLTRDVKDLFKENYKPLLNKIKEDTN KWNIPCSWIGRINIVKMAILPKVIYRFN AJHIKLPMTFFTELEKTTLKFIWNQKGVH IAKSILSKKNKAGGIMLPHFKLYYKATV TKTAWYQYQNRYTQCNRTPESEIIPHI YNHLMFDPKDNKKWGKDSLNFNKCW ENWLAICRKLKLDITLTPYTKINSRWIKD LNVVRPKPIKTLEENLGITQDIGMGKDFM SKTPKAIATKAKIDKWDLIKLSFCTAKE TTIGVNRQPTTELEKIFAIYSSDKGLISRIY KELKQIYKKKNNPIKKWVKDMNRHFSK EDIYAVNRHMKKCSSSLVIREMQIKTTM RYYLTPV |

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| 2306 | 10357 | A | 3239 | 1 | 1458 | GLSGDLLGAHQPLDVLGCVQPLDLLLP PQNLLALQSLQDDLLWALDPAAAAPWA MDRGAATQWAVGPVVS DPWVMEAVAS LPSAMDLDSAAQPTWLLGAASLLVTDQ PMDQPSADQLAEFPDLLSKVSQSLRIKY LGIKLTRNVKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVIYRFN AIPKLPMTFFTELENTTLKFIWNQKRACI AKSILSQKNKAGSIMLPDFKLYHKATVT KTAWYQYQNRDIDQWNGTEPSEIMSHIY NYLIFDKPEKNKQRGKDSLFSKWCWEN WLAICRKLKLDPFLTPYTKINSRWIKDLN VRPKIHKTEENLVNTIQDIGMGKDFMSK TPKAMATKAKIDKWDLIKQKSFCTAKET TIRVNRQPTWEKIFAIYSSDKGLISRIYK ELQQIYRKKTNNPIKKWAKDMNRHFSK EDIYAANRHMKKCSSSLAIREMQIKTTM RYHLTPV |
| 2307 | 10358 | A | 324 | 268 | 393 | DGRRKEKWHKVERRHRPYLLSSLSQHR W*TVTNFGEISGTIAIEVDEGTIHALNN GLFTLGAPHK/ERIALKPGYGKYLNSND ELVV/GRSDAIGPREQWEPVFQNQEVNRN GGPAEMGEEKRNGTKWREDTDHTSFPL FPSTGGQPKAHSNWRKVCH |
| 2308 | 10359 | A | 3240 | 1 | 2028 | |
| 2309 | 10360 | A | 3241 | 2 | 1547 | |
| 2310 | 10361 | A | 3242 | 3 | 1945 | |
| 2311 | 10362 | A | 3243 | 1 | 2124 | |
| 2312 | 10363 | A | 3244 | 1 | 2250 | |
| 2313 | 10364 | A | 3245 | 2 | 2483 | GKYYKLSSGTAPTCVSLGWGLARGDSA APALGSRTSACAPCSHGTWKLSPSDR LSPCDRSSEEAHTHAPHRLALVASLPW SRLPLLAPQSHSEAEATSQPTGVENHHQ KTRYVKAGGPVICRSLPESRGFLWASEG RKCMILIGSWAAMGRLRKSTISSRFGPQT LAGTGRPQAIPLVKKHSDAVLLGVCFLK LLHQHHQELGENADSQTLPTQTHWEFILS EDYNKMTVPKNYQVLEVLARAMRQEK QIKSIQLGKEEVKLSVFADDMIVYLENPI VSAQNLLKLISNFSKVSQYKINVQKSQA FLYTNNRQTESQIISELPFTIPSKRIKYLGI QLTRDVKDLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPRVIYIFNAIS IKLPMTFFTELEKTLKFIWNQKRARIAK TILSQKNKAGGITLPDFKLYYKATVTKT AWYWYQNRGVDQWNRIEPEIPIHNNH LIFDKPDKNKKWGKDSLFTKWCWENW LAICRKLKLDPFLTPYTKINSTWIKDLNV RPKTIKTLEENLGITIQDIGMGKDFMSKT PKAMATKAKIDKWDLIKLSFCTAKETT IRVNRQPTWEKIFTIYPSDKGLIPRIYKE LKQIYKKKSNNPIKKWAKDINRHFSKED IYAANRHMKKCSSSLVIREMQNKITIR/Y HLTPVRMAIHKSGNNRDMDEAGNHHS EQTIARTENQAPYLLTHR WELNNENTWT QVEEHHTLGPIVGVICRKVFPNGSGPSKP SGLHFSQPLPQVTSVVAKITIVPWEMKLI AMGVQDELNIAFHKNHLLMNDTTIHMT PYIQPAPKS |
| 2314 | 10365 | A | 3246 | 1 | 2622 | |

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| 2315 | 10366 | A | 3247 | 853 | 2831 | YPESTMNSNKFTRKKQTPPSKSG*RI*TD TSQKKTQMOPKDT*KNAQHHSLEKCK SKPQ*DTISHQLEWRSLSQDRKD*QSTL LAILIKKKGQKNQIDT/IKNDKEGITTDP EIQTIREYYKHLTYTNKVENLEEMDKFL DTYTLPTLKQKKEVKTLNRPITGSEIEAH NSLPT/KKSPGPDRTAEFYR/DIRSSGQG NQARERNKGYSIRKRGSIQVPVCR*HHCI FRKPHHLSPKSS*ADKQLQSSLRIQNQSA KITSIPHQ*QTNREPNE*TIHNCFKEN KMPRNPTYKGCEGSLQGELOTTAQ*NK RGHKRMEEHSMMLMDRKNQYRENGHTA QGNL*IQCHPHQATNDFHRIKKNYFKV HMEPKKSPHRQVNPKEQSWRHHTT* LQTLQGYSNQNSMVLVPKQHRPMEQ NRAPGNNTIHLQLSDL*QI*QKQEMGKG FPI**MVLGKLANHM*KAETGSLPHILYK N*FKMD*RLKC*T*NHKNPRRKPRQYHS GHRHGQGLHD*NTKSNGNKSQN*QMG N*TKELLHSTRNYHQSEQATYRMGENFC NLLI*QRANIQNLRQT*TNLQDKNKQPH QKVGKGYEQTLKRRHLCSQKTHEKML IITGHQRNANQNHNEIPSHTS*NGDH/SN QVRKQOVLERMWRN |
| 2316 | 10367 | A | 3248 | 1 | 4954 | MVFSIDAQKAFDKIQHRFMLKTLNKLGI DGTYLKIIIRAIYNKPTGNIILNGQKLEAFP LKTGTRQGCPPLSPLFNIVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDIIVYLENP IVSAQNLLKLIGNFSKVSQYKINQKSQA FLYTNNRQTESQIMSELPFTIASKRIKYL GIQLTRDVKNLFKENYKPLLNEIKEDTD KWKNIPCSWIGRIHVIMATLPKVIYRLH AIHIKLPMTFFTELEKTTLKFIW |
| 2317 | 10368 | A | 3249 | 25 | 527 | EFHRLRENPPMVAVSCPTKTNVKAWWG KVGGAHAVRSMCAEALERMFLSFPTTKT YFPFDLASHGSAQVKGATGKKVADAL TNAVANVDDMPNVAVRPEATLHAHKL RVDPVNFKLLKPLACLVDPGPAHLPRP SFTPGGATSSLGQSFLGFLKHRCLNLPN YR |
| 2318 | 10369 | A | 325 | 1 | 67 | |
| 2319 | 10370 | A | 3250 | 97 | 1360 | SACAWRLPSPGPSAMWPLWRLVSLAL SQALPFEQRGFWDFTLDDGPFMMNDEE ASGADTSGVLHPDSVTPTNYSAMCPFGC HCHLRVVQ/CSDLGLKSVPKEISPDITLL DLQNNDISELKDDFKGLQHLIALVLV NNKISKIHEKAFSPLRKLQKLYISKNLV EIPPNLPSSLVELRIHDNRIRKVPKGVFS GLRNMNCIEMGGNPLENSGFEPGAFDG LKLNYLRISAKLTGIPKDLPETLNELHL DHNKIQAIIELEDLLRYSKLYRLGLGHNQ IRMIENGSLSFLPTLREVHLADNNKLAR VPSGFPDLKLLQVV/YILHSNNIHQSGVF NEFLFPWGFGEAGPYYNH/ISLFNNPV PYWEVQPATFR/VVTDRLAIQFGQLQKV EAAAATLVSQWGS LGNRARHPDGEAEP GS |
| 2320 | 10371 | A | 3251 | 1 | 2535 | |

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| 2321 | 10372 | A | 3252 | 5 | 2333 | NPILWLETQMASNERDAISWYQKKIGAY DQQIWEKSIEQTQIKGLKNPKKMGHIK PDLIDVDLIRGSTFAKAKPEIPWTSLTRK GLVRVVFPLFSNWWIQVTSRIFVWLL LLYFMQVIAIVLYLMMPIVNISEVLGPLC LMLLMGTVHCQIVSTQITRPSGNNGNRR RRKLRTVNGDGSRENGNNSDKVRGIE TLESVPIIGGFWETIFGNRIKRVKLISNKG TETDNDPSCVHPHKKRRQCRPEIRMCQTR EKPKFSDGEKCRREAFRLNGVSDDLLS SEEDGEARTQMILLRRSVEGASSDNGCE VKNRKSILSRHLNSQVKKTTTRWCHIVR DSDSLAESEFESAASFQSGSRGVSGGSRS LNMSRRDSESTRHDESETEDMLWDDLLH GPECRSSVTSDEGAHVNTLHSGTKRDP KEDVFQQNHLFWLQNSSPSSDRVSAIW EGNECKKMDMSVLEISGIIMSRVNAYQQ GVGYQMLGNVVTIGLAFFFLHRLFREK SLDQLKSISAEIILTFCGAPPVTPIIVLSI INFFERLCLTWMFFMMCVVAERTYKQQR FLFAKLFSHIYFCQGLGKYEIPHRLKK VENIKIWLRLSYLKRGPQRSVDVVVS SVFLLTLIAFICCAQVLQGHKTSWDA YNNWGVFDLGETALLFLRLASLGSETN KKYSNVSILLTEQINLYLMEKKPNKKE QLTLVNNVLKLSKLLKELDTFRLYGL TMNPLIYNITRVVILSAVSGVISDLLGFNI RLWKIKS |
| 2322 | 10373 | B | 3253 | 73 | 358 | XVPGSRGPETKLWDDFSMSQATKRKHV VKEVLGEHIVPSDQQQIVRLRTPGNL HEVETAQQQRFLVSMPSKYRKNWIKRG DFLIVDPIEEGEK* |
| 2323 | 10374 | A | 3254 | 80 | 201 | |
| 2324 | 10375 | A | 3255 | 498 | 748 | FLPRRGDNDSTYPQ/WTACACRRRRTCW* T*TWIRSGQRKMWSCGRRSLTTCMP RTRTAARLMACGSGSWRRSGPCGRL SP |
| 2325 | 10376 | A | 3256 | 1 | 1764 | MTTSQKHRDFVAEPMGEKPVGSLAGIGE VLGKKLEERGFDKAYVVLGQFLVLKGD EDLFREWLDKTCGANAKQSRDCFGCLR E/WCAKSRPAAEVSELKADSKEGPQAQG PEQERTGL |
| 2326 | 10377 | A | 3257 | 842 | 1186 | FLPRRGDNDSTYPQ/WTACACRRRRTCW* T*TWIRSGQRKMWSCGRRSLTTCMP RTRAUTTWRSKNLALSCPSMTKSLKGS GHIPSAWSRAARLMACGSGSWRRSGPS CGCRLSP |
| 2327 | 10378 | A | 3258 | 526 | 1158 | SCGLSLIKMTTSQKHRDFVAEPMGEKPV GSLAGIGEVLGKKLEERGFDKGL/YVVL GQFLADIEKMKTSFREWLKDTCGANAK QSRDCFRMPFEKWCEALLVDALLGKFSI PPAPQSRSLASRSRDSSPCPSYEGKDICY CARTHLARRYFRGSFGEFSPLNHFQFFGI LRSWHAFPRPFPWPVSWVTVYQLFLE WDFPGPIPHPHFQSV |
| 2328 | 10379 | A | 3259 | 35 | 407 | |
| 2329 | 10380 | A | 326 | 163 | 552 | AGFSLSAQKSPGAMA*YSYVKSSKLVLK GT/SKKKKSKDKKRKREDEETQLD/IVGI W*TVTNFGEISGTIAIGMDEGTIHALDN GLFTLGAPHK/ERIALKSGYGYKLGINS ELVGHSDAIGPREQWEH |
| 2330 | 10381 | A | 3260 | 3859 | 4052 | ASCPNPKEFAPPRAGPPFWGPPPLARVN PGLGGPFSGTRTPPQPLPEQRVTLTSTN PWLAASV |
| 2331 | 10382 | A | 3261 | 493 | 712 | AHGRQLRKYSQQQGCWSRPFPGCHAV SGGGCGKCCSPANGPCGAAICLGFQPH NFPDPCETC/CGCHAVSGGGCGKCCISSK WSLWCSPAUVSSHTTSRIPVKLAGLPSP SFLPG |

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| 2332 | 10383 | A | 3262 | 51 | 539 | |
| 2333 | 10384 | A | 3263 | 742 | 4858 | |
| 2334 | 10385 | A | 3264 | 2 | 658 | AFRLMLFPESWMETRREGAPAPPAPRSET SHDLVATLMRCTPHYIR*SNPTRPRGPET GRRTA*TRSPQVPHLQHLPPTPRLVTPHP EGTQPTLPTRSSTRWNTWA*RTSGCES RLRLPPPVRQJPAEYAILTPETWPRWRGD EPRASSTCFGRSTWSPTRPDGEHQGLCQ EPRVAFPPGGGAKRKFDGFARTIQKAWR RTWLSGSTRRCGRKLPTSC |
| 2335 | 10386 | A | 3265 | 1 | 4095 | |
| 2336 | 10387 | A | 3266 | 26 | 173 | |
| 2337 | 10388 | A | 3267 | 387 | 1443 | PHRKQAEPPRHHERLGRRVRHHARHGR GSRPDTAAEAAGGCGDPRAQQLERRL RHPPLRWQGLLRQRLREPPRRSLLRP HRADAVQ*PGLPPDALPREAGWRQEGA PQHRRLQDYETCQLTWPH**GAHPTTS AALNPTRPRGPETGRRTESSTRWNTWA* RTSGCAEPASPTA/SQFAKFLQRYAILTP ETWPRWRGDERHGVQHLRAVNMEPD QYQMGSTKVFKNP/VVAFPPGGGARA KVRWLCPNHPEGLAAPRGCEVRGDA/R RKLPTSC*TRRSGGATASIGTSSGTTWG WRSGPSCVSSWARRSGWTSPIRSPSTTA ASSPSSGT*S*RPSVCM*LGERR |
| 2338 | 10389 | A | 3268 | 1 | 4496 | MEGNVNAHRASGAQIRTCRAPPATGC TALFKANSPEFTGLKSAQRGRGPVVGAP RKRFSGRLRGHREAERTLGWGSQAPPA AQAHTPAAGDSTLLRSAPVGTCLLYAP HPQDFPPAGFLREQWWPRLTLQVFLHL RTGGRVGPVDWVLLGGGRLLGHRMP GPCNLAEAVLLREARWPWGEAGGSEEG EPSSGSGVGGNCQARPLPSAHPEAQQGV GLEVGRGMVAPAASYFADEGRPNGDHP ARQPRLG |
| 2339 | 10390 | A | 3269 | 911 | 2827 | ERKHLGWMEFSIKQSPLSVQSVVKCIKM KQAPEILGSANGKTPSCEVNRECSVFLS KAQLSSSLQEGVMQKFNGHDALFFIPAD KLKDLTSRVFNGEPGAHDALRFESQE MKGIGTPNTTPIKNGSPEIKLKITYM NGKPLFESSICGDSAADVSQSEENGQKPE NKARNRKRKSIKYDSLLEQGLVEAALVS KISSPSDKKIPAKKESCPNTGRDKDHLLK YNVGDLVWSKVSGYPWWPCMVSAADPL LHSYTKLKGQKKSARQYHVQFFGDAPE RAWIFEKSLVAFEGEGQFEKLCQESAKQ APTKAEKIKLLKPISGKLRAQWEMGIVQ AEEAASMSVEERKAKFTFLYVGDQLHL NPQVAKEAGIAAESLGEMAESSGVSEEA AENPKSVREECIPMKRRRRRAKLCSSAET LESHPDIGKSTPQKTAEADP/RRRGVGS PGRKKTIVSMPSRKGDAASQFLVFCQ KHRDEVVAEHPDASGEEIEELLRSQWSL LSEKQRARYNTKFALVAPVQAEEDSGN VNGKKRNHTKRIQDPSENAIDLETPRK GLRTDKHSLRKRDTITDKTARTSSYKAM EAASSLKSAATKNLSACKPLKKRNR ASTAASSALGFSKSSSPASLTENEVK |
| 2340 | 10391 | A | 327 | 289 | 818 | EPSRGVWPHEARINGSKKKKSKDKKR KREEDDEETQFD/IVGIW*TVTNFDEISGTI AIEMDEGTIHALDNLFTLGAPHK/ERI ALKPGYGKYLINSDELVV/GRSDAIGPR EQWEPVFQNGACAAVFTVIGSEKQSECS LLRESRAKYHGCTHGQISSSLKQHPRWM YSHQEDLKV |
| 2341 | 10392 | A | 3270 | 3 | 114 | |
| 2342 | 10393 | A | 3271 | 328 | 471 | |
| 2343 | 10394 | A | 3272 | 1 | 190 | |

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| 2344 | 10395 | A | 3273 | 2 | 479 | SGLGRLPGPWQEAGSSRGPSSGDMAGV KALVALSFSGAIGLTF/LHMLGCALEDYG VYWPLFVLFFHAISPIPHIAKRVTYDSD ATSSACRELAYFFTGTIVVSLWISPVIL ARVALIKIWGACAFVLAGNAVIFPYN RGFSLYLGRGDDFSWAEQW |
| 2345 | 10396 | A | 3274 | 3 | 586 | ARAMGISRDNLHKRRKTGGKRKPYHKK RKYELGRPAANTKIGPRRIHTVRVRGGN KKYRALRLDVGNFWSGSECCTRKTRIIDI VYNASNELVVRTKTLVKNCIVLIDSTPY RQ/WTPEEEELNKKRSKKIQKKYDERKK NAKISSLLEEQFQQGKLLACIASRPGQCG RADGYVLEGELEFYLRKIKARKGK |
| 2346 | 10397 | A | 3275 | 2 | 727 | LFPASAEQMGISRDNWHKPRKTGGPRE SPYQOEAKSMSLGRPAANTKILAPRRIQ HSPVCRGG*QVNTVPLRFDVGNFSWG/S KECCTRKTRUIDVVYNAI**PSWVRYPRP LVERICNVLIDEQHPYRQWVRSPTYALP LGPQRKGAKLDSLREEIFPKPTDLK*IQ KKYD*/ERKKNCQNSASLPGRSSFQGGK ASLRCAFK/RPGQC/GRADGYMTRGHR VRSYYLRKIKARQSKINT |
| 2347 | 10398 | B | 3276 | 48 | 209 | XKNQCETRTMQENGYSSHAVDGTGPAG GAGRPAGSTGAQVSVQPNFQQDKFLGR X* |
| 2348 | 10399 | A | 3277 | 2 | 353 | |
| 2349 | 10400 | A | 3278 | 3 | 676 | SAVEFPPLSHTTGTRPRTPIILLQENG FIHTLWMGLALLGVLGDLGQHRPRSP CQPNFQQDKFLGRWFKRGLASNSSWL EKKAALSMCKSVVAPATDGGVNLSTF LQEKTSVETRMLALQPRGVPSASLQLTG VPHWGQA/HYSVSVVETDYDQYALLYT RASKGPGEDFRMATLYSRTQTPRAELK EKFTAFCKAQGFTEDTIVFLPQTDKCM EQ |
| 2350 | 10401 | A | 3279 | 154 | 522 | HVACGLLWIVVSPSAHLNLDGTITTK/EN LGTVNEILLGSNPTEAELQDMINEVMSD NGTIDFPEFLTMMARKMKVDTDSEGR KLVEEAFRVFGLRVGNGLYLACRNFRH VDGQTLGGGSLPD |
| 2351 | 10402 | A | 328 | 213 | 905 | YVQSLKQILS/GCI*ESIAIKKKKNKDKR KREDEETQLDIVGIWWTVTNFGESGTI AIEMDKGTIHALDNGLFTLGAPHKEVD EGPSPEQFTA/VKLSDSRIALKSGYGKY LGNSDGLVVGSRDAIGPREQWEPVFK MGKMALSTSNCFIRNHEAEDIEAKSKT AGEEEMI/KGSPNLCQFTFMTLPYLPEH RSLLLKIRSCAERETKKKDDIPEEDKGN KQCE |
| 2352 | 10403 | A | 3280 | 1 | 1446 | |
| 2353 | 10404 | A | 3281 | 774 | 3564 | VLSKGNERSQPRSLRLLAPQLKAEAAA DKGLAPVPPPFSSGHSGPCERELEGQRG RGRSRRGAHLELKPSPGLRAGAPTDRGR GGPAEVAAAAGGRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAGEDNPA GAGGAAVAGAAGGARRFLCGVVEEQL MTLISAAREYEIEFIYAI SPGLDITFSNPKE VSTLKRKLDQVSQFGRSFALLFDDIDH NMCAADKEVFSSFAHAQVSITNEIYQYL G |
| 2354 | 10405 | A | 3282 | 51 | 672 | VLSKGNERSQPRSLRLLAPQLKAEAAA DKGLAPVPPPFSSGHSGPCERELEGQRG RGRSRRGAHLELKPSPGLRAGAPTDRGR GGPAEVAAAAGGRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAGEDNPA GAGGAAVAGAAGGARRFLCGVVEEQL MTLISAAREYEIEFIYAI SPGLDITFSNPKE VSTLKRKLDQ |

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| 2355 | 10406 | B | 3283 | 506 | 2416 | MNPSAPSYPMASLYVGDLPDVTEAML YEKFSAPGILSIRVCRDMITRSLGYAY VNFQQPADAERALDTMNFVVIKGPVRI MWSQRPDLRKSJGVGNIFKNLDSIDN KALYDTFSAFNGILSCKVVCDENGSKGY GFVHFETQEAERAIEKMNGMLLNDRK VFVGRFKSRKEREAELEGARAKEFTNVYI KNFGEDMDDERLKDLPFGKFGPALSVKV MTDESGKSKGFGFVSFERHEDAQKAVD EMNGKELNGKQIYVGRAQKKVERQTEL KRKFEQMKQDRITRYQGVNLYVKNLDD GIDDERLRKEFSPFGTITSKVMMEGGR SKGFGFVCFSSPEEATKAVTEMNGRIVA TKPLYVALAQRKEERQAHLTNQYMQR MASVRAVPNPVINPYQPAPPSGYFMAAI PQTQNRAAYYPPSQIAQLRPSRWTAQG ARPHFPQNMPGAIRPAAPRPPFSTMRPAS SQVPRVMSTQRVANTSTQTMGPRPAAA AAAATPAVRTVPQYKYAAGVRNPQQHL NAQPQVTMQQPAVHVQGGQPLTASMLA SAPPQEQKQMLGERLFLIQAMHPTLAG KITGMILLEIDNSELHLMLESPELSRSKVD EAVAVLQAHQAKEAAQAVNSATGVPT V* |
| 2356 | 10407 | A | 3284 | 183 | 3080 | PRRCSTGNSGRPKIIRRAEAENEDRTL RLLPGNERSQPRSLRLLAPQLKAEAAV DKGLARVPPFSSGHSGPCEREGERGQRG RGRSRGAHLELKPFSGLRAGAPTDRI RGGPAEVAAGGRRMVQKESQATLEER ESELSSNPAASAGASLEPPAAPAGEDNP AGAGGAAGVAGAAGGARRFLCGVVEGF YGRPWWMEQRKELFRRLQKWELNTYLY APKDDYKHRMFWMREMSVEAEQLMT LISA |
| 2357 | 10408 | A | 3285 | 3 | 452 | |
| 2358 | 10409 | A | 3286 | 26 | 526 | NSTDSETHPWLLSPADKTTVK/APAWG KVGAHAGEYGSEALERMFLSFPTTKTY FPHFDLSHGFCPLRATGKKVADALTKR RGAPLDDMPNALVRPLSDLHAHKLRV GPGSTFKLLKPLACLTLGPAHLRPSFT PGGCKASLGQSFLGFLKHRCLNLPNYR |
| 2359 | 10410 | C | 3287 | 410 | 484 | |
| 2360 | 10411 | A | 3288 | 3 | 170 | IRGSVVLNLNLTFFTP*RSFISTSVMF* KPFIFSFLMLLL*VFIFSLKILSY |
| 2361 | 10412 | A | 3289 | 831 | 1559 | IAWAFKINWLPILFISVLFYPIFGFIFFYL LYFSNTCLSLFFHFLSETLDNIFIFLYSIF QFSSKFVHFAISFMFPLSFFFCILSRKF IFFSSKKYVFIFLISLSFIFF |
| 2362 | 10413 | A | 329 | 133 | 480 | GYGRRSVKVRWARCTGFSPKTPNPWV NSQHFGRLRWADHLRSGVRDQPGQHGE TLSELLKIQLPGCGGRCL*FQLFGRLRQE N*IRLNPGGGGCSELRSHHCTPAWVTEQ DSVSK |
| 2363 | 10414 | A | 3290 | 253 | 414 | |
| 2364 | 10415 | A | 3291 | 3 | 225 | |
| 2365 | 10416 | A | 3292 | 218 | 602 | SFLLLPRCTAEKQRWGHQQLYWSHPW KFGQGSRSICRVCSNNRHGLIRKYGLN MCRQCFRQYAKDIRFHLSWTKCSSFRGL SGASTSMKKPWINSFVYIIHFEKATEKK RKKNEIKRGPFCKGPL |
| 2366 | 10417 | A | 3293 | 33 | 494 | |
| 2367 | 10418 | A | 3294 | 1 | 609 | PLKRSDDGNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPEEKSAVTALWGKVVNDE VGGEALGRLLVVYPWTQRFESFGDLST PDAVMGNPKVKAHSKKGLRGAFGDGL AHLNLDLKGTFATLSELAHCDKAAPWIPE ELQAPWATCLVCVAWPITFGKRISTPPV AGLPNQENWLAWCWLNALGPTSNHLSL |

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| | | | | | | AFLAGPISN |
| 2368 | 10419 | A | 3295 | 8 | 519 | SAQMAVTTADPRVRPRVRTQLCSLASLI QTLLVHLTPEEKSAVTALWGKVNVD VGGKALGRLLVVYPWTQRFLAESFGDLS TPDAVMGNPKVKAHSKKVLGVAFSGGP GCTWDNLKGTFAHTEVSLHCDKILHRGS LKNFRLLGQRAWSVVAGPIHFWQKNFN PTSCRLA |
| 2369 | 10420 | A | 3296 | 3 | 333 | |
| 2370 | 10421 | A | 3297 | 35 | 717 | RRSSPSLLPLAERGGARARGRPERAPHPS TPATRTAPPWARRMMKLKSNQTRTYD GDGYKKRAACLCFRSESEEEVLLVS R/HPDRWIVPWKEGMEARRKEAKCGKQ VREVCERLGVKGTGLGRLVGIFENQER KHRTYVAVVLIVTEVLEDWEDSVNIGR KREWFKIEDAIVLQYHKPVQASYFETL RQGYSANNGTPVVAATTYSVSGFRASMF RAFRWT |
| 2371 | 10422 | A | 3298 | 81 | 426 | PSFHYAVLPLHNCLGFFPSLRHRWLHSM TDDPPTTKPLTARKFIWTHKFNVTGPQ NNMYLILPLERRFRSGSHLQHLTSKDNE EQLKHAKYGAFHVITLLFTIHYNSQLKL CD |
| 2372 | 10423 | A | 3299 | 180 | 484 | RQQAIFWHRWLHSM TDDPPTTKPLTAR KFIWTHKFNVTGPQNNMYLILPLERRF RSGSHLQHLTSKDNEEQLKHAKYGAFH VITLLFTIHYNSQLKLCD |
| 2373 | 10424 | A | 33 | 200 | 559 | KNFFFLEMEF/SVLLPRLECNGVISAHR LRLPLSSYPASSSQVAGDYRACTTTAG* ILYF**ETGFLHVGQAGLEFPTSGDQPAL ASQSAGITGVSHCPQLKKSILHETPKGLT GVTS |
| 2374 | 10425 | A | 330 | 27 | 201 | LQE*SRRPSRSEAADLHGECYSS*GSTSG VCCSSRWARGLAGLRSEAADLRSEYSS |
| 2375 | 10426 | A | 3300 | 591 | 942 | MAKTHFDVDGSMVPEWHRWLHSM TDDPPTTKPLTARKFIWDGTTKFORGLG HPRNNMYLILPLERRFRSGSHLQHLTSK DNEEQLKHAKYGAFHVITLLFTIHYNS QLKLCD |
| 2376 | 10427 | A | 3301 | 1 | 508 | NFALEAKNSARAISYVQTPMGHFTRG PRLTITSLWGKVNVEDAGGETPGKGS VVYPWTQRFFDSFGNLSSAFCSWPTP KVKAHGKVKVLTSLGDAHKSTWDDLKG HLLPKPEVNCTVDKPAWDPENFKAPG EMLLVTRFGQSLFRQKNFTPEGCRASLG KKDG |
| 2377 | 10428 | A | 3302 | 3 | 452 | |
| 2378 | 10429 | A | 3303 | 1 | 627 | TLLVPQDSERTHPWLLSPADKIVNKA WGKVGAAVSRMCAEALERMFLSFPTT KTYFPHFDLSHGISAQVKGATGKKVAD ALTKRRGAPLDDMPNAL/SSALEATLHA HKLVRVPGSTSKLLKPLACLVDPGPAHL PRPSSTPGGCNVFPGTKFPLFVEAPLLE PSKLPLKLSRLAIVFLPLWGFPAPPPL SCTRTPVVFEIKS |
| 2379 | 10430 | A | 3304 | 131 | 406 | EAMGILKLQVFLIVLSVALNHLKATPIES HQVEKRKCNATCATQRLANFLVHSSN NLGGILSSTNVGSNTYGKRNAVEVLKRE PLNYLPL |

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| 2380 | 10431 | A | 3305 | 154 | 1702 | IGHRDPARGRSCRCSGYYSRMVCEKLAP QSEMASAGVSLRATILCLLAWAGLAAG DRVYIHPFHLVIHNESTCEQLAEANAGK PKDPTFIPAPIAKTSPVDEKALQDQLVL VAAKLDTEKLRAMVGMLANFLGFP YYMGMHSELWGVVHGATVLSPTAVF GTLASLYLGALDHTADRLQAILGVPWK DKNCTSRDLAHKVL SALQAVTGLLVAP GRADKQAQLLALSTVGVFTAPGLHLK QPFVQGLALYTPVVLPRSLDFTELDVA ETIDRLMQAVTGWKTGCSLTGAKADST LAFNTYVHFQGMKGFSLLAEPQEFWV DNSTSVSPMLSGVMGTQHWSDIQDNF SVTQVPFTDASALLLIQPHYASDLADKVE GLTFQQMSFNWMRKLFPRTHLTMPQL VLQGSYDLQDLLRPGSSCPFLHTELNL GRISGNDRIRVGEVLN SIFFE LEADEREP TESTQQLNKPEVLEVPLTRPFLFAVYD QGATALALSWGRVGKPA |
| 2381 | 10432 | C | 3306 | 223 | 417 | |
| 2382 | 10433 | A | 3307 | 3 | 742 | HEASCRSERRRQMAFDITYDDRAYSSF GGGRSGRGSAGGHGSRSQKELPTEPPYT AYVGNLPFNTVQGDIDAIKDLIRSVR LVRDKDTDKFKGFCYVEFDEVDSLKEA LTYD\GALLGDRSLARVDIAEGRKQDKGG FGFRKGGPDDR\GFRDDFLGGRG/GLSR PGDRRTGPPMGSFRDGPPLRG\SNMDF REPTTEERAQRTTTPALKPRTVATPLNQ VANPNSSUFVGGARPREEVVQKEQE |
| 2383 | 10434 | A | 3308 | 1 | 861 | |
| 2384 | 10435 | A | 3309 | 1 | 2076 | |
| 2385 | 10436 | B | 331 | 396 | 809 | MAGCRSRALPHGEAAKAQRKVTAAGP GAKHLTAWGQQQLATPSVGPAEPHT QNSHWPASAVCSPSSRLRLSLHTYPQAE GAGSGLGQPRKGLPQCSSRLKGSSSAK VGAQAEVPRASEACEGCQHAVTSHKY * |
| 2386 | 10437 | A | 3310 | 34 | 657 | SDGRCGRCCAPRAPRAMHMSFAIS/RCA FYQLLLAALMLVAMLQLLYLSLLSGLH GQEEQDQYFEFFPPSPRVDQ\VKAHVRT ALASGGVLDVSGD\YRV\YRGLLKTTMD PNDVILATHASVEQTCLHLISGLLERW EGPAVPCSVFAAITKEEAQLATVLAYAL SSHCPDMPARVAMHLVCPSTRYEAAPVD PREPGEFALLRSCQEVFDKLARVAQPGI NYALGTNVSYPNLLRLNLA REGANYAL VIDVDMVPTEGLWRGLREMLDQSNQW GGTALVVPFAFEIRRARRMPMNKNEVLQ LYQVGEVRPFYGLCTPCQAPTNYSRW FNLPEESLLRPAYVVPWQDPWEPFYVAG GKVPNFRSGFRQYGFNRISQACELHVG GDFEVLNEGFLVHKGFKEALKFHPQK EAENQHNKILYRQFKQELKAKYPNSPR RRAQLATVLAYALSSHCPDMPARGHA PRVPLALRGSRRPPGAGGVCPAAVLPG GL |
| 2387 | 10438 | A | 3311 | 160 | 441 | |
| 2388 | 10439 | A | 3312 | 107 | 691 | RTAILSRMKIFLPVLLAALLGVERASSL MCFSCLNQKSNLYCLKPTICSDQDNYC VTVSASAGIGNLVTFGWSLSKTCFPCL APPPEGRSMLGVASMGHSAFCQSFLVAI FSCGPMAGLRGKRSPLL GARACCLSLAG RALLRFGPLDRPEPCSPDPAQEGKPSFF WIPQCMGAPDSSRALICALGPRSG |
| 2389 | 10440 | A | 3313 | 388 | 525 | |

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| 2390 | 10441 | A | 3314 | 194 | 1131 | PQHGGHFFRKIKSCSWQARPLEDEATLG QCGVEALTTEVTRPACLEVKSMVPWP VLEKVRGQTPKVAKHGEKKKKKTGRAK RRMQYNRRFVNVVPTFGKKKGTTFTKIF VGGLPYHTTDASLRKYFEGFGDIEEAVVI TDRQTGKSRGYGFVTMADRAAAERACK DPNPIIDGRKANVNLAYLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMYPPAI VQATVVIPAAPVPSLSSPYIEYTPASPAY AQYPPATYDQYPYAAASPATVRSFVGYS YPAAVPQALSAAAPAGTTFLQYQAPHV QPDRMH |
| 2391 | 10442 | A | 3315 | 1 | 407 | DAERQEALGIVRRIGTDTEAATEPAGAT VPAAAAAARIGTVGPQPAMPRRKRNA GSSSDGTEDSDFSTDLEHTDSSSEDGTSR RSARVTRSSARLSQSSSRISRSCSKSGSLL ALRSLLTLPEE*PVVSSSLPQ |
| 2392 | 10443 | B | 3316 | 78 | 316 | XSLLGQWPRDADGAFTCCTNDKATQT PLSWQELEGERASSCAHKRSASWGSTD HRKEISKLKQQLQRTKLSRSGKEKERX* |
| 2393 | 10444 | A | 3317 | 1 | 2319 | GHPAFLEDGSPSPVLAFAASPRPNHSYIF KREPPEGCEKVRVFEEATTRGKYGEGAK QETFTFALTIVFIQCVINAVFAKILIQFFD TARVDRTRSWLYAACSISYLGAMVSSNS ALQFVNYPTQVLGKSCCKPIPVMLLGVTL LKKKYPLAKYLCVLLIVAGVALFMYKP KKVVGIEHTVGYGELLLLLSLDGLT GVSQDHMRHYQTGSNHMMLNINLWS TLLGMAVSCPDQGPPELVPRCPFVQALE KPS |
| 2394 | 10445 | A | 3318 | 845 | 1343 | LSLGDSAQCLLPHASWCQVAGHPAFLE DGSPSPVLAFAASPRPNHSYIFKREPPEG CEKVRVFEEATS/RRVLTGPFLTSCPDKN KVHFQPTGSAFCPVNLMKPLFPGMGFIF RNCPSNPGISSSPGQPQATTSEGSGLQG LPTAIRAMAVAPHLQMSLCFSRAP |
| 2395 | 10446 | A | 3319 | 44 | 498 | |
| 2396 | 10447 | A | 332 | 130 | 249 | |
| 2397 | 10448 | A | 3320 | 1 | 164 | |
| 2398 | 10449 | A | 3321 | 2 | 438 | ARAARVFLHRSSLNLSNGETESVKTIV HDDVESEPAMTPSKEGTLIVRQTSASST LQKHKSSSFTPFIDPRLLQISPSGTTVTS VVGFSQDGMPEAIRQDPTRKGSVVNV NPTNIRQSDPPEIRKSGKG*L*ILGAGLW |
| 2399 | 10450 | A | 3322 | 3 | 174 | |
| 2400 | 10451 | A | 3323 | 2 | 4978 | RRTSAVSRGLLFMSFVQPLLQPPVHLLT ARVRVPGYLQIDGVKIKEHNGKLMNCF KTKMTYYSFMKCVGLPAQLTIGFSGPSR ETGSDPRAARRGEDPQSKDRGDLSEQT EAQRSGVHCPRSQLVGELAGQSPRTIPA ALRVCLYLLCITSYNHTSKDESSKDEEEE IKLEINMLKKYSHHRNIATYYGAFIKKSP PGHDDQLWLVMEFCGAGSITDLVKNTK GNTLKEDWIAYSISREILRGLAHLHHVI HR |
| 2401 | 10452 | A | 3324 | 197 | 332 | |
| 2402 | 10453 | A | 3325 | 1 | 1788 | |
| 2403 | 10454 | A | 3326 | 3 | 111 | |
| 2404 | 10455 | A | 3327 | 220 | 423 | HEELKSGPYLLTFRDCFLHFWALVSKR /LALNFM*TSAPT*KALSKRNICLVNKNR NIKIPYPKKKKK |
| 2405 | 10456 | A | 3328 | 273 | 499 | RSQVRDQPGQHGKITSLLKIQKLARRGG ACL*SQLLRRLRQENRLNPGGGGCSEPR SCHCTPAWETEQDSISKIK |
| 2406 | 10457 | A | 3329 | 1 | 1176 | |
| 2407 | 10458 | A | 333 | 1 | 3408 | |

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| 2408 | 10459 | A | 3330 | 245 | 394 | |
| 2409 | 10460 | A | 3331 | 458 | 701 | GPAPTRRGPAHPGAHTR**PAGTARAAC GSA*SAGTASPAHKKGKGGHHPGSRASGTG PGPCQRRRRSDHSSAGKWPLREASL |
| 2410 | 10461 | A | 3332 | 365 | 814 | AALRSSENSSRHRSLVKMSDKKAKDPV NKSGGQGPKRKNWSKGSSGTSFNNL VLFDKATYDKLCKEVPNYNLIITPAVGSE RLKIRGSLGQGKPFQELLSKGFIPNWFS KHRASSYFTPGITKGGADAPSLLEDGCMN RSNPPVHLEK |
| 2411 | 10462 | A | 3333 | 41 | 565 | APSPRRPWGHFTEED\KATIKNLWGKGE MWKIDAGGKNPWRLPWLSYPMGPQRF FDQLLANLSLCPIMGNPPKVKGTPWR KVLTSLS\SAHKSTWDDLKGHLLPKPEV NLHCIDKPAMWDPENFKAPGEMLLVTR FGQSHFRQKNFTPGGCRASWGRKMGDL ELASALVPSRYH |
| 2412 | 10463 | A | 3334 | 399 | 592 | KCIHFPGPPTKFCVGVIVVTAVP/TFGM* TVYV**LPFSILAQNVG*RDDCDPGWKL NLFYAKKKK |
| 2413 | 10464 | A | 3335 | 28 | 312 | |
| 2414 | 10465 | A | 3336 | 26 | 417 | |
| 2415 | 10466 | A | 3337 | 16 | 3567 | |
| 2416 | 10467 | A | 3338 | 6385 | 6599 | |
| 2417 | 10468 | A | 3339 | 2 | 758 | |
| 2418 | 10469 | A | 334 | 3 | 443 | SFQGGLEGEAWAGTGAAPGACGPAPVP GRRRLRGPRTRPAGPTGPGQ*G/VLAPGP AAAVL/RFLTGP*LPSRSRARDREGLQLH S*SQRDHEPTGRN/GTTPDAPP*EL*HSPR RSAASLCPQAPVSPQGSQVPALSGNSP QRLLPT |
| 2419 | 10470 | A | 3340 | 116 | 627 | |
| 2420 | 10471 | A | 3341 | 1830 | 2259 | |
| 2421 | 10472 | A | 3342 | 1 | 619 | |
| 2422 | 10473 | A | 3343 | 1830 | 2258 | |
| 2423 | 10474 | A | 3344 | 290 | 1377 | RSFRAIGEVGSIRGWGGGYAAQLQSPSR LPVLGGGKKGGSRGVGQGSRAEVGLG SQRERSGTCGAEAAAAAQLIAGTGSSL PYQGPQGNQTAIAPTAPLSPCKAAAVI MGNIFGNLLKSLIGKKEMRILMVGLDAA GKTILYKLLKGEIVTTIPTIGFNVETVEY KNISFTVWGC GVARDKIRPLAWRHVYFQ NTQGFILWSDSNDRERVNEAREELA MKNAGAETSLRDAVLLVFGQTNRICPN AMNAAGVQDKLGLHSLRHRNWIQAT CATRGN\GLYEGHLWLANSVPKQEVESR TALTKHSTSPLTYLLSPCPQLPLLSMOG LARA W GIMSTLPSRTLPLTSLPFCPP |
| 2424 | 10475 | A | 3345 | 292 | 574 | VTTENSGGQTQCGKQDRIQVPRHPARRG PPGSQY/PVTPPVPPGPHATQLPPGPIPL GKRKAGQERRLDPRPTTCQAAAPTRSSP FCPPQKVWR |
| 2425 | 10476 | A | 3346 | 3 | 142 | TISSIIRKARKPQDILLNNYTPRSSPLRSSG RTRMYKGNVRPGNSS |

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| 2426 | 10477 | A | 3347 | 1 | 1418 | MAAALFVLLGFALLGTHGASGAGEERA RKQPCGKSRFQGHSEALATRFSAAGNTG FVQAPLSQQRWVGGSVELHCEAVGSPV PEIQWWFEGQGPNDTCSQLWDGARLDR VHIHATYHQHAASTISIDTLVEEDTGTYE CRASNDPDRNHLTRAPRVKVVRAQAV VLVLEPGTVFTTVEDLGSKILLTCSLND ATEVTGHRWLKGGVVLKEDALPGQKTE FKVDSDDQWGEYSCVFLPEPMGTANIQL HGPPKVKAVKSSSEHINEGETAMLVCKS ESVPPVTDWAWYKITDSEDKALMNGSE SRFFVSSSQGRSELHIENLNMEADPGQY RCNGTSSKGSQAIITLRVRSHLAALWPF LGIVAEVLVLVTIIFIYEKRRKPEDVLDAL RRCTWPGMLMSCPEPLGVTEGRAGSTDA PARGLSGASADRLSSRPLFHGGGPSSDD DAGSAPLKSSGQHQNCKGKNVRQRNSS |
| 2427 | 10478 | A | 3348 | 3 | 896 | SCRGRRRQRLEVVRGFRRGIGIMAAALF VLLGFALLGTHGASGAAGTVFTTVEDL GSKILLTCSLNDSEATEVTGHRWLKGGV VLKEDALPGQKTEFKVDSDDQWGEYS CVFLPEPMGTANIQLHGPPRVKAVKISS EHINEGETAMLVCKSEFVPPVTDWAW YKITDSEDKALMNGSESRFFVNSSQGR SELHIENLNMEADPGQVRCNGTSSKGL RPRPLQFLRVRSHLAALWFLGIVGEVL VLVTIIFIYEKRRKPEDVLDLDDAGSAPL KSSGQHQNCKGKNVRQRNSS |
| 2428 | 10479 | A | 3349 | 870 | 997 | KWASNTYVISSNEESMIS*LSGRQ*NLRV WRLRKTWWLNWTL |
| 2429 | 10480 | A | 335 | 2 | 306 | |
| 2430 | 10481 | A | 3350 | 2 | 225 | GILKGLYYPLATNSFPATCWRL*VSPAHS KDPRNAATVHLSFFSPSGGPRYLLGHTT WQQGLGKRGRRTEQHS |
| 2431 | 10482 | A | 3351 | 1 | 336 | |
| 2432 | 10483 | A | 3352 | 1193 | 2524 | SKPPAASFAPRRPPATSRTLSAACAFRSR CRLAACSFVRPLPHTDTNMNGQLNGFH EAFIEEGTFLFTSESVEGHPDKICDQIS DAVLDAHLQDDPAKVACETVAKTGMI LLAGEITSRAAVDYQKVVRVAVKHIGYD DSSKGFYDKTCNVLVALEQQSPDIAQGV HLDRNEEDIGAGDQGLMFGYATDETEE CMPLTIVLAHKLNAKLAELRRNGTLPWL RPDSKTQVTVMQDRGAVLPIRVHTIV ISVQHDEEVCLDEMARDALKEKVIKAVVP AKYLDVTVIYHLQPSGRFVIGGPQGDAG LTGRKIIVDYGGWGAHGGGAFSGKDY TKVDRSAAYAARWVAKSLVKGGLCRR VLVQVSYAIGVSHPLSISIFHYGTSRKSE RELLEIVKKNFDLRPGVIVRDLDLKKPIY ORTAAYGHFGRDSFPWEVPPKCLKY |
| 2433 | 10484 | A | 3353 | 346 | 461 | |

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| 2434 | 10485 | A | 3354 | 3 | 1632 | MTEQLEPILMQAFIKSTAGLEARKLKAY RTMEYMAKSTDRSPGHILCCECGVPISP NPANICVACLRSKEDISQGIKQVVSISFCK QCORYFQPPGTWQCALESRGTFLLWCL EKNPKPLWSKVRLVDAGFVWTEPHFK RLKVKLTIQKEVMNGAILQQVFVVDYV VQSQMCGDGHSEKLLKDFWKAIVIQVR QKTLHKTFYYLEQLILKYGMHQNTRLRI KEIHDGLDFYSSKQHAQKMVEFLOCT VPCRYKASQRLISQDIHSNTYNYKSTFSV EIVPICKDNVCLSPKLAQSLGNMNQIC VCIRVTSAILHIDPNTLQVADIDGSTFW HPFNSLCHPKQLEEFIVMECSIVQDIKRA AGAGMISKKHTLGAEVWGTEGHLEMN RIKQYFCRTWLGTSCLNPGDRVLGFDL ANVCNLNDEHVNMNSDRVPDVVLIKKS YDRTRKQRRRNWKLKELARERENMDT DDERQYQDFLEDLEDEAIRKNVNIYRD SAIPVESDDEGAPRISLAEMLEDLHFS PGCPLVKEGASMLT |
| 2435 | 10486 | A | 3358 | 231 | 877 | PKPGGYSQCRRTSSRATERNRIDYVSSA VPYLTTPDLPRPEVVFVIGRNVGKSSL IKALFSLAPEVEVRVSKPGHTKKMNFF KVGKHFTVVDMPGYGFRAPEDFVDMVE TYLKERRNLKRTFLLVDSVVGQKTDNI AIEMCEEALPYVIVLTKIDKSSGHLK QVLHIQKFVNMTQGCFFQFPVSAVTF SGIHLRCFIASVTGSLD |
| 2436 | 10487 | A | 3359 | 3 | 234 | |
| 2437 | 10488 | A | 336 | 243 | 748 | PCQSFPQSGFGKDRPTSLEQRSQRERQA AIFAVSQPSLVIPPGTGKSEVNADRSP AYCSNLGRYSGPGPSLVIPPGTGKSEVN ADRSGPPAYCSNHFPALP**RSSMRSL LQQTSAWTCRHFHTSFEIQ/RGGSQILTL AFCAPAGPTPRGSHVLGLAPSEALT |
| 2438 | 10489 | A | 3360 | 25 | 546 | QSGDLGGRLSRSENCSSQVRVHRVGA VMAGVLKKTGVLVGLAVCNTPHERLR ILYTKILDLVEIPKINAAYRKYTEQITN EKLAMVKAEPDVKKVLEDQLAQGGQLAE VILAQAHEHNLAKKK*GEWKLWEPLIV EPPADQWKWANIIKLTLVVFMGKLD VIKIFCYI |
| 2439 | 10490 | A | 3361 | 2 | 367 | YAGFSLSAQKCPGAMAE*SYAKSTKLVL KGTKTKSKKKKSKEKKRKREDEETQF D/IVGTIAIEMDEGTIHALDNGLFTLGAP HKEGKMALLASNGCFIRCNEAGDIEAK SKTAGEEEMIT |
| 2440 | 10491 | A | 3362 | 268 | 393 | DGRRKEKWHKVERRHRPYLLSSLSQHR W*TVTNFGEISGTIAIEVDEGTIHALNN GLFTLGAPHK/ERIALKPGYGKYLINS ELVV/GRSDAIGPREQWEPVFQNGEVRN GGPAEMGEEKRNGTKWREDTDHTSFPL FPSTGGQPKAHSNWRKVCH |
| 2441 | 10492 | A | 3363 | 6 | 223 | TVTNFGEISGTIAIEMDEGTIHALDNGL FTLGAPHK/ERIALKSGYGKYLINSDEL VGHSDAIGPREQWEH |
| 2442 | 10493 | A | 3364 | 329 | 877 | RPWKQDRRAGDPWPRTHEFRSSEASLQ ASACKKKKSKEKKRKREDEETQFDMF GIW*TVTNFDEISGTIAIEMDEGTIHALD NGLFTLGSSTQRRIALKSGYGKYLINS ELVV/GRSDAIGPREQWEPVFQNGACAA VFTVIGSEKQSECSLLRESRAKYHGCTH GQISSSLKQHPRWY |

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| 2443 | 10494 | A | 3365 | 97 | 704 | AGFSLSAQKCPGAMAE*SYAKSTKLVLK GTKTKSKKKSKSEKKRREDEETQFD/ VGIW*TVTNFDEISGTIAIEMDEGTIHAL DDGLFTLGAPHKEGKMALLASNGCFIR CNEAGDIEAKSKTAGEEEMIKIRSCAERE TKKKDDFLEEDKGNVKQCEINYVKKFQ SFQEHKLKISKEDSKILKKAQKDGFLHET LLDR |
| 2444 | 10495 | A | 3366 | 24 | 981 | AIQRLGEDGGGFYRDVGCQGVFISRP FLRAPVLPRLTYSSRTGLSLSAQKLP MAEYSYVKSTKLVLKGTGKTKSKKKKSK DKKRKREDEETQLDIVGIWWTVTNFGE ISGTIAIEMDKGTIHALDNGLFTLGAP HKEISDEGSPPEQFTAIVKLSDSRIALKS GYGKYLGIIRDGLVVGGRSDAUGPREQW EPVFKMGKMALSTNSCFIRNHEAEDIE AKSKTAGEEEMIKIRSCAERETKKKDDIP EEDKGNVKNCEINYVKKFQSFQDHKLKI SKEDSKILKARKDGLHETLALDRRAK LEADRYCK |
| 2445 | 10496 | A | 3367 | 1 | 555 | PLKRSDDGNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPEEKSAVTALWGKVNVD EVGGKALGRLLVVPWTQRFESFGD LSTPDVAVMGNPKVKAHGGKVLGAFS GGPGCTWDNLKGTFAHTEVSLHCDKLH RGSLLKNFRLGNVLGLCLLAHSLGKEF QPHQLQAOLIKKIGWLGVG |
| 2446 | 10497 | A | 3368 | 1 | 390 | WEEIQELNEVARHRPRSTLVMGIQENR QIRELQENKELRTSLEEHQSALELIMSK YREQMFRLLMASKKDDPGHMKLKEQHS KELQAHVDQITEMAAVMRKPLKLTNR VARNKNEYFNLNKKTKA |
| 2447 | 10498 | A | 3369 | 769 | 912 | FPTPIPLFQELQAHVDQITEMAAVMRKIP LKLTNSNRVARNKNEYFNLK |
| 2448 | 10499 | A | 337 | 514 | 967 | APACCPAAVSPFLCEPTLIHPPHPPDLKE DTGQKHRGAQSHPTLAGAGLAGRSSKQ PSPSAISIWHSDDTSSCDRRQQCDRLPS ALLSPHLRCSQPATRQLESS*TPPGTADL FLASSGPNPRAFSNARSVRKCKATSEKS KPKSYQGS |
| 2449 | 10500 | A | 3370 | 1 | 463 | MKKNIAFLASMFVFSIATNAYADIQMT QSPSSLASVGDRTITCRSSQSLVHGIG NTYLHWYQQKPGKAPKLLIYKVSNRFS GVPSRFSGSGSGTDFLTISGLQPEDFAT YYCQHYSPLPYTFGQGTKEUKRTVAA PSVFIFPAHLMSS |
| 2450 | 10501 | A | 3371 | 2 | 166 | |
| 2451 | 10502 | A | 3372 | 39 | 1200 | FCGVAAMQLEIQVALNFIISYLYNKLPRR RVNIFGEELERLLKKKYEGHWYPEKPY KSGSFR/CIHIGEKVDPVIEQASKESGLDI DDVRGNLPQDLESFRIDPFVSYQIGEK GPVKVLYVDDNNENGCELDKEIKNSFN PEAIVFMPISDPASSVSSSPSPFGHSAV VSPTFMPRSTQPLTFTTATFAATKFGST KMKNSG/RGSSRFARTSPINLRGMWN DLLEGRKAISSMHSYGLGLGSSQQP QQQQQPAQPPPPPPPPQQQQQKTSALS PNAKEFIFPNMQGQGSSTNGMFP/GDSP LNLSPLOYSNADFVA/TYGLNEKSFV DGLNFSLNNMQYSNQFQPCYGLTKKK KMYRTKLKCTGPRGIFFFSPP |
| 2452 | 10503 | A | 3373 | 1 | 1197 | |
| 2453 | 10504 | A | 3374 | 66 | 632 | RRDPRTPANMALRVVRSVRALLCTLRA VPLPAAPCPPRPWQLGVGAVRTLRTGP ALLSVRKFTKEQESGNNQEKSMNQLGS GNFAQAEALGDVVYCSLPEVGTCLNKQ DEVGALESVKAASELYSPLASGEVTEINE ALAEENPGTCKTNFCYEDGWLIKMTLSN PSELDELMSSEAYEKYKISIE |

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| 2454 | 10505 | A | 3375 | 162 | 552 | VASEHSPKIGASQGLDYEPLLVVAKVWY LTRPTGTGKAGSVFSQYLPFLEPGILGPAS LPWLRQTLTGKEIEIDIEPTDKVERIKER VEEKEGIPPPQQORLHLQVAKQMNDEK TASWITKILRWVQSFT |
| 2455 | 10506 | A | 3376 | 77 | 427 | GRDKEGEYPPAPSSGWGKSVGIMLTELE KALNSIIDVYHKYSLIKGNFHAVYRDDDL KKLLETECPQYIRKKGADVWFKELDINT DGAVNFQEFLLVIKMGWQPTKKAMKK ATKSS |
| 2456 | 10507 | A | 3377 | 1 | 143 | |
| 2457 | 10508 | A | 3378 | 200 | 899 | GKSTGPVCVHMSLCEWTLSLATRVSLSS HPSHQSHSHLLVWLFGESRPGQGLRLGH ESSAYCPGQMQUIPCHGIPQKVLFFRWGK SVGIMLTELEKALNSIIDVYHKYSLIKGN FHAVYRDDDLKKLLETECPQYIRVRRGLG WRGLSAWSWGCPGPAVLPAHLRWLCL GSL*DL*TLASSSILT*KKGADVWFKE DINTDGAVNFQEFLLVIKMGWQPTKKA MKKATKSS |
| 2458 | 10509 | A | 3379 | 99 | 497 | RESGGKRLNIYHQTIVYHKYSLIKGNFVH AVYRDDDLKKLLETECPQYIRKKGADV WFKELDINTDGAVNFQEFLLVIKMGW QPTKKAMKESHKGVSLSLGPKGWAL GGHVTCRIKVINTEKSKKKKVDAA |
| 2459 | 10510 | B | 338 | 1 | 456 | MKLRTLAVSATALKVARLEFVFPDVRM CSEFLSSGVKLQTFVAVSVTALNRLLEF VPPGGLMVSLASGVKLQIFTVSVTAHKS SVDPKTLGWSMGLGAVEQGAALIGEAW AAQEPMEGVGGSGMAGCRSRALPRGKA AKARREIERSAGH* |
| 2460 | 10511 | A | 3380 | 1 | 282 | PLKRSDGCGNDGRPTRPPTRPDTTFTSNL KQTRMVHLNTPEEKSAVTALWGKVNVD EVGGKALGRLLVVLPLGPPKGLKSFG GICPNSLNAG |
| 2461 | 10512 | A | 3381 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLLDLKGT AQLSELHCDKLHVDPENFKLLGNVLTV LAHFGKEFTPEVQASWQKMVTGVASA LSSRYH |
| 2462 | 10513 | A | 3382 | 3 | 549 | FCPRGQEFEGGNKLLVPDAMGHFTEED KATITSLWGKVNVEDAGGETLGRLL VVYPWTQRFFDSFGNLSSASAIMGNP KVKAHGKKVLTFLGRCCQSTLDDLKGH LLPKPEVNCTVDKPAWDPENFKAPGE MLLVTRFGQSHFRQKNSPPGGCKASWA ERWVTGVASALVPSRYH |
| 2463 | 10514 | A | 3383 | 347 | 716 | REPCVSRSTCCPLPWMEPRAMCPPVGA MRGSRDPASSSLSPDHLAQLQPGAGFL FCSAPALSGFPPRPPQGHLAGSWL/ CPPVQAQPAPALCGRRGVAVWGIAW EDSGKSVGEVAS |
| 2464 | 10515 | A | 3384 | 1 | 1362 | |
| 2465 | 10516 | A | 3385 | 284 | 540 | KLFQKKNKKSSCISDNFFLLAIMVNLLQ IVRDHWVHVLVPMGFVIGCYLDRKSD ERLTAFRNKSMFLKSFPHRELQPSEVT WK |
| 2466 | 10517 | A | 3386 | 194 | 353 | |
| 2467 | 10518 | A | 3387 | 57 | 880 | DPHSVSSTGGPLPIWFWPLSSGPGAVAA DPAPQSGPTVDAGVPIPHIRARDSARLP LCPWHASALELGIATPGTVTTQAPGSYP AWRSRCLLPQSPVLLASLGVGLVTLG LAVGSYLVRRSRFPQVTLDPSEKYLRL LLDKTVSWGRKGQEGGDQSAPGM*GT APTUVGMSKGRGSARRAW*NTCVLHPP TVSHNTRKRFALPTAHTLGLPVGKES VEWAPFGYPQKVTPLLGSHETRCFNRF APHTISPSPTWLCILQAVRCHWA |

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| 2468 | 10519 | A | 3388 | 430 | 483 | NQPCLTLPTRKSECTDTVISWSLSFGFLF TRWVTGMAVLLRLSLRQAEYTHSQQLL PLDT*RLGNVVKFRGPSGLLSYTGKGFH NIQPNKKSPPPEPRVAKKLGMIAGGTGITP MLQLIRAILKVPEDPTQCFLLFATQTEKD IILREDLEELQARYPNRFLWFTLDHPPK GILPISGHPTIPSSSKSKPCPFVNSGFIEINL ASHCQLGSLSAQTQ |
| 2469 | 10520 | A | 3389 | 3 | 1007 | HACAHASAHASGRLVVRWGRKRRSVMGI QTSPVLLASLGVGLVTLLGLAAGSYLVR RSRRPQVTLDPNEKYLLRLLNKTTVSH NTRFRFALPTAHHTLGLPVGKHLYLST RIDGRVRVKPYTPVTSDEDQGYVDLVIK VYLKGVQPKFSEGKMSQYLDLKVVG DVIVEFRGPSGLLYTGTGKGFHNIQPNKK SPPEPRVAKKLGMIAGGTGITPMLQLIR AILKVPEDPTQCFLLFANQTEKDIFAGG LKRNLQARYPNRFLWFTLDHPPKDW YSKGFVTADMIREHLPAPGDDVLVLLCG PPPMVQLACHVNLGQTGVT SQKMAISP Y |
| 2470 | 10521 | A | 339 | 1 | 1519 | MAPELSSKEQPGSEWKKACQMEGTVCA KAQRDLLDGFQDQADDDMDNEIQAE VSDGDEELVGNWSKEPTTLGAATMGLG TEKQLGMGWAGRKGPIEDLEPLQAAC KLHAVAHTTWEEAVQCGSLPRRNSNLL LEQGVLEETRNLQEHGGEIDLEKKRWL GTVAHTCNASTLGGRGVKLQFTVTSITA PKAARLELFVPPGGLVLLASGVKLQIF AVSVTAHKSSVDPKTLGWSMGLGAVEQ EVVLVGEAPAAQEPMEWVGSGMGAA GPGALPRGKAAKARREIEHSAGLYKLLP HSEYSRPNRVFNSQGSNPVRVSFVNLN DQSGNGDRLCFNVGRELYFYIYKGVK TIP*GICRTEILISVLTEAADLSKPIDKRIY KGTQPTCHDFNHLTATAESVLLVGFSA GQVQLIDPIKKETSKLFNEEAFEGRYATF FTI/WYECSHGKLHISSALGLVFFGGDISY SLSSQPAPLEGASRDSGSRGHELWSESSR KRNNKRH |
| 2471 | 10522 | A | 3390 | 2568 | 2781 | RSPGRPPHPPNAPV/RRPASCHS/AAESQ HGGWKKSISASRKLQKTLTLLQIAKQE/ LEREAEEERRGEKGRAL |
| 2472 | 10523 | A | 3391 | 2 | 409 | |
| 2473 | 10524 | A | 3392 | 3 | 490 | SSPEETVGPWDPEGHPGGPLTDPPNAPV LALPPAIPGLSLIMADGSSDAVRAAG*GV AGTPRARAREPRPAPAPIRRRSSNYRAY ATEPHAKKKSISASRKLQKTLTLLQIAK QELEREAEEERRGEKGRALSTRCQPLELA GLGFAELQDLCRQLHARVDK |
| 2474 | 10525 | A | 3393 | 2023 | 2613 | |
| 2475 | 10526 | A | 3394 | 150 | 848 | VSAWRNGSSDAAREPRPAPAPIRRRSSN YRAYATEPHAKKKSISASRKLQKTLTLL QIAKQELEREAEEERRGREGARSLAPRC QPLELAGLGFADLPGLCCROFHARVD KVDEERYDIEAKVSKNITEIANLTQKIF DLRSKFKRPTLRRVRISADAMMALLG ARAKESLDLRAHLKQVKEDPEKENRE VGDWRKNIDALSGMEGRMKKWRELSLP AYCPCPEEGH |
| 2476 | 10527 | A | 3395 | 1 | 2880 | |

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| 2477 | 10528 | B | 3396 | 61 | 5070 | MGPTSGPSLLLLLTHLPLALGSPMYSIT PNILRLESEETMVLEAHDAGDVPVTVT VHDFPGKKLVLSSEKTVLTPATNHMGN VTFTIPANREFKSEKGRNKFVTVQATFG TQVVEKVVLVLSQSGYLFQTDKTIYTPG STVLYRIFTVNHKLLPVGRTVMVNIENPE GIPVKQDSLSSQNQLGVLPLSWDIPELVN MGQWKIRAYYENSPOQVFSTEFVKEY VLPSFEVIVEPEKFFYYINEKGLEVTI |
| 2478 | 10529 | A | 3397 | 3 | 560 | EGKGQGTLSVVTMYHAKAKDQLTCKNF DLCLPGSRQKYEVLGPCLQPGTFLWSR NRRVLGFPSMNGEDMGLFLCSEWERS EGWLCNREGSGHSEPHCCTFLHLTHR SLAFSLLAGVSCTCASSCKCKEACKCTSC KKSECGAISRNGLWLKVGREP KAVPEV RASGEPAFLCPCRLSLPV |
| 2479 | 10530 | A | 3398 | 3 | 1584 | SNQPLRREAFPETPKGLRQGIPGEPENG RSHFFSFDVTAVMILYKESQALTGNLPG PQLPRRLAAGRGHPSVPAPSRRGALS RFPASGRSAVPTIGWLCRSHYPHSIRGAN GWDRELVRASHTMSATAQTNHRAEK AGRELSQANNDRTGRLAHPAPPSQARQ VPRLEHLASPRCRWPAVISRPFWSHCIL EIRFRKGKLGGRASPENEGAGEIRVKVP KDRDWLTAKLQGDLLTVSQTAKLEDMV LQTAKSTQDFLTPTARSYSPTTKLKGV NTKSPILLTPTARGHYLLGAPIASWRC HTSTIRYHTVVVMSMTLSEHQAGSVD MSANDYAHYSGASGDNEMCVVIACPTP LFLSPRAWKPCDAGSKVKNWGIENGNL VHTVLSSTQHGDPHEVHAPFGMEAEYA HPLETLILGTGFFIGIVLLCDHVILLWAW VTIRLLETIDVHSGYDIPLNPLNIPFYAG SRHHDFFHMMNFIGWYGFQHFTRWDW NFLGTDSDQYNAYNEKRKKFEKTE |
| 2480 | 10531 | A | 3399 | 2 | 873 | GRVGEMSQGRKYDFYIGLGLAMSSSIF IGGSFILKKGLRLARKGSMRAGQGGH AYLKEWLWRAGLLSMGAGEVANFAAY AVAPATLVTPLGALSVLVRALLSSYFLNE RLNLHGKIGCLLSILGSVMVIHAPKEEEI ETLNEMSHKLGDPGFVVFATLVVIVALIL IFVVGPRHQTNILVYITICSVIGAFSVSC VKGLGIAIKELFAGKPVLAGIPWAWILL LIVCVSTQINYLNRAPWDIFNTSIVTIYY VFFTTSVLTCSAILFKGVGKDMPVGRCP LVL |
| 2481 | 10532 | A | 34 | 2583 | 3580 | DRVSLLLPRLECNGAILAHCNLCLSGSSD SPASASQVTGITGKCHHTQLIFVFLVEMG FHHIAQAGLELLTSDSPTLASQAGITGV NHHAWLFFFCR/RTVSLCYPGWSRVA* SRITATSA/PGLK*FACFSLPSSRDYRHVP PHPGNFCIFGRDEVSPCWPGWF*TPDLR/ YPPASASQSAEIIIGVSHHTWPQEVFLFN LFIYLRWSL/DSVAQARVQRRDLGSLQA PPPRFKPFSCLSLPSSWDYRRPPHPANFF VFLVETGFATVLARRVLIS*PRDLPASASQ SAGITGVSHHTR/LIF/NFFETGTHSVTWA AVQWYTI/GSLQPRTPELK*SSHLILTSN WDYRCTPPCPPNLFIYLFYFHRDEGSLC CPGWS*TPELK |
| 2482 | 10533 | A | 340 | 759 | 1034 | |
| 2483 | 10534 | A | 3400 | 90 | 458 | HFSRGYLEAFSEISNIRFVPPHSVTVVVV FGACFLCILGIWPWACLPGPGGEGSGGF GEGRGSEAGRLGSVELTPATLPLQAPEA YPVFEPVPPVPEAAQGDTEDEGAPPLK RICPNAPDP |

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| 2484 | 10535 | A | 3401 | 3 | 787 | PGSTISWRPGLARSLSPDGRRPRRGLGP GPSPASMAGRTVRAETRSRAKDDIKKV MATIEKVRRWEKRWVTVAATPFRLNW VAIVVDPQEEERRRAGGGAERSRGRER RGRGASPDGGG/PLFILLDLNDENSQR FPLRKGSQLRGTEVSPGGTPKPNRQCVT LPDPPEGGPCTRAQPPT/RLGQEERSPGGI TVAGSTDEPP/MLTKEEPVPELEAEPEA VPVFEPVPPVPEAAQGDTEDFGSAPPLK RICPNAPDP |
| 2485 | 10536 | A | 3402 | 1 | 172 | |
| 2486 | 10537 | B | 3403 | 1 | 5501 | MVSKLSQLQTELLAALLESGLSKEALIQ ALGEPGPYLLAGEGPLDKGESCGGGRGE LAELPNGLGETRGSEDETDGDEDFTPI LKELENLSPEEAAHQKAVVETLLQEDPW RVAKMVKSYLQQHNIPQREVVDTTGLN QSHLSQHLNKGTPMKTQKRAALYTWYV RKQREVAQQFTHAGQGGLIEPTGDELP TKKGRRNRFKWGPASQQILFQAYERQK NPSKEEREAAQGLGSLNLTVEVRVYNWFA NRRKEEAFRHKLAMDTYSGPPPGPGGP ALPAHSSPGLPPPALSPSKVHGVRYGQP ATSETAEVPSSSGGPLVTVSTPLHQVSPT GLEPSHSLSTEAKLVSAAGGPLPPVSTL TALHSLEQTSPGLNQPPQNLIMASLPV MTIGPGEPASLGPTFTNTGASTLVIGLAS TQAQSVPVINSMGSSLTTLQPVQFSQPLH PSYQQPLMPPVQSHVTQNPFMATMAQL QSPHALYSHKPEVAQYTHGTGLLPQTMLI TDTTNLSALASLTPTKQVFTSDTEASSES GLHTPASQATTLHVPSQDPAGIQHLQPA HRLSASPTVSSSLVLYQSSDSSNGQSHL LPSNHSVIETFIQMASSSQ* |
| 2487 | 10538 | A | 3404 | 158 | 755 | RGGRPAWPCGSRAMVSKLSQLQTELLA ALLESGLSKEALIQALGEPGPYLLAGEGP LDKGESCGGRGELAELPNGLGETRGSE DETDGDEDFTPIILKELENLSPEEAAHQ KAVVETLLQEDPW RVAKMVKSYLQQH NIPQREVVDTTGLNQSHLSQH/HQQGHS HEDAEAGRPVHLVRPQAARGGAHVHPC RAGRAD |
| 2488 | 10539 | B | 3405 | 133 | 2369 | MVSKLSQLQTELLAALLESGLSKEALIQ ALGEPGPYLLAGEGPLDKGESCGGGRGE LAELPNGLGETRGSEDETDGDEDFTPI LKELENLSPEEAAHQKAVVETLLQEDPW RVAKMVKSYLQQHNIPQREVVDTTGLN QSHLSQHLNKGTPMKTQKRAALYTWYV RKQREVAQQFTHAGQGGLIEPTGDELP TKKGRRNRFKWGPASQQILFQAYERQK NPSKEERETLVEECNRAECIORGVSPSQA QGLGSLNLTVEVRVYNWFANRRKEEAFR HKLAMDTKVHGVRYGQPATSETAEVPS SSGGPLVTVSTPLHQVSPTGLEPSHSLLS TEAKLVSAAGGPLPPVSTLTALHSLEQTS PGLNQPPQNLIMASLPVMTIGPGEPAS LGPTFTNTGASTLVIVPTLDQSLCYISDT WVNQTDQNLSSSREAGTKHNTSILWY LRRPGLHAGTECAGHQHQHQQPDHLQP VQFSQPLHPSYQQPLMPPVQSHVTQSPF MATMAQLQSPHX* |

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| 2489 | 10540 | A | 3406 | 1 | 2112 | MMLKGKAHCSILDFGLDQCSTNSAAE FIRSWEDPWVAKMVKSYLQQHNPQR EVVDTTGLNQSHLSQHLNKGTPMKSQK RAALYTWYVRKQREVAQPHIPYPIPENS TGTEWLIETWLDPTHAKNDQEHRTDSP VNYGKKKGKENKNLKPPEVYVSLIKA CGGPGNFCPSFSELQRNFVKHRPTKLKS LLRLVKHWYQQWLQPHREWKEEVLDA VRTVEEFLRQEHFQGGKRGDLQDVRVLK VVKVGSFGNGTVLRSTREVELVAFLSF HSFQEAAKHHKDVRLIWKTMWQSQD LLDLGLEDLRMEQRPDALVFTIQTGRGT AEPITVTIVPAYRALGPSLPNSQPPPEVY VSLIKACGGPGNFCPSFSELQRNFVKHRP TKLKSLRLVKHWYQQYVKARSPRANL PPLYALELLTIYAWEMGTEEDENFMLDE GFTTVMDDLLEYEVICIYWTYYTLHNA IIEDCVRKQLKKERPIILDPADPTLNVAEG YRWDIVAQRASQCLKQDCCYDNRENPI SWNVKRARDIHLTVEQRGYPDFNLIVN PYEPIRKVKEKIRRTRGYSGLQRLSFQVP GSEKQLSSRICSLAKYGIFSHTHIYLET IPSEIQVFVKNPDDGGSYAYANPNNSFIL GLKQQIEDHQGLPKKIQQQLFQGGQVL QGLVGWGFYGIQDSDTLNLSVKKKGE ALFPAS |
| 2490 | 10541 | A | 3407 | 108 | 442 | ALLSWEMSAACWEEPWGLPGGFAKRVL VTGGAGFIR*WRR*PSSGSPETPTFSRSS ACPSASHMIVSLVEDYPNYMIINLDKLD YCASLKNLETISNKQNYKFIQGDICDS |
| 2491 | 10542 | A | 3408 | 115 | 1196 | ALLSWEMSAACWEEPWGLPGGFAKRV LVTGGAGFUSASHMIVSLVEDYPNYMII NLDKLDYCASLKNLETISNKQNYKFIQ DICDSHFVKLALFETEKIDIVLHFAAQTHV DLSFRTCPWSFTHVNV/YMGTHVLVSAA HEARVEKFIYVSTDEVYGGSLDKEFDES SPKQPTNPYASSKAAAEACFVQSYWEQY KEPVVITRSSNVYGPYQYPEKVIKFI QHNRKCCIHGSLQTRNFLYATDVVEAF LTVLKKGKPGIYNIGTNFEMSVVQLAK ELIQLIKETNSESEMENWVDYVNDRPTN DMRYPMKSEKIHGLRWRPKVPWKEGK KTIEWYRENHFNWKNVEKALEPPV |
| 2492 | 10543 | A | 3409 | 359 | 532 | IVMCHCLELVIGEPCHICGSVCVCVYA AVCVLCVCVHTCICFGACV/CVCVCRRV CPVCLCTYLYLLWGLCVVCYQRVNFWK |
| 2493 | 10544 | A | 341 | 587 | 1097 | QKIINKVVPITGRQCCFVRLSPLESKFQS KEEIRNTSHRANVTKRNSANRKTDAILA TPGPPPAQPHGA/PGGYAPRLPQHPAPGC FPKCGNPAPRPWYGPFGPPLRKEQKRN PRKGTG*MQGVSPVPFPPT*NAGPLPGGS LGPPISGHHLVSHTWPPPPRSPTAPP |
| 2494 | 10545 | A | 3410 | 27 | 1389 | GQPRSQQAGSWGKRRQESYRAREGDG GSGSLTGLLRTAAGWLLPARASPRERAT RHPVRSPPQRRARRSLQRGPERPRDPPQ TAWAARMCTKMEQPFYHDDSYTATGY GRAPGGLSLHDYKLLKPSLAVNLADPYR SLKAPGARGPGPEGGGGSYFSCQGS TGPSLKLASSELEVRILVPSNKTANTTPT PPIGQYFYPRGGSGGGAGGAWGGVTE EQEGFADGFVKALDDLHKMNHVTPPNV SLGATGGPPHGP/GIRASPEPPPVYTN LSSYSPASASSGGAGAAGVTGSSYPTTTI SYLPHAPPFAGGHPAQLGLGRGASTFKE EPQTVPEARSRDATPPVSPINMERPRAPS KLEPSGLRNRLAGHQSAKGRKLRKFAR LEDKVVKTLKAENAGPVEVPPGLPPGSR LAQAQTRKVIDPRVSNGLSLLFGVVRGH AFLNVPCPL |

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| 2495 | 10546 | A | 3411 | 1 | 3589 | IRRPLDQRGGIPLRKKPLEDLVCKLADISI NYVNERKSEQHLRFLSTLLDSFSSSRVFK MLLGDEKQSIVQAKPLEIAKLQKNPAV QFLYQKLIGWLNEDQQRKDFGLVDILYS ALRCCDNDMERKKVLDLTKVDLKWN SLLKIIKACPSSDKHALVTPWLKGDILG EKLVLNADCLCNEDLESRVSSSESHFSE WTLISLVLSQHVKN DY LIGDVYVERIIV RLHETLFTKTKLSEAESSDSSVSFICDV |
| 2496 | 10547 | A | 3412 | 112 | 828 | PVFKTPLPSHRRRAHAAALDLGASSSDP HADSGTGNWAEVDPGSAQHLPRPSSQLP HFLLSGGGPGQCRRGQRGELLPSGGTA TPCAPRGLGWGLRSCALRAAAAPTAPQ TLRRRAPRPARPRAGPGLAPQPSISDFL GQAACASGTMLRWLRDFVLPTAACQDA EQPTRYETLFQALDRNGDGVVDIGELQE GLRNLGIPLGQDAEEVGRRRGAA*AGG LRALGTLRGPRRAA |
| 2497 | 10548 | A | 3413 | 1 | 1413 | RDARRYSGTTPHPSISRDLGQAVCASG TMLRWLRDFVLPTAACQDAEQPTRYET LFQALDRNGDGVVDIGELQGLKNLGI LGQDAEEKIFTTGDVNKDKLDFEEMK HLKDHEKKMKLAFKSLDKNNDGKIEAS EIVQPLQTLGLTISEQQAELILQSIDVGT MTVDWNEWRDYFLFNPVTDIEIIRFWK HSTGIDIGDSLTPDEFTEDEKKSQWWR QLLAGGIAGAVSRTSTAPLDRKIMMQV HGSKSDKMNIFFGFRQMVKEGGIRSLW RGNGTNNVIKAPETA VKFWAYEQVMKT RLAVGKTGQYSGIYDCAKILKHEGLGA FYKGYVPNLLGIIPYAGIDLAVYELLSY WLDNFAKDSVNP GVMVLLGCGALSSTC GQLASYPLALVRTRMQAAMLEGSPQL NMVGLFRRIISKEGIPGLYRGITPNFMKG LPAVGISYVVYENMKQTLGVTVQK |
| 2498 | 10549 | A | 3414 | 1 | 222 | |
| 2499 | 10550 | A | 3415 | 2 | 528 | SRVDPRVRHSARLTMCHSRISCHPTMTIL QAPTPAPSTIPGPRRGSGPEIFTFDPLPEP AADPAGRPSASRGHRKRSRRLVYPRVV RRQLPVEEPNPAKRLLFLLLTIVFCQIL MAEEGVPAPLPPEDAPNAASLAAPTIVS PVLEPFNLTSPLDYASWNLSTFLQQHP AAF |
| 2500 | 10551 | A | 3416 | 1623 | 2346 | TFPSGAKPPLAASHHHRHLRDASRLWRG RSGGPSVTRRPTFLPSYPPAPAHAPASAP GPSDSDCSPPFRRRSPTRTDCFVCRPVC PFPFIVPPGRAPSRMAEVL L L L L L L LPSA AAKIQGYPCPGPQLSRDILSSGDGWWA GLSGHHRVCGGPGVQEPQTTVVHNATD GIKYIHHRLIHLTPADYDDFVNAIRSARS AFCLTPMGMMQFNDILQNLKRSKQTKE LWQRV SLEMATFSP |
| 2501 | 10552 | A | 3417 | 256 | 657 | KGLSLSKKAGENHYFYLPHSFPEKAPPG AIGHLSPRGTIEEALDLSARIVAEFIVLP ASHHPRHLRDASRLWRGRSGGPSVTRRP TFLPSYPPAPAHAPASAPGPSDSDCSPF RRRSPTRLARMRGLLG |
| 2502 | 10553 | A | 3418 | 294 | 573 | SHLLGLHEPSRHNRA SPGLFCTHRRGIH SASSKPSSPTSP*CKSPRSPGAAPRRG*L E*AGLLGFSTGFRGFPNRRRPRRLGVAI AHQAP |
| 2503 | 10554 | A | 3419 | 1 | 931 | |

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| 2504 | 10555 | A | 342 | 462 | 1238 | SFYETKLLISGSETLDSKDQYRINKYNH YFQTLHYTHLKFSSGLSSATQ*KLSWSK GNG*GERPVSPPLMAPSGQLLAHVWS EVKSVSSCFLSCQQGHVLTSPGSSFPQCQ PAQCYLIPCSSEKYTNW/PGIPIPSLGIQ SS/SSPGS*SGPISSSKYSGDAQVCFSSPNL FPSFRPVTGCIQSPPNISPGAEGKGCGLQPI PVHSFLTSTFSPVSP*RSRSTHPETHS MSHSSQSSPQAPSALPPSISLPLSP |
| 2505 | 10556 | A | 3420 | 640 | 757 | |
| 2506 | 10557 | A | 3421 | 865 | 1314 | TPLPSTTPPKQPNRGPSPGAESLETEEEE EEEKGSERPPPPRRSRSLRPPWRWRGD PVGQIETGPPKLRPWDGAEAGVAIGH AAAFPH/ITEGPRLVPLGGVRLTPSPVTL LRTGAGLLHYERLWNLVGPCLHPRQ DHTLGLGSWG |
| 2507 | 10558 | A | 3422 | 2 | 310 | ARDVHPLPLPFLGNSLALGMQMRPQL LLSRCRLPATCASSCKCKECKCTS/TAR KKSCCSLNPCLVPKCAPRACICKRGHR RSASLLRLMTGTALLPTYK |
| 2508 | 10559 | A | 3423 | 41 | 317 | LLKFFFETGSHSFIQVGVQWCDHDSLD LPGSGDPSS/AS/RVAGTAGMHDHTWLIF VFLVRRWSLTVLLRLVFNSWAKVILHL GLPKGWGLQV |
| 2509 | 10560 | A | 3429 | 781 | 949 | LLCLGLAYRRHFEMSLWLGMAHVHCNP SAWGGRRGGQIT/R/QEFETSLVNMVKT CLY |
| 2510 | 10561 | A | 343 | 2 | 384 | |
| 2511 | 10562 | A | 3430 | 3 | 1029 | RAFRDDTMAGGGCRAGPGATCSGDGA GSDQRQNEEIEAMAAIYGEEWCVIDDCA KIFCIRISDDDDPTWTLCLHVMPLNEY CTAPPIYQLNAPWLKGQERADLSNSLEEI YIQNIAESILYLWVEKIRDVLIQKSQMT PGPDVKKKTEEDVECEDDLILACQPESS LKALDFÆVSEARTEVEVEELPIDHGIPIT DRRSTFQAHLPVVCVKQVKMGLSKLY ENKKIASATHNIYAYRIYCEDKQTFLOD CEDDGETVAGGRLLHLMEILSVKDVGMG VRARWYVGMGLGPDPRFKHINNCVRNIL VEKNYTSSLEESSKALGKNKKVRKDKK RNEH |
| 2512 | 10563 | C | 3431 | 153 | 224 | MVAHACNPSTLGDRGGRFTRSGD* |
| 2513 | 10564 | C | 3432 | 20 | 58 | MTQLTKRKETIL* |
| 2514 | 10565 | A | 3433 | 837 | 1125 | LDVTTSKNQFVLRTWLKIPGNCYRRHFF FFETESCSVAQAGVQWHNLSSLQAPPPG SRHSPTSASQAAGTYRYPAHHAWPNFV FVFLVETGFHPC |
| 2515 | 10566 | A | 3438 | 56 | 290 | |
| 2516 | 10567 | A | 3439 | 468 | 993 | VLLACFWPGSDFWPSRRKTYGTAPQSC YSFYVALDCGGVSRLVIFVSWRNPQVAP TSAHQNRPSRNPVSRPPNTQVARRKHY ALADGYTERRWTNAPCRAESSFPNCPS AAPIPDSYDK*PSRATLFTSHLTVEAFPV WSYLYPGETPRLHPRAHTRTVPAAIRYP DRQTPNGLRGANTMHSQMDTLNGDGR THLAGQRARSPTARPQRQYRIHTSDL PGLVRKYASGCCLRIWYCCAWIERALSL QVGGGVFGDPLSEGQAECDHGST |
| 2517 | 10568 | A | 344 | 2 | 624 | SDSRASCKMLLILLSVALLALSSAQNLINE DVSQEEPSLIAGNPQGSPQGGNKPQGP PPPPGKPQGGPPQGGNKPQGGPPGKQGP PPPGQDKSRSPRSPGKQGGPPQGG*LQ GPPPRGGIKPQGGPPGKQGGPPAQGGSK SQSARAPPKQGGPPQEGNPPQGGPPP AGGNPQQPQAPPAGQPQGGPPRPPQGGP SRPPQ |
| 2518 | 10569 | A | 3440 | 1 | 3114 | |

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| 2519 | 10570 | A | 3441 | 3 | 401 | TSSL SLSGKSGRYIVFLRRSVGIQSPSAVA TVRLLLAGSDRRFAAGSAGCAVLSRAER S*EPGCCYRIRRSARLRAGSIGNRDKPV AWPDTGSGDNTEVYFRAHQAGILPDTVL AGPAQRVAVSGGTPVDW |
| 2520 | 10571 | A | 3442 | 2874 | 3062 | |
| 2521 | 10572 | A | 3443 | 2766 | 3323 | MPDLVEGREKSDKGAQPQRTQSRSA NGSGVRILHSLWRIIGIPLLGYSLVCSR VLLACFWPGSDFWPRSRRKTYGTAPQSCY SFYVALDCGGVSRLVIFVSWRNPQVAPT SAHQNRPSRNPVSRPNTQVRARKHYA LADGYTERRWTDAPCRAESSFPNCPL* RQYRIHIVDASVCGP |
| 2522 | 10573 | A | 3444 | 968 | 1440 | |
| 2523 | 10574 | A | 3445 | 3 | 640 | LSVVRSRIHMGVGVGVGCPVRYRNQDD HELQITHGNKILCGIVCDKGAQPQRTQS RSARTNGSGVRILHSLWRIIGIPLLGYS VCSRVLACFWPGSDFWPRSRRKTYGT VPQSCYSFYVALDCGGVSRLVIFVSWRN PQVAPSAHQNRPRNPVSRPNTQORVA RRKHYAPADGYTERRWTIAPCRAESSFP PNCPSAAPIPDSYDK |
| 2524 | 10575 | A | 3446 | 1 | 3140 | MVYKMRYSRQHPYSIKEKQMKSEVLSV KEKIGYGMGDAASHIIFDNVMLYMMFF YTDIFGIPAGFVGTMLVARALDAISDPC MGLLADRTRSRWGKFRPWVLFALPFG IVCVLAYSTPDL SMNGKMIYAITYLLT LLYTVVNIPYCALGGVITNDPTQRIQS LQSWRFVLATAGGMLSTVLMPLVNLIGGD NKPLGFQGDLSPMFSTPEEIARPGPYEND VHVVGASSLAAGHKTILPELVRSAEQHM GTR |
| 2525 | 10576 | A | 3447 | 750 | 1340 | ILHAPAPFASASHEQPEWSDKGAQPQ RTQSRSAARTNGSGVRILHSLWRIIGIP LLGYSLVCSRVLACFWPGSDFWPRSRRK TYGTAPQSCYSFYVALDCGGVSRLVIFV SWRNPQVAPSAHQNRPSRNPVSRPNTQ RVARRKHYALADGYTERRWTNAPCRAE SSFPNCPFAAPIPDSYDK*PFRIVS |
| 2526 | 10577 | A | 3448 | 93 | 699 | RASVQOKKLSTDDKGAQPQRTQSRSA RTNGSGVRILHSLWRIIGIPLLGYSLVCS RVLLACFWPGSDFWPRSRRKTYGTAPQS CYSFYVALDCGGVSRLSYLYPGETPRV APSAHQNRPSRKPGTRPPNTQVARR KHYALADGYTERISATNAPCRAESSFPPE LPVPQVPNTGFIRQVTFRDCFVNTPQAA ASGFW |
| 2527 | 10578 | A | 3449 | 1000 | 1530 | QRYSDNPPNDKGAQPQRTQSRSA RTNGSGVRILHSLWRIIGIPLLGYSLVCSR VLLACFWPGSDFWPRSRRKTYGTAPQSCY SFYVALDCGGVSRLVIFVSWRNPQVAPSA HQNRPSRNPVSRPNTQVARRKHYAL ADGYTERRWTNAPCRA/VEFPNCPWE AQYRIIRK |
| 2528 | 10579 | A | 345 | 85 | 194 | |
| 2529 | 10580 | A | 3450 | 106 | 375 | |
| 2530 | 10581 | A | 3451 | 232 | 376 | KKGVLSCVRRHSMET*NEKPALLKMSGI KIPSPVHHFVFHKQSEKGA |
| 2531 | 10582 | A | 3452 | 481 | 781 | IKDKKVSNSQLCGYLVAMTDVETTYA DFIASGRTGRRNAIHDLVSSAGNSNEL ALKLAGLDINKTEGEEDAQRSSTEQSG EAQGEAAKSESLTPHF |
| 2532 | 10583 | A | 3453 | 15 | 369 | RVGEYDGYEAGPAPCPPRASLCQ/PGPD QGPSPCTQAIPAPRKPHPCWPQGPKKL GELPGLCLQGSPTAGHPCCPPQETGAQG GAPASPWFQNNAAACGLICFCPPQPRIFL CINSNS |

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| 2533 | 10584 | A | 3454 | 201 | 711 | KKMARTKQTARKSTGGKAPRQTAG/LA TKAARKSAPSTGGVKKPHRYRPGTVAL REIRRYQKSTELLNRKLPFQRLVREIAA GFSKTALRFQ SARIRCACRLAKRYLVG LFEDNNLCVAIHAKRVTIHAPKTIQLARR DTGEKRALSEGSFYGVLLVKFLLKYFGLI C |
| 2534 | 10585 | A | 3455 | 758 | 1188 | GKLSGRGTGSLLRGDALPRLQKTGCPKA GGNRPPAVSQSRGGAVRDEGLLAAQTA EGGPRVEEARPPQLPQARGSLPETPPPPA PDAITPPPPSGSHISPSSAEGPSRPPVGVAV DSGGAPQPQDPGPAPAPALLRHRHQTP RP |
| 2535 | 10586 | A | 3456 | 2 | 297 | |
| 2536 | 10587 | A | 3457 | 1 | 1128 | |
| 2537 | 10588 | B | 3458 | 58 | 1282 | MRTLLKNTVIVLLPYKSGSKLYGESSTE LNVEVLNCTASQFKCASGDKCIGVTNRC DGVFDCSDNSDEAGCPTRPFGMCHSDEF QCQEDGICIPNFWECGDHPDCLYGSDEH NACVPKTCPSYFHCNDNGNCIHRWL DRDNDCGDMSDEKDCPTQPFRCPSWQW QCLGHNICVNLSVVCDFGIFDCPNGQMSP HFALVAAAVDWLSQDSKWLQDSHIVPD VKLCVVASAYRQSYQSLGNDISLGYRCQ PKFSRSIDPTGKAVQTADIRLSARATLWL GGSIESPVLCSLTLRLLRLRPPLTWTS NRPTQPCTAQQTQNSVGIAAPS AIRVIY PESVVLNAV IYLPGDPEVSGLPRAFRRF SVEVRLDCGTFKLLLVYCTHPGDIK VNT CKTGALVAFRCFLPX* |
| 2538 | 10589 | A | 3459 | 1 | 1870 | MGKVP MRSEKPAHEVRASTISTTDLSSI ESFFSRGPSTNHTSIKGRPLTAE LKNKT NRAEEKIKKEELAISGVDEDDGGKGIKD TGDLVEMVDLAFRCDRHNDGCDYS DER GCLYQTCQQNQFTCONGRCSKTFVCDE DNDCGDGSDEL MHLCHTPEPTCPPHEFK CDNGRCIEMMKLCNHLDDCLDNDSEKG CGEFIFRASSPGAILILIVAVSTIHAI TDPR LGNALPVR RIVQPQYSWTPLTLKLWASR VSNCQGLLSAAKTHHTVQFSILMALPKG HLFSARLTGKCVAQVIVEGFFAGRD K FV CVLNVA FVPYQFVLSLVRTGTASKSTVG FYRNNISVITGFLIGFLCQSSALDLETFV VSHFYFGINECHDPSISGCDHNCTD L TS FYCSCRPGYKLMSDKRTCVDIDECTEMP FVCSQKCE NVIGSYICKCAPGYLREPDG KTCRQNSNIEPYLIFSNRYLRNL TIDGY FYSLILEGLDNVVALDFDRVEKRLY WID TQRQVIERMFLNKTNKETIINHRLPAAES LAVDWVSSALKGGFVHPALNGGSQHFTL LVD*VIKWLYLISNSVPC*KRRWGLPVF WFGGKREMSWEMMGH*LVEGLCGCCH |
| 2539 | 10590 | A | 346 | 617 | 711 | |
| 2540 | 10591 | B | 3460 | 1 | 2973 | MEKQSINOQLPYPDQLPTQCSPLTGLNE YPLSGVSIPDESWDRKSKHSAAMTLRQV HQRHQNNFLDHNTNVEEYSAQMRIGT HCCCTSSSELLLLVASQNKIADSVTSQV HNIYSLVENGSIYAVDFDSISGRIFWSD ATQGKTWSAFQNGTDRRVVFDSSILTET IAIDWVGRNLYWTDYALETIEVSKIDGS HRTVLISKNL TNPRGLALDPRMKLLYFM DSYLDYMDFCDYNGHHRRQVIASDLGF EV |

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| 2541 | 10592 | A | 3461 | 257 | 3561 | RHKKPFKKSMNPGAG/MLYWSDDQGTDS GVPKIASANMDGTSVKTLFTGNLEHLE CVTLDIEEQKLYWAYVTGRGVIERGNVD GTDRMILVHQLSHPWGIAVHDSFLYYTD EQYEVIERVDKATGANKIVLRDNVFNLR GLQVYHRRITEP/CPN*PKTIKIGHYIKDK PTCSSE/AKWYLPHPGQM*IA/DKPEAQR GSRRLTDLEGGNNEIDWSISCDIYPSSQ VFDLSAKIEGKVDKRTCCPSSFPKGYGPI |
| 2542 | 10593 | A | 3462 | 1 | 10725 | MAGAPPPASLPCCSLISDCCASNQRDSVG VGPSEPGVGYSLVVRFLSRSEKRNIRV GVTRFSRELDPDLRFPEHLFFTDWRLGAI IRVRKADGGEMTVIRSGIAYILHLKSYDV NIQTGSNACNQPTHPNGDCSHFCFPVPN FQRVCGCPYGMRLASNHLTCEGDPNTNEP PTEQCGLFSFPCKNGRCVFNYYLCDGVD DCHDNSDEQLCGTLNNTCSSAFTCGHG ECIPAHWRCDKRNDCCVDSDEHNCNP T |
| 2543 | 10594 | A | 3463 | 3 | 14105 | SWRRCRPKGAFASRGAAVAVCYARPPP GEGTARPGTIAEMDRGPAAVACTLLAL VACLAPASGQECDSAHFRCGSGHCIPAD WRCDGTKDCSDDADEIGCAVVTCCQGY FKCQSEGQCIPSSWVCDQDQDCDDGSDE RQDCSQSTCSSHQITCSNGQCIPSEYRCD HVRDCPDGADENDCQYPTCEQLTCDNG ACYNTSQKCDWKVDCRDSSDEINTEIC LHNEFSCNGECIPRAYVCDHNDCCQD GSDEHA |
| 2544 | 10595 | A | 3469 | 2 | 230 | WQDFYQC*HIFGAFFTHPDGPNWAFS NFVMFCHCLPKCWDYRGESPRPAHFIF VDQCTVVKKKKIRKIKNKFL |
| 2545 | 10596 | A | 347 | 2 | 343 | SSVRAVEFPEDASGSSPSGTSKSDANR ASSGGGGGLMEEMNKLLAKRRKAAS QSDKPAEKKEDESQMEDPSTSPSPGTRA ATSHLTPQRLAGSPSGATRWRLCPRF CPG |
| 2546 | 10597 | A | 3470 | 134 | 929 | RTAARGCNGIPGAAWEAALPRRRPRR HPSVNPRSRAAGSPRTRGRRTEERPSGSR LGDRGRGRALPGGRLGGRGRGRAPERV GGRGRGRGTAAPRAAPAARGSRPGPAG TMAAGSITTLPALPEDGGSGAFPPGHFK DPKRLYCKNGGFFLRHPDGRVVDGVREK SDPHIKLQLQAEERGVSISKGVVC/SNRY LAMKVEDGRLLASKCVTDECFFERLESN NYNTYRSRKYSWYVALKRTGQYKLG KTGPGQKAILFLPMSG |
| 2547 | 10598 | A | 3471 | 1 | 2604 | |
| 2548 | 10599 | A | 3472 | 478 | 697 | YLIYQSRFFLFSSIRYCQMPMPMG/YCNP YAYGQYNMPYPVYHQSPGQAPYPGTQ QPSYPFP/QPPQSYYPQQ |
| 2549 | 10600 | A | 3473 | 21 | 194 | |
| 2550 | 10601 | A | 3474 | 2 | 767 | APLSPGAQLGRGAPTSAPPPAAEAHPA ARRGLRSPQLPSGAMSQNGAPGMQEE LQGSWVELHFSNNGNGGSPASVSIYNG DMEKILLDAQHESGRSSSKSHCDSPAS SQTPQDTNRAFETDTHSIGREKQLTVLR EDDIERRKEVESILRKNSDWIWDWSSA GKIFPPKEFLFKTPGSRTATLSMRINTSVL KKGIFSAEFLKVLFPFAALSIAWPIGL GIYIGKASDQSTSTFGWKEPGSLDLVR |

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| 2551 | 10602 | A | 3475 | 1 | 4220 | MLNIVQDSALLEAIGCQMEMGGGENNL KSHSRTNSGISSASGGSTEPTTPDSEPA QALLRDYALNTDSAAGLLIRSIHLVTQRL NSQWRQDMSISLAALELLSGLAKVKVM VDSGDRKRAISSVCTYIVYQCSRPAPLHS RDLHSMIVA AFQCLCVWLTEHPDMLDE KDCLKEVLEIVELGISGSKSKNNEQEVK YKGDKEPNPASM RVKDAAEATLTCLVN ETTLIKYSRLPTINKHSFRYFVLDNSVILA ML |
| 2552 | 10603 | A | 3476 | 3 | 1676 | HASDSFRYFVLDNSVILAMLEOPLGNEQ NDFFPSVTVLVRGMSGRLAWAQQCLLL PRGAKANQKLFVPEPRPVKNDVGFKYS VKHRFPPEEVDKIPFVKADLSIPDLHEIVT EELEERHRKLRSGMAQQIAYEIHLEQQS EELQKRSPDPVTDCKPPPAQEFQTAR LFLSHFGFLSLEALKEPANSRLPPHIALD STIPGFFDDIGYLDLLPCRPFDTVFIFYMK PGQKTNQEILKNVESSRTVQPHFLEFLLS LGWSVDVGRHPGWGTGHVSTSWSNCCD DGEQSQQEEVISSEDIGASIFNGQKKVLY YADALTEIAFVVPSPVESLTDLESNISD QSDSNMDLMPGILKQPSLTLELFPNHT DNLNSSQRLSPSSRMKLPQGRPVPLGP ETRIVSVVWVERYDDIENFPLSELMTEIS TGVETTANSSTSLRSTTLEKEVLVIFHPL NTGLFRIKIQGATGKFNMVIPLDGMIVS RRALGFLVRQTVINICRRKRLESYSPP HVRRKQKITDIVNKYRNKQLEPEFYTSL FQEVGLKNCSS |
| 2553 | 10604 | A | 3477 | 288 | 589 | WCSRRRGWYLLLG FHN YWRSSTFLVRC TPSCPGGCCPRYGIYPVRSCPRLP GGVS R YGSIHSG/RWCSWSPSWSPWLTSVTPRL YVALM*AVVCPVVGKQP |
| 2554 | 10605 | A | 3478 | 1250 | 1909 | GAGPDMVWDTELELALKISKGLQRPIKA HREEREDIGKHESRCVIYFGTAKKWILK DKNGRSRVDVISHRLKVSSGLCKTHEIG FDPLALKCPLRSRTAPWWPLDRVSFDLH HLVIGNFFVGNRKIFLDYLVYGFHNNR WKLLVQSWSDGCVHRTFGLVKSFSKAS FCIFITKQRKSSDLALKQICANTARVIL KLKHFHFVS YMCTFLFTCENGHL |
| 2555 | 10606 | A | 3479 | 3 | 246 | AAAMSALSLILGLLTAVPPASCQQ/GEP AHMILTVGNKADGVLVGTDGRYSSMAA SFRSSEHENAYENVPEEGKVRSTPM |

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| 2556 | 10607 | A | 348 | 2 | 2355 | WCDLGSLOPPPPRFKQFSCLSLPRHS*TS Q*POPPKTQLNFTVAIDFTASNGETRMSE KVGGNPLQPTSLHYMSPYQLSAYAMAL KAVGEIIQDYDSKLFPAVGFGAKLPPE GRISHQFPLNNDEDPNCAGIEGVLESYF QSLRTVQLYGPTYFAPVINQVASNSWSS VTLGTDSEPAVEVPQYVGIRLLVEGFTIK KPMAMCHRRMGVRPAVPLLTQRGSSEG KDSGTPTHSLHTKAQLPSPHVLRHQGV LRRQHSKLVGTALSTTGKALRTLPTAK VFISLPPNLDFKVAPSILKPRKSIREDRNG RSQKTVHTEGDMNMNIKKIVKOATVLT FTTALLAGGATQAFAKENNQKAYKETY GVSHITRHDMLOIPKQQQNEKYQVPQFD QSTIKNIESAKGLDVWDSWPLQADGTV AEYNGYHVVFALAGSPKADDDTSIYMF YQKVGDNISDSWKNAGRVPKDSKDFDA NDPILKDQTQEWSGSATFTSDGKIRLFYT DYSGKHGKQSLTTAQVNVSKSDDTLKI NGVEDHKTIFDGDGKTYQNVQQFIDEGN YTSGDNHTLRDPHYVEDKGHKYLVFEA NTGTENGYQGEESLFNKAYYGGGTNFF RKESQKLQSSAKKRDAELANGALGHIEL NNDYTLKKVMKPLITSNTVTDEIERANV FKMNGKWYLFDTSRGSKMTIDGINSNDI YMLGYVSNLTGPYKPLNKTGLVLQMG LDPNDVTFTYSHFAVPQAKGNVVTISY MTNRGFFEDKKATFAPSFLMNIKGKNTS VVKNSILEPGQLAVN |
| 2557 | 10608 | A | 3480 | 162 | 530 | ELLQPMASALLILGLLTAVPPASCOQGL GNLQPMQGLIAAAFLVLAIAFAVN HFWGAKEEP/ESPAHMILTVGNKADGV LVGTDGRYSSMAASFRSSEHENAYEN VPEEEGKVRSTPM |
| 2558 | 10609 | A | 3481 | 4 | 409 | NAATSLTANPDATTVNIEDPGETPKHQ GSPRGSGREEDDELLGNDSDKT/EGTV SGNDSSEVNDTWPLPWGKQANRPLLS LLAGQKKSSPFWTFEYYQTFDVTYQV FDRIKGSLLPIPGKNFVRLYIRSIV |
| 2559 | 10610 | A | 3482 | 160 | 518 | |
| 2560 | 10611 | A | 3483 | 12 | 197 | |
| 2561 | 10612 | A | 3484 | 2 | 321 | ARGVYGYSLFYIPTAILWIIPKAVRWI LVQJALGISGSLLAMTFWPAVREDNRRV ALATIVIVLLHMLLSVGCLACFFDAPE MDHLPTTTGTPNQTVAAAKSS |
| 2562 | 10613 | A | 3485 | 187 | 1280 | PLARLNLCSLSPLSNLSLFLIGTSL GCTCSLKHSHKPCQIFFLIIGRRLTGRMA AVDDLQFEFGNAATSLTANPDATTVNI EDPGETPKHQPGSPRGSGREEDDELLGN DDSDKTELAGQKKSSPFWTFEYYQTF DVTYQVFDRIKGSLLPIPGKNFVRLYIR SNPDLYGPFWICATLVFAIAISGNLSNFLI HLGEKTYHYVPEFRKVSIAATHIYAYAW LVPLALWGFLMWRNSKVMNIVSYSFLEI VCVYGYSLFYIPTAILWIIPKAVRWILV MIALGISGSLLAMTFWPAVREDNRRVAL ALVVTIVLLHMLLSVGCLAYFFDAPEMD HLPTTTATPNQTVAAAKSS |
| 2563 | 10614 | A | 3486 | 112 | 563 | LDSSHCCSCSTALFRTQTAAAVPRMVI RVYIASSSGSTAI/RGKRQQDVLGFLEAN KIGFGRKDIAANGENRKWMRENVENS RPGTGVPPLPPQIFNESQYRGDYDAFFG RPEENNAVYCLRLGTAPPGVSKGRQE GAKPKAGQALTL |
| 2564 | 10615 | A | 3487 | 105 | 335 | GRLFPKVLSYHSVGYLPLILFCHFLANC ILCLMHFL*FFQSYRF*G*KFGFTQHHC HYIFHKQWPLLWKNFPEH |

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| 2565 | 10616 | A | 3488 | 993 | 1338 | QNCLKPHFFFFFETRVSLLLPKREAMGTI STHCNLCPLPGFQGNPASASQGR/AGLH GMGPPCR/RGTFVFLIGDRGFLHVGSSWS WNSQPQVIRPPRPSPKCWGLQGMEATV PSP |
| 2566 | 10617 | A | 3489 | 2 | 454 | PLLPPALPGCHALAPSSYIPVAIRALEPPS PYHGQLKMQSIPGPPQPRSFFLSSPLDVD SPQAPRHCTGLPAPSLSSPPWSCPTLFSW FFEASGVCHHWTSVIAASNSSPIPELPH HPLRISAWLFPPWRDHSQDPLCRGATSP VLNS |
| 2567 | 10618 | A | 349 | 1129 | 1821 | AWGSGKQQRQEAQCEVAEFTPAWRR APDTPAPLVLEPARA*HTSPKKHPPMWC RFFFRQSFALVPQIGVQWRNLGSLQPLP PRFKAFFSYPPPPSSWHYRHHVPIVFSA NFCIFNKRWGFTMLAKLVLNS*PHEIHP PGPSQSAGIMGVSHCTWLVSFVKVVLV DYFFEKFPN*GNRFEFYFYLFETGSHSVN QAGVQR/PYHASLQPPQAQVSLPSSW DYRHVPF |
| 2568 | 10619 | A | 3490 | 1109 | 1448 | PRLISKCFLLLFRRQSHFVAQAGVQWC DLRSVYHLPPGLKRFSCSLPSSWDYRH LPPCPANFCNFSRDRVSPCCPGWFRTPD PGDPPASAPKWWEYTL*PPGPDHPKAF |
| 2569 | 10620 | A | 3491 | 14 | 250 | VLSVGLPTGDTGIGLSRKTSPAPVALIHS HSLKQAH*TLGSRGTGNIHAIYRGVLK YCNFICLGFMLRYQLVSPSF |
| 2570 | 10621 | A | 3492 | 1 | 1065 | |
| 2571 | 10622 | A | 3493 | 90 | 1937 | AGGNQRTQSPRKNFMAFQASHRPAWGK SRKKNWQYEGPTQKLFLKRNNSVAPDG PSDPSISASSEQSGAQPPGLQVERIVDK RKNKKGKTEYLVRWKGYDSEDDTWEP EQHLVNCEEYIHDFFNRHTEKQKESTLT RTNRTSPNNARKQISRSTNSNFSKTSKPA LVIGKDHESKNSQLFAASQKFRKNTAPS LSSRKNMDLAKSGIKILVPKSPVKSRTAV DGFQSESPKLDPVEQQQEDTVAPEVAA EKPVGALLGPGAERARMGSRPRIHPLVP QVPGPVTAAMATGLAVNGKGTSPFMDA LTANGTTNIQTSVTGVTASKRKFIDRR DQPFDKRLRFSVRQTESAYRYRDIVVRK QDGFTHILLSTKSENNSLNPAEVLREVQS ALSTAAANDSKVVLPRAVGSVFCCGLN FNYFKPRLPNARKRESIKMAEAI RNFN TFIQFKPIIVAVNGPAIGL GASILPLCDV VWAN EKAWFQTPYTTFGQSQEGCSPV MFPKIMGGSICILDAVLGDRNLTAQEAC GKGLVSRVFWPGTSPRKVMVRIKELASC NPVVLEESKALVRCNMKMELEQANERE CEVLKKIWG\SAQGDGTRMLKVLCRGKI E |
| 2572 | 10623 | A | 3494 | 2 | 572 | WCLQHD/LGHASIFKKSWWNHVAQKFV MGQ/LKGFSAHWWNFRHFQHHAKPNIF HKDPDVTVPVFLGESSVEYGKKRRR YLPYNQQLHYFFLIGPPLTLVNFEVENL AYMLVCMQWAVSGVAQDPGHTAAVA GGGASGDSTCP*RTGCTDLLWAASFY ARFFLSYLPFYGVPGVLLFFVAVRYGRE WR |
| 2573 | 10624 | A | 3495 | 25 | 430 | YKNSFPPIALGKCAMLTFPLPLSHQA QSQGHRAEYTCESRPFPPVGLPWGQ AAMRAGGWVGR TAECFSGMESRPG*R VSGRGAGGQPRPSGMSLGGPVPPAPSS PLLPPAGRCNPRTERTWNLPTRSWA |

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| 2574 | 10625 | A | 3496 | 821 | 1412 | GSARASPOGPGKPLVRVDHTDEPHQGD RPREAPGLGQLSAGSHLQRGALTFHQL VQRAPQLPDRAPPLPQDAETQLQPGCPA CQVAVCQVARPQLRSEALPHRAGGHR QVPEESLVTSCWTPPTSISEGNTQAGREGL RAPATKPSPRDRIPPTPLTSLGVPCLPS WYCCPLGLPLTCVFSSPMALALGLMQ G |
| 2575 | 10626 | A | 3497 | 32 | 616 | VLQCSHGCFSPSSGG\LTDEAASSCCSD ADPSTKDFLLQQTMLRVKDPKKSDFY TRVLGMTLIQKCDPIMKFSLYFLAYE DKNDIPKAEKDEKIAWAVSRKATLELTQ QFGALKDDATQSYHNGNSDPRGFHIGI AVPDVYSACKRFEELGVKFVKKPPDDG KMKGLVAFIQDPDGYWIEILNPNKMATL M |
| 2576 | 10627 | A | 3498 | 77 | 403 | |
| 2577 | 10628 | A | 3499 | 18 | 753 | TQPQLTSTCYRAFASWTRSLLEPATILP TTCCPAPAAMCRTLAAPTTCLERAKEF KTLGIFPHKSSELGFDTGSTGKFEWGSK HSKGDLKTSQKDVLGWRESFDLLSSK NGVAAFHAFKTEFSEENLEFWLACEE FKKIRSATKLASRAHQIFEEFICSEAPKE VNIDHETRELTRMNLQTATATCFDAAQ KTRTLMEKD/SPYPRFLKSPAYRDLAAQ ASAASATLSSCSLDEPSHT |
| 2578 | 10629 | A | 35 | 45 | 819 | RLALSPLRECNGAISAHCKLRLPGSRHS PASASRAAGTTGAHHRARLIFFVLVET GFHRVSQDGL/PLDL/DDPPASASQSAGI TGVTAAAPSRACSFKLARGRACPGWDWA EELTGTSHTRRVHPGQALWGWDWRCS CGSRSWQT*LQRCPAVLRGWLACLTQ EEQIGPYVSVPVIPAACCFIDVLR*KI SDKDVFKAGRGAQPKTFSLLRKSL/NPV TQARVQWCDLSSLQLLPPRFK*FSCFSLP SRTIT |
| 2579 | 10630 | A | 350 | 325 | 608 | LMPNPRHFERLRQADHLRSGVPRPALV QHGETLSVLKIQKLGHHGSTCL*SQLLRR LRQKNLLSLGGRGCSKLRSHHCTPAWV TEPDSVSKKK |
| 2580 | 10631 | A | 3500 | 28 | 342 | PGSTHASADAWVHPKNI/SSVNALSPGPH CAQTEV/IVSPAPRCLCHRRGPRPSCCPN PVPSLTSLTRFPLCRATLKNGRKACLN PASPIVKKIEKMLNSDKSN |
| 2581 | 10632 | A | 3501 | 1 | 274 | MARATLSAAPSNPRLLRVALLLLLVA SRRAAGASVVTELRCQCLQTLQGIHLKN IQSVNATLKNGKACLNPAAPMVQKIE KILNNP |
| 2582 | 10633 | A | 3502 | 1 | 893 | MSSREVTTPGKDVARSRLRSGKSGDPRRT ALGSRSSASSQAVISVSLRAAGSRSRSDS GQKENIPQLAGVTQDSQTRTSLVSAPTPL HPRGGAIAFLPNSGSIWSSGNFPGPLRA FQPQPCIKGVRRSRATEPGPQAAPCQLS SSHRSNRLLSPMARATLSAAPSNPRLLR VALLLLLVAASRAAGAPLATELRCQC LQTLQGIHLKNIQSVKVKSPGPHCAQTE VM*VSPIAAAATAGVPDSPAAPNPVLS TSCLTRFPLCRATLKNGQKACLNPA MVKKIEKMLKK |
| 2583 | 10634 | A | 3503 | 1 | 407 | ATEPGPQAPPRQLFRSSHRSQTRLLSPMA RAALSAAPSNPRLLRVALLLLLVAAGR RAAGASVATELRCQCLQTLQGIHPKNIQ SVNVKSPGPHCAQNEVHKHTQEMGGKA CLNPASPIKKIEKMLNSDKSN |

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| 2584 | 10635 | A | 3507 | 47 | 891 | KQPFVWPAGGERLSGARPKKEARLLR WCPMSFKRNRSDRFYSTRCCGVCCHVR TGTHLGTWYMVVNLLMAILTVEVTHP NSMPAVNIQYEVIIGNYYSISERMADNA C/VFFFAVSVLKVYNPVPMLVYGSNFLY PSGVGWIPFFCYRLFDVLSICLVAISSLT YLPRIKEYLADQLPDFDKDDLRLALDSAS CLLFIVLVFFALFIIFKAYLINCWNCYK YINNRN/VCPAIAVYPAFEAPQYVLPY EMGREKWPEKEHPPLLTWPEGNSGLW TINP |
| 2585 | 10636 | A | 3508 | 246 | 559 | MPVAVMAES/AFSFKLLDQCENQELEA PGGIATPPVYGQLLALYLLHN/GQRIWQR DFPGIYTTINAHQWSETVQPIMEALRDAT RRRAFALVSQAYTSIIADDDFA |
| 2586 | 10637 | A | 3509 | 2 | 250 | |
| 2587 | 10638 | A | 351 | 3 | 218 | |
| 2588 | 10639 | A | 3510 | 2 | 119 | |
| 2589 | 10640 | A | 3511 | 197 | 921 | GTWVGLAVRTVQRRGPAAKMPVAVMA ESAFSFKLLDQCENQELEAPGGIATP KVYQQLLALYLLHNDMMNARYLWKRI PPAIKSANSELGGIWSVGQRIWQRDFPG IYTTINAHQWSETVQPIYKHFDRDATR/ RDRAFAPGLLQAVYFQSIRPMIFAFAVGV LPVVEAVKGILAEQGWQADSTRNGSC PGKPVCRGPWDVFPFNKFISLYSEPAPV PPIPNEQLARLTDYVAFLEN |
| 2590 | 10641 | A | 3512 | 3 | 354 | |
| 2591 | 10642 | A | 3513 | 1 | 179 | |
| 2592 | 10643 | A | 3514 | 63 | 386 | LRTLISCHLVVLMLLFLHTGGDDGLLRG WDTRVPKGFLFTSKR*PPKGQHSVPTPA PAFPGSPALPPGWVCVLDTGSEASAC RHTMGVCSIQSSPHREHILATGR |
| 2593 | 10644 | A | 3515 | 1 | 147 | |
| 2594 | 10645 | A | 3516 | 450 | 1154 | KSHVLEPLSSLALEEQCLALS LDWSTGK TGRAGDQPLKIHSSDSTGQLHLLMVNETR PRLQKVASWQAHQFEAW/TCCFQLPWH PEIVYSGGDDGLLRGWDTRVPGTFLFTS/ IKTHHGCVASIQSKPSSGAHPWPRESYDE THPTVADTRNMKQPLADTPVQGGVWRIK WHPFHHLHLLAACMHSGFKILNCQKAM EERQEATVLTSHLTPDSL VYGADWSWL LFRSLQRAPLVVLS |
| 2595 | 10646 | A | 3517 | 73 | 168 | |
| 2596 | 10647 | A | 3518 | 322 | 671 | RLWASPAAPGKKKEMGNSMKSTPAPAE RPLNPEGLDSDFLAVLSDYPSPDINPPIF RRGEKLRVISDERGWWKAISLSTGRESY IPAICVARSYHGWLRLRGPCKNMAEELL QLPD |
| 2597 | 10648 | A | 3519 | 624 | 1580 | KAATSENKIIICCEWRTSQAALMLHRLW ASPAAPGKKKEMGNSMKSTPAPAERPLP NPEGLDSDFLAVLSDYPSPDISPPIFRGE KLRVISDEGGWWKAISLSTGRESYIPGI CVARVYHGL/WLFEGLGRDKAEELLQL PDTKVGSFMINRESETKKGFYLSVRHRQ VKTYRIFRLPNNWYIISPRLTFQCLIEDL VNHYSEVADGLCCVLTTPCLTQSTAVAP AVRACSSPVTLRQKTVDWRRVSRLQED PEGTENPLGVVESLFSYGLRESIASYLSL TSEDISSFRKKKSISLMYGGSKRKSSFFS SPPYFED |

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| 2598 | 10649 | A | 352 | 319 | 1979 | VPGVPAARPERECRAHPASFPPPPGGLDS GFVPSVQDFDKKLTADAYLQILIEQLKL F**QASKRKEDQQRKKIETLKETTNSMV ESIKHCIVLLQIAKDQSNAEKHADGMIST IKSCRCNIPA*SLGTCDAQCLPRLPYLQ NPLSCVSSSVHLS*QVGPVLSYLGTSDD SNTQIVPGSGNFTNLAASLTPSQAMSTLS PNTVPEFSYSRQ*/EDEFYDAD/ENSIKVG SSPKRLIDSSGSASVLTHTSSSGNSLKR PDT TESLNSSLNNGTSDADLFDSDHDDRDDDA EAGSVEEHKSVIMHLLSQVRLGMDLTK VVLPTFILERRSLLEMYADFFAHPDLFVS ISDQKDPKDRMVQVVKWYLSAFHAGRK GSVAKKPYNPILGEIFQCHWTLPNDTEE NKELVSEGPVPGVSKNSVTFVAAEQVSH HPPIFSLFMLECFNKKIQFNAHIWTKSKF LGMSIGVHNIGQGCVCCLDYDEHYILTTP NGYGRSILTPWVELGGEKNINCSKTGY SANIIFHTKPFYGGKKHRITAEIFSPNDKK SFCISIEGEWNG |
| 2599 | 10650 | A | 3520 | 24 | 688 | VDHPPYKRTEKVRQSPKSDIYLGLL VKLYRFSGPEEPNSNIQTRVVLKARLFMS RTNRPPLSLSRMIREDEAFLAGKKKNP AVVVGPKLIMCGVQKGTPLKVCALG GTQAGPHKRILRARGQSRITFDQLALD/S PLRGCGTVLLASGPKGQREVYRHFGKAP GNPHSHTKPYVRSGRKFARARGVRA SRGYKKLTLDPTLLYKKIFADSEKKKK |
| 2600 | 10651 | A | 3522 | 195 | 391 | PGVAGARHPLLGAAPKGRLEVLAVGFH GSAANQVWVSKSHPPQFIPTDQIEGGDRA LKGTCLRLPLS |
| 2601 | 10652 | A | 3523 | 112 | 492 | AHSRTPARPENRAAASAPRKPRRAMSSP PEGKLETKAGHPPAVKAGGMRIQKHP HTGDTKEEKDKDDQEWESPPKPTVFI SGVIARGDKDFPAAQAQVAHQKPHASM DKHPSRPTQHIQPRK |
| 2602 | 10653 | A | 3524 | 3 | 982 | GTRVGVAWRSVRLLLGPGAGLRGGVVL KVSPSPCRGRRVPVRAEGARGRGRPN KVPGASSGA AVGAARLTAPLLAKAMAS KLLRAVILGPPGLGKAPVCQRIANFG LQVHLSGHFLRENIKAISTEVGEMANQV YREKVFLVPDHVITRLMMSELENRRGQ HWLLDGFPTLQGAELDKICEVDLVIS LNIPFETLKDGLNRRWIHPVSGARVYNLA DENPPHVHGIDDTGEPLVQEDDKPE AVAAIRLRQYKDVAKPVIELYKSRGVL HQFSGTETNKMWPVYVYTLFSNKITPIQ SKESILTLAQWEEPWNVDVGHFSQ |
| 2603 | 10654 | A | 3525 | 19 | 445 | |
| 2604 | 10655 | A | 3526 | 1 | 622 | QAAWILKARALTEMVYIDEIDVDQEGIA EMMLDENAIAQVPRPGTSLKLPGTNQTG GPSQAVRPITSHSEKPTGFLRPSTQSGRP GTMEQAIRTPRTAYTARPITSSSGRFVRL GTASMLTSPDGPFIN*SRNLTKYSQKPK MAKALPEYIFHHENDVKTALELAALSTE HSQYKDWWWKVQIEKRYRRLGMYREA EKQLISAMKQ |

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| 2605 | 10656 | A | 3527 | 1 | 1509 | MKAEICKSRTVKDWHNHQKLGEKNKTD SPQOPSEGTNTANTLILDFWPLEMIACCW ETFPQRLTAELFMNPTHWRWHGYKNQSV GALRAPLGQGPSRRGLPGRVGRRLFTP RPPLSWSAGPSLAAPAAAMSSEMEPLLLA WSYFRRRKQFQCADLCTQMLEKSPYDQ EPDPELPVHQAAWILKARALTEMVYIDE IDVDQEGIAEMMLDENAI/PSSTPITQAG RPITGFLRPSTQSGRPGTMEQAIRTPRTA YTARPITSSSGRFVRLGTULGMYREAEKQ FKSALKQQEMVDFTFLYLAKVYVSLDQP VTALNLFKQGLDKFPGEVTLCCGIARIYE EMNNMSSAAEYYKEVLKQDNTHVEAIA CIGSNHFYSQPEIALRFYRRLQMGYIN GQLFNNLGLCCFYAQQYDMTLTSFERA LSLAENEEEAADVWYNLGHVAVGIGDT NLAHQCFRLALVNNNNHAEAYNNLAVL GDAEG/RHVEQARALLQTASSISPHMYE PHF |
| 2606 | 10657 | A | 353 | 27 | 749 | STCCFQELVTL*GCKLCTFHPGRKWETR LAEPLQORDPSYRVVMLGELRGIVFLTGI VSPRTENDQEISEDTRSHGVLLGRFQKD ISQGLKFKEAYEREVSLKRPLGNSPGERL NRKMPDFGQVTVERS*PPGEREA/RKYN DFGNSFTVNSNLISHQRLPVG/DTRPHKC DECSKSFNRTSDLIQHQRHTGEKPYECN E/CGKAFSQSSHLIQHQRHTGEKPYECS DWGKTFSCSSDLILH |
| 2607 | 10658 | A | 3531 | 1 | 174 | |
| 2608 | 10659 | A | 3532 | 1 | 189 | MDAVAVYHGKISRETGEKLLLATGLDG SYLLRDESVPGVYCLCVLAFQKPDQIV IPLQYPV |
| 2609 | 10660 | A | 3533 | 3 | 210 | CPRVHQAMD VAVYHGKISRETGEKLL LATGLDGSYLLRDESVPGVYCLCVL*V *YVCCEYDTPCLWYLVMAA |
| 2610 | 10661 | A | 3534 | 1 | 386 | GISLAQFSSSACPRVHQAMD VAVYHG KISRETGEKLLLATGLDGSYLLRDESVP GVYCLCVLYHGYITYRVSQTETGSWS A/EAFQKPDQGIVPLQYPVEKKSSARST QGTGIREDPDVCLKAP |
| 2611 | 10662 | A | 3535 | 224 | 751 | LVPGCCSSGISLAQFSSSACPRVHQAMD AVAVYHGKISRETGEKLLLATGLDGSY LLRDESVPGVYCLCVLYHGYITYRVS QTETGSWSAETAPGVHKRYFRKMKKS HFQHFQKQDQIGIVPLQYPVEKKSSARS TQGTGIREDPDVCLNAPLIKISPLRPLFS ITFNIC |
| 2612 | 10663 | A | 3536 | 3 | 199 | SIRAEMSRSVLAVLALLSLSGLEAIQRT PKIQVYITSSSREWVKFPPELLCVWVSST PTLKLTY |
| 2613 | 10664 | A | 3537 | 134 | 404 | |
| 2614 | 10665 | A | 3538 | 415 | 533 | |
| 2615 | 10666 | A | 3539 | 1 | 3349 | MDQPEAPCSSTGPRLAVARELLAALAE LSQEQLKFRHKL RDVGPDGRSIPWGR ERADAVDLAEQLAQFYGPEPALEVARK TLK RADARDVAAQLQERRLQRLGLGSG TLLSVSEYKKKYREHVLQLHARVKERN ARSVKITRFTKLLIAPESAAPPEALGPA EEPEPGRARRSDTHTFNRLFRDEEGRRP LTVVLQGPAGIGKTMAAKKILYDWAAG KLYQQQVDFAFFMPCGELLERPGTRSLA DLILD |
| 2616 | 10667 | A | 354 | 69 | 378 | KGGSLGAPRVEGPNFGLAKDSSSPKKRE FPALPPPGGN/KRAGPPCPGKFGFLKKK GVPPGGKRG LNPRPQGDSS*PPKGGGI TGGAPRPGKKRSFSLQKIL |
| 2617 | 10668 | A | 3540 | 3 | 261 | |
| 2618 | 10669 | A | 3541 | 3 | 429 | |

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| 2619 | 10670 | A | 3542 | 1 | 859 | ALGKQKCEEWRSKY/EALK/ED/WRNLG AQHRELESQHLVLSKLQAGDSRDLQM NQALRSLQNEHQQLQAKIECLQADRDLQ SLYTQDLQDQLKRSEAEKLTLVTRVQQL QGLLQNSQLQLEQEKLLTK/KRSANLL PQILRYCSFSYLPRGSGMDYMTSWSPSQ FWEFC*VRDVWELFKD*SLALRTLQLVS LLS*DQALPVWSPKSPNEVEPEGTGKE KDWDLRDQLQKKTLLQQAKEKECRELH SELDNLSDEYLSCLRKLQHCREELNQSQ QLPPRRQCGRWLP |
| 2620 | 10671 | A | 3543 | 392 | 2016 | AKRNRCLVIMISPDPRPSPGLARGAESY EAKCERRQEIRESRRCRPNVTTCRQVGK TLRIQQREQLQARLQQFRRRNLELEE KGKAQHPQAREQGPSRRPGQVTGTSSEV FPAQHPPPSGICRDLSDHLSQAGGLPPQ DTPIKKPPKHHRGTQTKAEGPTIKNDAS QQTNYGVAVLDKEIQLSDYLKEALQRE LVLKQKQMVILQDILLSTLIQASDSSWKQ LNEDKLKGLRSLNQLYTCTQKYSWP GMKKVLLMEDQKNSYEQAKESLQK VLEEKMAEQQLQSTQSRSLALAEQKCE EWRSSQYEALKEDWRTLGTQHRELESQ HVLQSKLQAGDSRDLQMNQALRFLNE HQQQLAKIECLQGDRDLCSLDTQDLQD QLKRSEAEKLTLVTRVQQLQGLLQNSL QLQEKEKLLTKKDQALPVWSPKSPNEV EPEGTGKEKDWDLRDQLQKKTLLQAK EKECRELHSELDNLSDEYLSCLRKLQHC REELNQSQQLPPRRQCGRKGLPVLMMVI APALAVFLANKNNLMI |
| 2621 | 10672 | A | 3544 | 35 | 219 | |
| 2622 | 10673 | A | 3545 | 293 | 479 | |
| 2623 | 10674 | A | 3546 | 1 | 968 | VKLPSCPDAMPSTLLCWMALCLLGAD HADTGVSQNPRIHNRKQNVTFRCDFPI SEHNRLYWYRQTLGQGPFLTYFQNEA QLEKSRLLSDRFSERPFGSFTLEIQRTE QGDSAMYLCASSLAGLNQPHFGDGTR LSILEDLNKVFPEVAVFEPSEAEISHTQK ATLVCLATGFFPDHVELSWVWNGKEV HSGVSTDPQLKEQPALNDSRYCLSSRL RVSATFWQNPRIHNRKQNVTFRCDFPI DEWTQDRAKPVTVQIVSAEAWGRADCGF TSVASYQQGVLSATILYEILLGKATLYAV LVLSALVLMAMVKKRDF |
| 2624 | 10675 | A | 3547 | 278 | 1283 | GGIGEIKQRPSCLRCLDPSLSVLMNLSL ELGSVFSAVISQKPSRDICHRGSLTIQGG VDSQVTMMFWYRQPGQSLTLIATANQ GSEATYESGFVIDKFPISRPNLTFSTLTVS NMSPEDSSIYLCVVEEQGFVGAETQYF GPGTRLLVLEDLKNVFPPEVA/VLFEPSE AEISHTQKATLVCLAICFYLDHVELSWW VNGKEAHSGVSTDPQLKEQPALNDSRY CLSSRLRVSAITFWQNPRIHNRKQNVTF GLSENDEWTQDRAKPVTVQIVSAEAWGR ADCGFTSGKISYQQGVLSATILYEILLGK ATLYAVLSALVLMAMVKKRDSRG |
| 2625 | 10676 | A | 3548 | 151 | 286 | |
| 2626 | 10677 | A | 3549 | 28 | 177 | |
| 2627 | 10678 | A | 355 | 213 | 660 | KPVILGYAEPAPGQFSRGP/WSRAE/WP GTASPLLV/SCATSALL*SIPKGPDSHRGH QHGTPTPSKPEKGTAGQLSRYITPQE KEIAPLNPPALKSPSKENRDPDLTGPGQ TSRALTVPAGCALGPQVEPMKALRRQM GGAVFPLGS |
| 2628 | 10679 | A | 3550 | 422 | 671 | RIYPALRMPISINTASIAQARKLVEQLFMF VANIDRIKVSAAAADLMAYCEAHAKEDP LLTPVPASENPFKEKKFFCAHPLSL |

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| 2629 | 10680 | B | 3551 | 62 | 299 | MFSLKKWNAVAMWSWDVECDTCAICR VQVMDEGIGVRNWSEALNLIYASEMGF DLDMGSQTSLSPLAHWLLNNLGWMNL X* |
| 2630 | 10681 | A | 3552 | 1 | 602 | ADVEDGEETCALASHSGSGSKSGGDK MFSLKKWNAVAMWSWDVECDTCAICR VQVMDEGIGVRNWSEALNLIYASEMGF DCRSSTALAVPSVSLASHQPCLDHR* QPIGSIQSSLF*RNSQVS*GRK*KVASYEL LKEGFCVNACLRCAENKQEDCVVW GECNHSFHNCCMSLWVKQNNRCPLCQ DWVVQRIGK |
| 2631 | 10682 | A | 3553 | 2 | 428 | SGGSTPLGLSAPKPTSSAVGSVGAAM ADVEDGEETCALASHSGSGSKSGGDK MFSLKKWNAVAMWSWDVECDTCAICR VQVMDACFRCAENKQEDFFVVLGECN HSFHNCCHVPCGSKQNNRCPLCQ/QDW VVQRIGK |
| 2632 | 10683 | A | 3555 | 3 | 378 | |
| 2633 | 10684 | A | 3556 | 2 | 299 | LLNSRPRRRQQAQPSLEMQNDAGEFVD LYVPRKCSASNRIIGAKDHASIQMNVAE VDKVTGRFNGQFKTYAICGANRRMGES HDSFLRMAKADGIVSK |
| 2634 | 10685 | A | 3557 | 1 | 392 | RRYLCRVTSCLSLRAVWWPARRSPAF EMQNGRRRSSDLYRARGKLSASNRIIG AKDHASIQMNVAEVDKVTGRFNGQFK TYAICGAJRRMGESDSSILARLAKADGIV FKELFDWREITDVGFCHK |
| 2635 | 10686 | A | 3558 | 1 | 415 | FRDIVNENGEIEQDEEDGYDDDEM GTGMKES*NSPWVMAG/HGGSNPQANR QTSOSSAKMSTPADKVLKFKENKINLD KLNVTDSVIYKATEKF/DTKGIKYVLDPT TRMILFKMLTRGIITDIDGCISTGREANV |
| 2636 | 10687 | A | 3559 | 139 | 1914 | AVPFHRAAASGGALQSWTTGGLMSR VVPQGQDDADSSDENRDLKTVKEKDDI LFEDLQDNVNENGEIEDEE/WKEGYD DDAEMTGTGMKELENSPRVMSGIGRKQP TGKSTD/PDSSSAKMSTPADKVLKFKEN KINLDKLNVTDSVINKVTEKSRQKEADM YRIKDKADRATVEQVLDPRTRMILFKM VTRGIITEINGCISTGKEANGYHASTANG ESRAIKIYKTSILVFKDRDKYVSGEFRFR HGYCRGNPRKMVKTWAEKEMRNLIRLN HSR/GYHCPEPIMLRHGLAMSFIGKDD MPATNFGKMFQLSESKARELYLQVIQY MRRMYQDARLVHADLSEFNIMYHGGG VYIIDVVSQSVEDHDPHAEFLRKDCAN VNDFFMRHSVAVMTVRELFEFVTDPIPL HHENLDAYLSKAMEIASQRTKERTV/SS QDHVDEEVFKRSYIPRNLADEVKNYERD MDIIMKLKEEDMAMNAQQDNILYQTVT GLKKDLSGVQKVPALLENQVEERTCSDS EDIGSSECSDDSEEQGDHARPKKHTTD PDIDKKERKKIEVKEAQREKRKNKIPKH VKKRKEKTAKTKKGK |
| 2637 | 10688 | A | 356 | 629 | 1007 | KGTIYKQERLENLRNHLDKYYNPPMK QNYQKLCQKGMASRTHREESR*MRGNR CRLRITRNA*FEGENLQNKVAQGENLEKK PEPATYI*EA*ESKRDGV*KSYCVSSFPT MQ*KSD*SEYSYG |
| 2638 | 10689 | A | 3560 | 129 | 567 | SYKSRLARKSITGOKAPRKQLAYKKPA SQECGPLLGGLKKPHRYRPGTVLREIR RIVQKSTELMIRKILRFQRLVREIAQDF KTDLRFQERSNQVALQEAARRAYLVWP FLKDTNLVCLSMKRVPMKPRHSSAR RHHVENVL |
| 2639 | 10690 | A | 3564 | 194 | 338 | |

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|------|-------|---|------|-----|------|--|
| 2640 | 10691 | A | 3565 | 197 | 522 | GSAAMKVKIKCWNGVAHWLVVANDE NCGICRMAGNGCCPGCECSPSMLSERPR LQGAPATDCPAGCGGPVLPFCFQHALHP QVGLHAQQVQALAPMLPPRIGKFKE |
| 2641 | 10692 | A | 3566 | 1 | 6521 | MLRKRKWLGVVAHACNPSTLGGQGHF DKQPQVRRLLSAPGSRIAGQWVLDLKS PHLLKGENDKNSLSQKAFLYVAHVLE SERGVLTMTTETGPDSEVKKAEQEEAPQ QPEAAAAVTPVTPAGHGHPEANSNEK HPSQQDTRPAEQSLDMEEKDYSEADGLS ERTTPSKAQKSPQKIACKYKSAICRVTL DASEYECEVEKHGRGQVLFDLVCEHLN LLEKDYFGLTFCDADSQKNWLDPSKEIK KQIRSE |
| 2642 | 10693 | A | 3567 | 1 | 1232 | GCTGTWGEALFIKEKGFFWSPATGPMA AVQMDPELAKRLFFEGATVVLNMPKG TEFGIDYNSWEVGPKLRGVKMIPPGIHL HYSSVDKANPKEVGPRMGFFLSLHQRG LTVLRWSTLREEVDLSPAPESEVEAMRA NLQELDQFLGPYPYATLKKWISLTNFISE ATVKKLQPENRQICAFSDVLPVLSMKHT KDRVGQNLPRCGIECKSYQEGLARLPEM KPRAGTEIRFSELPQMFPEGATPAEITK HSMDSLAYALETVHNKQFPSSQDVLGEL QFAFVCFLGNVYEAFEHWKRLNLLC RSEAMMK/HATRLWINLISILHHQLGEIP ADFFVDIVSQHNFLTSTLQVFFSSACSIA VDATLRKKAKEFQAHLTKKFRWDFAE PEDCAPVVEELPEGIEMG |
| 2643 | 10694 | A | 3568 | 2 | 166 | |
| 2644 | 10695 | A | 3569 | 56 | 1072 | ARGGGAMEGLEENGGVVQVGELLPCKI CGRTFFPVALKKHGPICQKTATKKRKT DSSRQRAEGTDIPTVKPLKPRPEPPKPS NWRRKHEEFIATIRAAGLDQALKEG KLAPPPPPPSYDPGFIIQW/CPYQCQRKIP MENAADRHINFCKEQAARISNKRFFSTD TKGKPTSRTQVYKPPALKKSNSPGTASS GSSRVPPSGAGKTVVGVPSQGVVSSS SSSLG/NTKLQTLSPSHKGIAAPHAGANV KPRNSTPPSFARNPAPGVLTNKRKTYT ESYIARPDGDCASSLNGGNIGIEGHSPG NFPKFCHECGTKYPVEWAKFCECGIR RMIL |
| 2645 | 10696 | C | 357 | 1 | 555 | MLYVLIESERARIKKLQEEKTRNLESSRK LEPTIVSEHKGGLRTEQTDIDVLGQHLTK EHVSSHSQSPIRDSQWFTLSPQEKYACSY ERKDPLIKRAFIIFYHRNAVVS HGGNGPA VVLPISRFVLTPTTFESTLPFLSSRLAWGT SSKDPRIAAGQQSPLEKKILVSKLSSHHT VWNYTEKES* |
| 2646 | 10697 | A | 3571 | 32 | 469 | |
| 2647 | 10698 | A | 3572 | 659 | 1149 | EVTACRQPSVAFSTSLALALTALLEEPP SLLHHCESPLLGWASSCGGCAGSPSSAG PAGIVLK/SLAGQLPPCRVGLGTCSLPY LSLPPAVGSFMARASLMSAAPCSMARVP STTQGLLSRTPQCGQMAQDWQAAPPAS PVQDPLEEASWAPESSGDLENFYV |
| 2648 | 10699 | C | 3573 | 361 | 501 | MLFLRYAPLVGGSFCIWSHPLQFFLTSIK VNFVETLFCFQSFKDIF* |
| 2649 | 10700 | A | 3574 | 124 | 579 | EPLPGLAKAGAGSLSCSVRPCAAGASPT SATPCSIAPSIDHPRAEECGRMVQDWQ AAPAPRCGIHWVKPAGLLSLLMSMVR INMIVKLLVFVILLVT*FTVKVCLYIFQGL CCGLLFCILHGSPSHHRPKDLWHHCDL DVRHEVKGDH |

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| 2650 | 10701 | A | 3575 | 2765 | 3138 | YSLKSGSVMPPALFFWLRIALAMQALF WFHMFNFVVFNSLKKVIGSFMGMALN L*ITLGSMAIFITILIPTHEHGMFFHLFVSS FISLSSGL*FSLKRSFTSLVSWIPRYFILFE AIVNGSSL |
| 2651 | 10702 | A | 3576 | 265 | 663 | GRASGVVRSPRWVCDLAGFRGEAADLH GVCYSRLRSPAGFTQWIHQHQSRSWCLP VPRRAPALLVALGWSMGWAPPQPLAWV LSPSLPGAGSADWLLQVRGPPSPRPPGTP AGPPAPCAALVPARVSPSTLPS |
| 2652 | 10703 | A | 3577 | 82 | 361 | LRSPAGFTQWIRTGAAGGAACQFRAVRP ALLSPWVVDGTGRRGAGGGAYRGGSG RTGAHGTGGGSGMACRSRAVPRRCAA KTRPCEVQKRQHNVNLYFPVVETKAQT VKWFVLA*ASPCSVGSCAARASPIAAP CSTAPSPIDHPRAECWAHGTLAGSSTC SPGADPLGEASWAPE |
| 2653 | 10704 | A | 3578 | 806 | 934 | KILSSKFPFSFLPSYVCTSSFP*THPSIIST SSSSHVPTN |
| 2654 | 10705 | A | 3579 | 1034 | 1393 | AVTLTGKVCSTPEASETTNPPGGTNN RRASLRAATLTVKVRSTPRGSAASFFKS VRPRTHQFRTQYSPRMSKIRDCSRSCFI SFLASWRIICLL*VLISLCAW*RYRLF LPSS |
| 2655 | 10706 | A | 358 | 4627 | 5052 | LSTKAPRKDTLNFNKCWENWISICRRLQ LGSYLLPY*KINQKWIKGLNDRSETMKL LKENIGEMLNIGLGKDFMVKTSKA*AT KQKIGRWDIKLIKICTAKKT/IRVKRPTV DGNNIFKLSNRGLISRVYKEHNSTVKKK KK |
| 2656 | 10707 | A | 3580 | 529 | 750 | REFRVGVASADPAFGAAGRCPQGG*G A*HTGQWLRRVYVWPQQCQPTGVALDF SPGLSCLPAGQSGSPAARHA |
| 2657 | 10708 | A | 3581 | 2 | 343 | HAVFFISIRSFMFFFLVILVSNSSKLFSTF LVSLHWVRTCSFSSEEFVITHFLKPTSVN SSNSFSVQFCSLAGEEL*SFGGEEAFWFL EFSALHWWFLIFMDLSTFGLCCC |
| 2658 | 10709 | A | 3582 | 289 | 422 | |
| 2659 | 10710 | A | 3583 | 189 | 309 | |
| 2660 | 10711 | A | 3584 | 587 | 801 | |
| 2661 | 10712 | A | 3585 | 76 | 1740 | SLLTAASSFQQLKQSSHLSPSGWDYR LRMTQNKLLKCSKANVYTEVPDGGWG WAVAVSFFFVEVFTYGIKTFGVFFNDL MDSFNESNSRISWIISCVFVLTFSAPLAT VLSNRVLGHLVVMMLGGLLVSTGMVAA SFSQEVSHMYVAIGIISGLGYCFSFLPTVT ILSIFYGTRRSIVTAVAISTGECFAVFAF APAIMALKERIGWRYSLFVGLLQNLNVI FGALLRPIFIRGPASPKIVIENRKEAQY MLENEKTRTSIDSIDSGVELTTSPPKNVPT HTNLELEPKADMQQVLVKTSRPPSEKK APLLDFSILKEKSFICYALFGLFATLGFFA PSLYIIPLGISLGIDQDRAAFLSTMAIAE VFGRIGAGFVLNREPIRKIYELICVILLTV SLFAFTFATEFWGLMSCSIFFGFMVGTIG GLTFHCLLKMMSWALQKMSSAAGVYIF IQSIAGLAGPPLAGLLVDQSKIYSAFYF CAAGMALAAVCLALVRPCKMGLCQRH HSGETKVVS HRGKTLQDIPEDFLEMDLA KNEHRVHVQMEPV |

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| 2662 | 10713 | A | 3586 | 1 | 2472 | GFVFLLLLAPLSRLEFHKSRLKNVFEGL EAEFCFYKVHLDGGEELWVRPDAETT THQGRVSQEKHQALGCKWPKLCGDALC VILSAPSPIDHPKAECCRARRDWAAPP AAPVRDPLGEASWAPESGQOMKEAAEL GVSCMGPDLEKLTLYEVKLRQLQGCKAA QRPLGCTLLAIQGTLYQRIFSPLTQPELV NGKGWHLTQESLSQNGSLEFLTSEPHSP NPNEGSSRRQSLHTNANNMAFASEQFPN LPSGSGSRGFPGRARVLHDCQNCQRLT AGPAQLQGSRAANRRKALVSPSSVARE DGFAEEMVFTYGIKTFGVFFNDLMDSF NESNSRISWIISICVFVLTFSAPLATVLSN RFGHRLVVMLGGLLVSTGMVAASFSQE VSHMYVAIGIISAIMALKERIGWRYSLLP VGLLQLNIVIFGALLRPIFIRGPASPKIVIQ ENRKEAQYMLENEKTRTSIDSIDSGVELT TSPKNVPTHNTLELEPKADMQQVLVKTS PRPSEKKAPLLDFSILKEKSFICYALFGLF ATLGGFAPSLYIIPLGISLGIDQDRAAFL STMAIAEVFGRIGAGFVLNREPIRKIYIEL ICVILLTVSLFAFTFATEFWGLMSCSIFFG FMVGTIGGLTFHCLLRMMSWAL/QKMS SAAGVYIFIQSIAGLAGPPLAGLLVDQSK IYSRAFYSACAAGMALAAVCLALVRPCK MGLCQHHSGETKVVSHRGKTLQDIPE DFLEMDLAKNEHRVHVQMEPVVRRRFA AAGPAGLGAAGDSDAFPAAREGPERRAG YSGPAAACDFSTAAPKREQRGPLSLVG LEM |
| 2663 | 10714 | A | 3587 | 323 | 1303 | STLYLPAMDNTNQEIPDLLALGTSAWSS TLAALEEFPSLPLHCGSPFLGWSRPELAP SACREVWREKPEWELGLRTVLAGQCEF RVGVGSGDSTRSSWPPLAPGNEGLSTR ASSCGGCTGSPSRAGPPVLCISQCQALAA FPRGRARGLQAPAMPEPPRLRGLLCSPEP PRLVPPAPGHPVPLTTQGLRSTGKTHR DWQAAPPAAPVRDPLGEASWAPESANL VGKWRFTVSSSGTANAPISTLSKQTTGL YQSAGCGWGQNLGAKYRA/LCRPVKSD *HGRQTKDTGVRLSGKGLSNP*LFRVG TVGSHRPHFTYMDGLASGV |
| 2664 | 10715 | A | 3588 | 1 | 3552 | |
| 2665 | 10716 | A | 3589 | 375 | 646 | KKSLLSINSRLQLVMKSGKYVLGKYQT LKMIROGKAKLVILANNCPALSGNNIEL GTACGKYRVCTLAIDPGDSDIIRSMPE QTGEK |
| 2666 | 10717 | A | 359 | 1 | 366 | KKQIFLELISIYSRVAGYKNTQKSVAFLY NSNKQLNL*IK/DTMPFILAC/NK*KHLPL NLTK*VQEIYEGNYDTFMK*IED/DKQRN ISSIW*KRFIKMPILPNLIYRYNAFPVKIS ESYLVDI |
| 2667 | 10718 | A | 3590 | 75 | 335 | LRILKFLSCSLSLGWGPSLRLQEDGGR KRRRKKSLESINLRLQLVMKSGKLLPGG TSQTLKMIROGKAKLVILANN/CGPALR KSEIEYYCYVWLKTGC/HHPLTVGNNE LGATA/CGKITRYVLHTGLFIDPG*LLTSF RKACPEQTC*KMVAAKEDEKSRWSRST LGSNSLWKSGKLLPGGTSQTLKMIQTRQ SEMWSFSLTTGPSFEEI |
| 2668 | 10719 | A | 3591 | 1 | 2580 | |
| 2669 | 10720 | A | 3592 | 1 | 1386 | |

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|------|-------|---|------|-----|------|---|
| 2670 | 10721 | A | 3593 | 2 | 1419 | RPPGIRAPRQLHPAAGRPPDASARPRFRP TVLLHDPFQLSFPPLSYPSVFPVAVARV LPQRSGDYRAAGMPQLSGGGGGGGGDP ELCATDEMIPFKDEGDPQREKIFAIVNP EEEGDLADIKSSLVNESEIIPASNGHEVA RQAQTSQEPYHDKAREHPDDGKHPDGG LYNKGPSYSSYSGYIMPMNNDPYSMS NGSLSPPIRPTSNKVPVVQPSHAVHPLTP LITYSDEHFSPGSHSHIPSDVNSKQGMS RHPPAPDIPTFYPLSPGGVGQITPPLGWQ GQPVYPITGGFRQYPSSLSGDTMSRFS HPMIPGPPGPHITIGIPHPAIVTPQVVKQ DHPHHSSDLMHVKPQPEQRKEQEPKRP PTKKPLNAFMLYMKEMRANVVAECTL KESAAINQILGRRWHALSREEQAKYYEL ARKERQLHMQLYPGWSARDNYGKKKK RKREKLQESASGTGPRMTAAYI |
| 2671 | 10722 | A | 3594 | 59 | 435 | STCPAPQSARVQWCNLSLQPPPTPTPR SSNSPASASQIAGVTGVRHHTQLIFVFLV GDGGFHCVGSGWVSNCWPSGWRPLWP HLFLGFHKDLEVVGFLVFASISFRSWRW DLKNSSVLTHFFK |
| 2672 | 10723 | A | 3595 | 54 | 442 | |
| 2673 | 10724 | A | 3596 | 360 | 1023 | GQGRLPERGYLEAGVYRICGRQSRHED GTHRGAQVIEQRRKWLPALGFQPIILQL CGKRVPAPSRASTGQPQASRAWSGPL/P HPQCGSDIRLRVRAEYCEHGALEQGV SRRPQALARQLDVFQATAVLRSDLG VVCDFKFSLSYLDFAFWGDYLSGALLQA LRGVFLTEALREAVGREAVRLLVSDEA DYEAGRRLLLMEEEGRRPTEAS |
| 2674 | 10725 | A | 3597 | 3 | 370 | QMYCVFNREDACRY/GS/AIGVLAFLAS AFFLVVDAYFPQISNATDRKYLVIDLLF SGVLAFLAYQRYKAGVDDFIQNYVDPT PDPNTAYASYPGASVDNYQPPFTQNAE TTEGYQPPVY |
| 2675 | 10726 | A | 3598 | 1 | 1356 | |
| 2676 | 10727 | A | 3599 | 3 | 706 | GGSGGDGDMESGAYGAAKAGGSFDL RRFLTQPVVARAVVLIVFALIVFSCIY EGYSNAHESKQMYCVFNREDACRYGS AIGVLAFLASAFVLVDAYFPQISNATD RKYLVIDLLFSALWTFWVFGFCFLT QWAVTKPKTVLVGADSVRAAITFSFSI FSWGVLASLGIYQRYKAGVDDFIQNYV DPTDPNTAYASYPGASVDNYQPPFT QNAETTEGYQPPVY |
| 2677 | 10728 | A | 36 | 2 | 424 | |
| 2678 | 10729 | A | 360 | 241 | 583 | NGPPFFFFFEMEFSLLLPRLECNGAISAH RNLRLPGSSDSPASAGLL*SQVAGITRL RHHD*LILY/FLVEMRFHRVG*AGLELLT SGDPPSSASQGAGITGMSHSAGHYGKIF |
| 2679 | 10730 | A | 3602 | 1 | 171 | RILMAINGKVFDTVTKGRKFYGPVKYHH VGKLLTAGEEPAVYSDEEEKDESARK ND |
| 2680 | 10731 | A | 3603 | 3 | 253 | LSLQEFGTSFAGRDSRGLATFCLDKEA LKDEYDDLSDLTAAQETLSDWESQFTF K/LLKEGEEPTVYSDEEEKDESARKND |
| 2681 | 10732 | A | 3604 | 3 | 701 | PARHSLAQREEKVASSGSLPSAAQPLLSE IMAAEDVATGADPSDLESGLLHEIFT SPLNLLLGL/CIFLLYKIVRGDQPAASG DSDDDEPPPLRLKRRDFTPAELRRFDG VQDPAPYSWAINGKVFDTVTKGRKFLT GPEGPYGVFAGRKCIQALPTFLLDKEA LKDEYDDLSDLTAAQETLSDWESQF TFKYHHVGKLLKEGEEPTVYSDEEEKD ESARKND |

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| 2682 | 10733 | A | 3605 | 3 | 678 | KRLPKMAEVQVLVLADGRAHSSLGRLA/ AIVAKIQVLLGRKVVVVVARCEGNNISGNF YRWKLLKYLGFPPPSGMNTNPSRGPYHF GAPSRILLAGTVRGMLPHKTKAEAKAA LDRLKVFDPGPYPYGQEKSGMVVPA LKVVRULKPTRKFCLIWGRLAPEVGWK YQAVTATLEEKRKREKPRFHYRKKENSI MRLARKQAREETWRKKIDKYTEVLKTHG LLV |
| 2683 | 10734 | A | 3606 | 114 | 353 | |
| 2684 | 10735 | A | 3607 | 104 | 342 | |
| 2685 | 10736 | A | 3608 | 211 | 241 | NFNGRGGLAAGRKKPDWLDSTLNS*PS H |
| 2686 | 10737 | A | 3609 | 37 | 116 | |
| 2687 | 10738 | A | 361 | 654 | 942 | CHACNPQHFRPRQVDHLRSGV*DQPG QHGETPSLLKNQKLAGEHGGVHL*S*LLR RLRQENRLNLGGGGCSEPRSHHCTPAW VTE*DSVSRRKKKK |
| 2688 | 10739 | A | 3610 | 104 | 516 | ALSSRGVMAEYGTLLQDLTNNITLEDLE QLKSAFKEADIPSEKSEEITGSAWFSFLE SHNKLDKDNLSYIEHIFEISRRPDLLTMV VDYRTRVLKISEDELDTKLTRIPSAKKY KDIIRLPSEEEIKLAAPPPKKA |
| 2689 | 10740 | A | 3611 | 569 | 838 | PTVLWEPPSFPPPPQGIPIHSG/PDILTGR RRASPSGLCYSENGGLEEGSTRPPAH/S PGATVSSPPPPPPSSSLPCCLGNRHFD RV |
| 2690 | 10741 | A | 3612 | 268 | 356 | |
| 2691 | 10742 | A | 3613 | 489 | 605 | QLQVCYCT*RPYSGTRCGVSNVQLLCS LLSHLCCSAS |
| 2692 | 10743 | A | 3614 | 391 | 561 | |
| 2693 | 10744 | A | 3615 | 367 | 855 | GARRQAHTMALKRINKELSDLARDPPA QCSAIGPVGDDMFHWKATINGDLMDK PIFKGGVFFLTTHFPTDYPFKTPKVAFT TRIHYPNINSNGSICLDILRSQWSPALTIS KVLLSICSLACDPNPDDPLVPEIARVY KTDRDKYNRISREWTKQYAM |
| 2694 | 10745 | A | 3616 | 1002 | 1480 | MLLLKTTERFEVSVMCTYVSNLGGK QRSVSFLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSKRVAHP FSPGPACFLLCDLARVGSPPKINRVPHFT RTQTSTQRSCTVFVWQRCSLVGPQVTV FTMYFHHSLSRSIRFSSG |
| 2695 | 10746 | A | 3617 | 223 | 415 | |
| 2696 | 10747 | A | 3618 | 1 | 858 | |
| 2697 | 10748 | A | 3619 | 144 | 1339 | DPEQPDMEQPWPPGPWSLPRAEGEAE ESDFDVFPSSPRCPQLPGGGAQMYSHGIE LACQKQKEFKSSVACKWNLAEAQKQL GSLALHNSESLDQEHAKAQTSIRTEGN GKKNRQKEEALRQREKMLCWSTDAI SKDVFNKSFNQDKRKDEDEKSESFM QKYEQKIRHFGMLSRWDDSQRFLSDHP YLVCEETAKYLILWCFHLEAEKKGALM EQIAHQAVVMQFIMEMAKNCNVDPGRC FRLFFQKAKAE EEGYFEAFKNELEAFKS RVRLYSQSQSFQPMTVQNHVPHSGVGS GLESPLQNPDLQYSISTALCSLNSVVH KEDDEPKMMGHCIWVKTA EAKCYFVT GKGGTWAIFLDTFMGLALYFCSVFDG RERV LKCFVNFF |
| 2698 | 10749 | A | 362 | 1 | 2322 | |
| 2699 | 10750 | A | 3623 | 44 | 420 | |
| 2700 | 10751 | A | 3624 | 20 | 421 | |
| 2701 | 10752 | A | 3625 | 1 | 346 | LRPQSAQSSFPSPGSPDVQLATLAQRV KEVLPHVPLGVIQRDLAKTGCVDLTITN LLEGAVAFMPEDITKGTQSLPTASAKF/ PRQESLQERKQALY EYARRRFTERRAQE |

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| | | | | | AY |
| 2702 | 10753 | A | 3626 | 162 | 461 |
| 2703 | 10754 | A | 3627 | 39 | 260 |
| | | | | | DCKPVARPSTKAKTDQSGPFLSLLPHRY LSLSLTLRSSPESMTWCWMEGREKESA SQ*VTTTFRASMSSYTA |
| 2704 | 10755 | A | 3628 | 1 | 2160 |
| | | | | | FRPGAPEAAVMELSSWPGERLFDHSHRL PGDCFLLLVLLLYAPVGFCLLVLRFLGI HVFLVSCALPDSVLRFRVVRTMCAVLGL VARQEDSGLRDHSVRVLISNHVTPFDHN IVNLLTTCSTVSESEADSATVRFGAQLK APLSPLAFPMEDTEALPLTPILYPTCQFFF FIFLNIFLLAFSSPGSQPLLNKSPQAFVIC WSRGFMEMNGRGEVLSLKRFCSTR LPPTPLLLFPEKKATNGREGLRFSSWPF SIQDVVQPLTLQVQRPLVS/VGECVLNRE SLGLEGEISHPWWRPHLMPSQTVSD ASWVSELLWSLFPFTVYQLVAKELGQT GTRLTPADKAEHMKRQRHRLRPQSAQ SSFPSPGSPDVQ/IWATLAQRVKEVLP H/VGPLGVIQDLGMGKGPTLGDGHRE EKWVVKETKTGCVDLTITNLEGAVAF MPEDITKGTQSLPTASASKFPSSGPVTPQ PTALTFAKSSWARQESLQERKQALYEYA RRTFPQVTRSHIISTALEDPCLSKISTTCQ RGNSLRSCQRATMTSQPLRLAEYGPSP GESELAVNPFDLFPSSRYELLKQRQA LPIWAARFTFLEQLESNPTGVVLVSGEFG SGKSTQIPQWCAEFALARGFQKQGVTVT QPYPLAARSLALRVADMDLTGHEVG YSIPQEDCTGPNILLRFCWDRLLQEVA STRGPGKLGRAGTR |
| 2705 | 10756 | A | 363 | 8453 | 9757 |
| | | | | | APCLLGWLSLPSRAKTYAYLFSHPSRMP VYPKWVGADHADDIYVFGKPFATPTG YRPQDRTVSKAMIAWTFNFAKTG*DVG *VQGGGQPRRASHHEALFPHLPVEGLW ASHLTSPCIGIHVCLRMVTRGRAPSPCTC TASAQYAVRGMVPRASSEGGDGSQVQV ESRASAPWESPAPAQPLLTLQDPNMGD SAVPTHWEPTYTENSYLEITKKMGSS MKRSLRTNFLRYWTLTYLALPTVTDQE ATPVPTGDSEATPVPTGDSETAPVPPT GDSGAPPVPPTGDSGAPPVPPTGDSGAPP VPPTGDSGAPPVPPTGDSGAPPVPPTGDS GAPPVPPTGDSGAPPVPPTGDAGPPVPP TGDSGAPPVPPTGDSGAPPVPTPTGDSETA PVPPTGDSGAPPVPPTGDSEAAPVPPTDD SKEAQMPAVIRF |
| 2706 | 10757 | C | 3631 | 44 | 340 |
| | | | | | MKCSQPXRCHFQSDFOKCAPCPRAQTH WLEPPGRVQTISSMRNAQKGFADSIRLW RLPASGVGWVVSPEGAGDPSHLLDPPGH SAPYSPAPRQLSRVP* |
| 2707 | 10758 | C | 3632 | 2037 | 2426 |
| | | | | | MKCSQPXRCHFQSDFOKCAPCPRAQTH WLEPPGRVQTISSMRNAQKGFADSIRLW RLPASGVGWVVSPIQTQEVAPEGMYLV GSSSGTLGGCRALTQVFLSLSLGCVCA CACACLCFSLWAHQDVSS* |
| 2708 | 10759 | A | 3633 | 184 | 9818 |
| | | | | | IEEPRDTRLQVCSGVHIWCLDKFKMRKH RHLPLVAVFCLFLSGFPTTHAQQQQADV KNGAAADHFLVDSSWTIGEEHFQLVREF LYDVVKSLAVGENDFHFALVQFNGNPH TEFLNTYRTKQEVLSHISNMSYIGGTNQ TGKLEYIMQSHLTKAAGSRAGDGVPO VIVVLTGDHSGDGLALPSAELKSADVNV FAIGVEDADEGALKEIASEPLNMHMFNL ENFTSLHDIVGNLVSCVHSSVSPERAGDT E |

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| 2709 | 10760 | A | 3637 | 312 | 805 | GPQAGSSPEILLPEDNSLIRWAGAGCHTQ DSATTVTASWAPLCAGAGREEDGTPCV CLGRSARPKLVFGRPLRTSAALRPGACIP HGLLCYPREPVDFRPGSGRAWPPRSPSP/ CQDPRPSRSAPGSEPGW/CPDPPAPPRLV TLGRASPHLTLPRAAPPPCRWRP |
| 2710 | 10761 | B | 3639 | 199 | 286 | XSELESALQMEPAAFQALYSAEKPLED EHLVFFCQMKGRLQAHAAAGPESWIHW GSQLRWSL* |
| 2711 | 10762 | A | 364 | 10 | 548 | FRLVLSRLEGIGAILAH*NLCLLGSNDSP ASATRVAGITGRHHAPLIFVFLVEMGF RHVGQAGHKLLISGDPPA/SASQSAGITG VSH/ARLAALSNF*GLGQVPTLKQATLL SLLDTSPLPAIFFLFFF*DRFS/SVTQAEV QWGDHCSLHP*PTGLKIDPPASARLGTT RTRHHSR |
| 2712 | 10763 | A | 3640 | 754 | 1082 | GMVHICCLGAPRTQPFQAQLPNLSAKLL AFPSTLSTPPVSELESALQMDQPAFQAL YSAEKPKEDEHLVFFCQMKGRLQAT QLARSLGYTGARNYAGAYREWLEKES |
| 2713 | 10764 | A | 3641 | 113 | 737 | AGPDSFCNFSVCPSSSTAWILVLAQFLL SPTLLSPRMLTVALLALLCASASGNAIQ ARSSSYSGEYSGGGKRFSGNQLDGP ITALRVRVNTYYIVGLQVRYGKVSQDY VGGRNGDLEEIFLHPGESVIQVSGKYKW YLKEAGYLVPTKGPFLSFGKSKGPSFN AVPLHPNTVVRFISGRSGSLIDAIGLHWG CFHTHTSCSRC |
| 2714 | 10765 | A | 3642 | 1724 | 1818 | |
| 2715 | 10766 | A | 3643 | 1 | 894 | RGESRVLWSELEGEAGGAGGWASSLNA RMDNRFATAFVIACVLSLISTIYMEGVSIG TDFWYEYRSPGQENSSDLNKSIDEFIS DEADDATYNDAFLRYNGTVGFLRRVY SPYPKTLHWVLAHHERTESFDVVTKICV SFTLATEQFMEKFVDPGK/HTNSRGLDLL RTYLWRCQFLFPVSLGFDVLWGALIG LCAICICRSLYPSIATGILHLLAGLCTLGS VSCYVAGIELLHQKLELPDNVSGEFGWS FCLACVSAPLQFMASALFIWAAHTNRK EYTLMKIAYRVGMSKKPACF |
| 2716 | 10767 | A | 3644 | 323 | 898 | |
| 2717 | 10768 | A | 3645 | 816 | 1171 | LFKHFVGPVANWGLPIAAINDMKKSPG DYSVGRMTFALC/CYSILTFMEILPYKVQ PSGTWASCFACHGTNEVRPSFIQEGEGLI PNTRMDLKRASGINQWGKGKNKVFECD SLCPGCC |
| 2718 | 10769 | A | 3646 | 205 | 369 | |
| 2719 | 10770 | A | 3647 | 3 | 451 | CSGAGAEPAAANPRSPRSLVPSLESTSTSV PPAPGTMATDSWALAVDEQEAASG AVVKTNANAECTDEEEKEDRAAQSLN KLIRSNLVDNTNQVEVLQRPNSPLYSG KSFEELRLKPQLLQGVYAMGFNQPSKIQ ENALPLMLAEPY |
| 2720 | 10771 | A | 3648 | 1 | 186 | |
| 2721 | 10772 | A | 3649 | 2 | 261 | SSANNISILGAFRSVTKWLS*THPL*FFCQ CLCLSPTYELALQTGKVEIQMGKFYPEL KLAYAVRGNKCEYGRRQLNSEQGRGLG V |
| 2722 | 10773 | A | 365 | 252 | 934 | LCASRLLPAPMLSLSHRISHPWPVGVH YGC*GGRSGDIGSCRETGLCRGFSPGCI KTSTSPWAPAG*APSTGPGQETCTAHS PFIPAPA*AQGLKF*GVTESICAGAAGTA GGTETAVSAGSPAGQAQPGPGAGQSLSA GSQMA*GSDHPGPIWQTC*SVQGAFLD G*GG*LHPHPP*GPATLPEGGGGVCFAA KNASGATREVPVAVLQAVHAPGATWLRP P |
| 2723 | 10774 | A | 3650 | 1 | 2613 | |

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|------|-------|---|------|-------|-------|---|
| 2724 | 10775 | A | 3651 | 3 | 550 | LCSSR/DEKFKALCNLPG/AITMAQAMIF CHTRKTAISWLAELSKEGHQVALLSGE MMVEQRAAVIERFREGKEKVLVTNVC ARGEQRTCPTWSARLGVPGPIRARNPCI QGSRMVSGRWVGLVTLFLSRDCLDFP EVVRTHTCQVRWLMPAIPRQENCLNPG DRGCSEPRMCYSTPSWVTE |
| 2725 | 10776 | A | 3652 | 1 | 1571 | CRGAGAEPANPRSPRSLVPSLEYTSTSV PPAPGTMATDSWAILAVDEQEAAAESLS NLHLKEEKIKPDTNGAIVVKTNANAECT DEEEKEDRAAQSLNKLIRSNLVNTNQ VEVLQRPNSPLYSVKSFEELWLKQPQS QGVYAMGFNRPSKIQENALPLMLAEPPO NLIAQSQSGTGKTSPLVLAMLSRVEPI RPDTPQCLCLFPTYEAGGFKQKGVIEQM GKFYPELKLAYAVRGNKLERGQKISEQI VIGTPGT/VGLNWCFQLKFIDPKKIKVFV LDEADVMIATQGHQDQSIRIQRMLPRNC QMLLSATFEDSVWKFQKVPDPNVK LKREEETLDTIKQYYVLCSSRDEKFAQAL CNLYGAITIAQAMIFCHTRKTASWLAEE LSKEGHQVVMVLSGEMMVEQRAAVIERF REGKEKVLVT/TPNLCRSGIDVDQVSVVI NFDLPVDKDIGNPDNETYLHRIQRTARF GKVRGLAIVNMVDSKHSMNILNRIQEH FNKKIERLDTDDLDEIEEN |
| 2726 | 10777 | A | 3653 | 3 | 421 | |
| 2727 | 10778 | A | 3654 | 209 | 435 | |
| 2728 | 10779 | A | 3655 | 126 | 775 | APAKVRTAQEDRDTFSSQRTRWKEQNTI DNMALLGPKGLLFLAIFIITSDWIPLGV NSQVRGDDVTQATPETFTEDPNLVNDPA ATDETVLAVLADIAPSTDDLAASLEKNT TAECWDEKFTCTRLYSASGPNQMH FIQLCFHPVLRMYIVQPREICSSVLVC KGTPKPMKDELCRQMAGLPPLGRUARP QLLPDFPPCENVDLQRPNGL |
| 2729 | 10780 | A | 366 | 169 | 457 | SLEVS LGDHFQKCRFLEKRERFWKGMFS FCSMAVSGFLAAGAGLKP RSG/WH*VFH SPRRSWTENFKFQRDEVSASPLGAWRAL TKEKGGAQPLEGL |
| 2730 | 10781 | C | 3660 | 162 | 425 | MVGPSLHAGXXVYIPRFLYIRSWLPCIF FSGGVTVGNIGRQLAMGVPEKPIVIESSK PXILEXGRFLEENLXLVDYXKGLSFFLK * |
| 2731 | 10782 | A | 3661 | 89 | 308 | |
| 2732 | 10783 | A | 3662 | 2 | 454 | |
| 2733 | 10784 | A | 3663 | 570 | 1418 | PMPLRHDHFWSCSAHSARRRGPPRAIA AGLAAKVGEMIIIVFSGPSLMAVLSASD ADPAPRGRSAVKS GYPYGPYPNTWHHS LMQKSLVLFVSGEVLALVNLQIQRV TLFPEEVIAIFSSA WWPICCGTAPAD VGLLYPCIDSHLGEPHKFKERMGOVSMR CIAVFVGINHASAKLDFANNVQLSLTLA ALSGLWWTFDRSRSGGLGVTIAFLAT LUTQFLVYNGVYQYTSDFLYIRSWLPCA IFFSGSVTVGNIGRQLGYGVFLEKPHSD |
| 2734 | 10785 | A | 3664 | 195 | 462 | RIFSMTSGRLRWCTWRPATALWSASLR LGTSSMHPSPRSISLP/PVHVHTHNSGKE VLGLQVQRSGTG PACSQAGSGAVQG GNWCIF |
| 2735 | 10786 | A | 3665 | 12102 | 12327 | |
| 2736 | 10787 | A | 3666 | 535 | 992 | RIFSMTSGRLRWCTWRPATALWSASLR RLGTSSMHPSPRSISLPLSMMLSPLPS NTRGLSPTALVRSPNSEHATSCPRLHL WRCRAPLRSPSPLGRLP GATPGVP SHVH TVHNSGKEVLGLQVQRSGTG PACSQA GSGAVQGGNWCIF |
| 2737 | 10788 | A | 3669 | 76 | 419 | |

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| 2738 | 10789 | A | 367 | 186 | 370 | QIRETS GTGT*YTSASQSAGIEVSHHAR QMFQFYSQKYTLNCKL*ILMFKIKFFL TQK |
| 2739 | 10790 | A | 3670 | 71 | 350 | AFIPAMAELIQKKLQGEVEKYQQLQKDL SKSMSGRQKLEAQLTENNIVKEKRYES QLRDLERQSEQQRETLAQLQQEFQRAQA AKAGAPGKA |
| 2740 | 10791 | A | 3671 | 334 | 1191 | GLLPHLGPRVQRLPRLSLSTLACGLTRGP HPFLLPOIHIHLTRIVGIGGTFDVSKLPFL SSPDLSKMSGRQKLEAQLTEYNIAKEV RDWDLWGEEGPVLAMVLITYVPSLHQE LALLDGSNVVFKLLGPVLVKQELGEARA TVGKRLDYITAEM*VFIPPPCAAPCDASE PLE*RC*TIAEQLSIVAPSPVPPTLSFPF*P PFFSLPWISRFSTYLFALFSTLHSESY*FLP FCLSPSLSKRYESQLRDLERQSEQQRE TLAQLQQEFQRAQA AKAGAPGKA |
| 2741 | 10792 | A | 3672 | 210 | 617 | AFIPAMAELIQKKLQGEVEKYQQLQKDL LSKMSGRQKLEAQLTENNIVKEELALL DGSNVVFKLLGPVLVKQELGEARATV GKRLDYITAIEIKRYESQLRDLERQSEQQR ETLAQLQQEFQRAQA AKAGAPGKA |
| 2742 | 10793 | A | 3673 | 3 | 266 | |
| 2743 | 10794 | A | 3674 | 31 | 500 | ARVTA AVSAAVAKRVWRDGFDCSGY YSLTILLVQPTKRPAEGRTYADYESVNE CMEGVCKMYEEHLKRMNPNGPSI/TH NTTSQLFDFIDDLADLSCLVYRADTQT YQPYNKDWIKDEPTVLLSSGKAQQA REIIVGSHWGGWGGAWDTGV |
| 2744 | 10795 | A | 3678 | 1 | 134 | |
| 2745 | 10796 | A | 3679 | 162 | 437 | RRGLFPAGPGPRQEPSRASSPMPSELRN IKD/FLLTARRKDAKS/VKIKKNKDNVVK FKVRCRYLLHPWSSPDKEKAELKQS LPPRF GK |
| 2746 | 10797 | A | 368 | 150 | 799 | QC*DPETSETV*EKL RAGRHRQRCCHGGQ SCFDKSATRALPPPRKWRHRGTRCAATK RTRLGEMAVLGP*E*RQPEEFRTTSILA EPTVLSRRKCRPSEKRGSA TEKFGATSA VTENPPLGAAGERANKTL/RCCHRD TDF RTPASDGERRRSHTGEPINRSLAMRMGK GGSIGTENRADWAGPGCKVCESCS/RVL HLCVYGSHHRIWHMEGYQHMLV |
| 2747 | 10798 | A | 3680 | 60 | 216 | |
| 2748 | 10799 | A | 3681 | 505 | 794 | NVVECLFKDALPQLSADRFLASSILLGDL GVVEVHFVSNSLTGEELWHLLRSTSLGI ASPPHIEVPFLEVDGDRTKTQVFPLTNLH VRAHASAHAS |
| 2749 | 10800 | A | 3682 | 685 | 1484 | LRLTFPEFSHTKVRTMSLFPSPPLLLLSM VAASYSETVTCEDAQKTCPAVIACSSPGI NGFPGKDRDGTGKEKGEPGQGLRGLO GPPGKLGPPGNPGPSGSPGPKGQKGDGP KSPDGDSSQAASERKALQTEMARIKKW LTFSLGKQVGNKFFLTNGEIMTFEKVKA LCVKFQASVATPRNAAENGAIQNLKEE AFLGMPDEKTEGQFVDLTGNRLTYTNW NEGEPWNNAGSDEDCVLALLKNGQWND SPCISTSHLAVCEFP |
| 2750 | 10801 | A | 3683 | 427 | 751 | |
| 2751 | 10802 | A | 3684 | 31 | 558 | EFVPHSEKMLYDQAQLAVAYLYAFQLS GDEFYSDVAKGILQYVARSLSHRSGGFY SAEDADSPPERGQRPKEGAYYVWTVKE VQQLPEPVLGATEPLTSGQLMKHYCL TEAGNISPSQDPKGETCRARMLDRPVL RWELTAARFGLDV/EKAVRLLNTGLEK LFQARKHRPKP |

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| 2752 | 10803 | A | 3685 | 3 | 399 | KCVCLLTAFSERMRRVPVALPEMVRALS AQQQTLKQIV/VWRPSSGQRTPKALVQC VHSVYIPNKVLILADGDPSSFLSRQLPFLS TLRRLLEDQATAYVCENQACSVIPITDPCE LRKLLHPLTCPYPLGWGR |
| 2753 | 10804 | A | 3686 | 2 | 2238 | NVAAMLGARAWLVRVLLLPRAGAGLA ASRRGSSSRDKDRSATVSSSVMPAGGK GSHPSSTPQRPVNRILIHEKSPYLLQHAYN PVDWYPWGQEAFFDKARKENKPIFLSVG YSTCHWCHMMEEESFQNEEIGRLSEDF VSVKVDREERPDVDKVMYTFVQATSSG GGWPMNVWLTPNLQPCVGGTYFPED GLTRVGFRVLLRIREQWKQNKNTLLEN SQRVTTALLARSEISVGDRQLPPSAATVN NRCFQQLDEGYDEEYGGFAEAPKFPTPV ILSFLFSYWLHRLTQDGSRAQQMALHT LKMMANGGIRDHVGQGFHRYSTDRQW HVPHEKMLYDQAQLAVAYSQAFQLSG DEFYSDVAKGILQYVARSLSHRSGGFYS AEDADSPPERGQRPKEGAYYVWTVKEV QQLLEPVLGATEPLTSGQLLMKHYGLT EAGNISPSQACELADKGHSPQDPKGELO GQNVLTVRYSLELTAARFGLDVEAVRTL LNSGLEKLFQARKHRPKPHLDSKMLAA WNGLMVSGYAVTGAVLGPRLQNYAT NGAKFLKRHMFDAVSGRLDADLLHRH LGGLWSTATPPCWGFLEDYAFVVRGLL DLYEASQESAWLEWALRLQDTQDRFLW DSQGGGYFCSEADWGAGLPLRLKDAQ DEAEPSANSVSAHNLLRLHGFTGHKDW MDKCVCLLTAFSERMRRVPVALPEMVR ALSAQQQTLKQIVICGDRQAKDTKALGA VRPLCLHS |
| 2754 | 10805 | A | 3687 | 5 | 188 | |
| 2755 | 10806 | A | 3688 | 132 | 341 | GFTSFISRLSCLSFCLLLET/CPVTCWCWE APRCNQKCTDPAARRDPQTCASQDRLR CAPCTCHQPLASR |
| 2756 | 10807 | C | 3689 | 4 | 204 | MCFQRKSYFHIQTLYCPLICISALRYSTG PAPAMWKCHTAPVQKDWLTPITLISS PNFLTINL* |
| 2757 | 10808 | A | 369 | 1200 | 1678 | RYKLLSYRKPETAIEQKENIPFQNLRSFS KNLHFWK*SPKETSRLYHECLQLNSSCLI LTLAYPVQII/CHLFLDEPGRMSDQRRQA NVPEMGFHHVGG/ACLNLSTSDRPASAS QSARIEVSHHARQMFQFYSQKYTLNCP CKL*ILMFKIKFFLTQKQN |
| 2758 | 10809 | C | 3690 | 57 | 209 | MEVXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXGRLLFGPL* |
| 2759 | 10810 | A | 3691 | 363 | 424 | |
| 2760 | 10811 | A | 3692 | 2 | 264 | KFSLIKLRKENFPTARICRLVYPLYPLKIF IFPKALNFCREVGPIPPPKK/GSFPKIPK AFNRPLRKKIIPSQPALNWGPVRP |
| 2761 | 10812 | A | 3695 | 2 | 201 | GRVGSQSCQRRQQGDTKRRRLSSYPWR RRQRWRRRR/TSSRRKPQFLRQRQRPRQ ARRRWRATRA |
| 2762 | 10813 | A | 3696 | 31 | 445 | EKAVVTSAASSLVYTVYTAQAPRPSFHP FCSTWSAKEPNTTAGEGGSTNECQLSA /CPGANCPGLGTLKSPQNCPSLPRPPLP ACRGSYESVWARLLQSVHAIQRRRES WSPKLYWVHPPQEVVGAFTFLFLV |
| 2763 | 10814 | A | 3697 | 73 | 404 | AYSRTSSLSTMNQTAILICLIFLTLGI QGVPLSRTVRCTCISISNQPVNPRSLEKL EIPASQFCPRVEIATMKKKGEKRCCLNP ESKAIKNLLKAVSKERSKRSP |
| 2764 | 10815 | C | 3699 | 250 | 495 | |
| 2765 | 10816 | B | 37 | 44 | 307 | MVAVSCRQRPTSRPAWGKVGHAHAVRS MCAEALERMFLSFPTTKTYFPHFDLSHG FCPGLRATGKKVADALTNVAHVGRHA |

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| | | | | | | QRRCP* |
| 2766 | 10817 | A | 370 | 1 | 1107 | MTLEATHLLLRVLLVLLASGGSFQSP VKSILGVAVTVVLLLLLALLNRYLQK ARGRARKPYTEDVSVDKKTETWEWAR GEGESYHVYDDVQKEKTTDRMIRSSM CVHKINTSVSMCAQETPNSSKAKLGQK IPVQKDEILHKALCFCPWLKGKGMPL RLILLFVTELSGAHNTTVFQGVAGQSL QVSCPYSMKHWGRRKAWCRQLGEKG PCQRVVSSTTCGLLSFLRRWNWEHSHS QTIPWGGTLTITLRNLQPHDAGLYQCQS LHGSEADTLRKVLVEVLADPLDHRDAG DLWFGDLRASRMPMWSTASPLRAR EGR*WEEKPRRSPTRDQPSLHTCHLATR TPCSALARDYSA |
| 2767 | 10818 | A | 3700 | 226 | 854 | RVPGLNMSGIALSRLAQERKAWRKDH PFGFVAVPTKNPDGTMNLMNWECAIPG KKGTPWEGGLFKLRMLFKDEYPSPPKC KFGPPLFPNCVTSGASCLSFLEEDKDW RPAITIKQILLGIQELLNEPNIQDPAQEA YTIYCQNRVEYEKRVRAQAKKFAPSCRS SLEPSRTWAVLLLSLRPQVSVLRHFLC VYMAFCLCCCLE |
| 2768 | 10819 | A | 3701 | 813 | 1637 | TCQGIALSRLAQEYKAWRKDHPFGYN AVPTKNPDGTMNLMNWECAIPGKKGT PWEGGLFKLRMLFKDDYPSPPKCKFE PPLFSPRIVYPSGAKCACPSLEEDQRTW RPSFTIQTFRLLRNYRNLKWNPNIQDP SFQAEAYTIYCQNRV/ESYEKRVSTKP RKFCAPHKQRPCGNRQKERDWFQELV YNIFCKSKVCSHTMTSHLGGVGRAPSSH CPPRGVRSRIRLNCVSIQGSFLRCFCIF GLLCKTRLFILMSSISTAVKL |
| 2769 | 10820 | B | 3702 | 236 | 362 | KQEPQIPCQGGKDAAVLQGSQPSLAGIR TTRLRDPSSKKWPKGX* |
| 2770 | 10821 | A | 3703 | 1 | 808 | TPPFLAMAPALLIPAALASFILAFGTGV EFVRFTSLRPLGGIPESGGPDARQGWL AALQDRSILAPLAWDLGLLLFVGQHS MAAERVKAWSRYFGVLQRSLYVACTA LALQLVMRYWEPIPKGPVLWEARAEPW ATWVPLLCFVLHVISWLLIFSIFLVDYA ELMGLKQVYYHVLGLGEPLALKSPRAL RLFSHLRHPVCVELLTVLVVPTLGTDR LLAFLTLVGLAHGLDQDLRYLRA QLQRKLHLLSRPDGEAE |
| 2771 | 10822 | A | 3704 | 221 | 1728 | GQAGCSDTMGSCCCLNRDSVPDNHPT KFKVTNVDEGVELGSGVMELTQSELV LHLHRREAVRWPYLCLRRYGYSNLF ESGRRCTGHGIFAFKCSRAEIEFNLLQD LMQCNSINVMEEPVIITRNSHPAELDPR APQPPNALGYNVSSFSNGCPGEGPRFSA PQRLSTSSLRHPSLGEESTHALIAPDEQS HTYVNTPASEDDHRRGRHCLQPLPEGQ APFLPQARGPDQRDPQVFLQPGQVKFVL GPTPARRHMKVCQGLCPSLHDPHHNN NNEAPSECPAQPKCTYENVTGGLWRGA GWRLSPEEPGWNGLAHRAALLHYENL PPLPPVWESQAQQLGGEAGDDGDSRDG LTPSSNGFPDGEEDETPLQKPTSTRAAIR SHGSFPVPLTRRRGSPRVFNDFRRPGPE PPRQLNYIQVKLKGWGGDRPKGPQNP SPQAPMPTTHPARSSDSYAVIDLKKTVA MSNLQALPRDDGTARKTRHNSTDLPL |

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| 2772 | 10823 | A | 3705 | 1143 | 1849 | PAILSPNLDDLNFVSVRASVPTLAPSAPSA SSSPARIPAATROGRRSPRIPPAPSNEASP APGRPRVPGAAVPRFPKPTIQASGADRA VDCGILKLQKSPARLARPRWRPSPKRF WSAAGSVEEQPKPPKAP/PAKSPEQSPQL SVLPLATITPQAYGASFEKMKNLKTRRG GRSRWHFFPNVIPQAPSLKWGFQTS SAEVFHVDRSLASHKMGPGRRPRSPLW APFFWNPRH |
| 2773 | 10824 | A | 3706 | 130 | 360 | SLPKKKNPDLHGFGVGFYQTFKEKIPASS SSNKF/PQDIYEASITL/TPKPDQDFRKKEN CSSVSLIIFPEINKILEN |
| 2774 | 10825 | A | 3707 | 46 | 292 | DQASSNGVMTIARRNPDTLRLFLPDEAR SLPPPCLTDPRLLYIGFLGYCSGLIDNVI RRRIATADKKTYGEIFEKHFPIR |
| 2775 | 10826 | A | 3708 | 269 | 476 | STCLGLPRCWNRYRREQRLVYM*FVHL YYF |
| 2776 | 10827 | A | 3709 | 448 | 894 | DQASSNGVMTIARRNPEPLRFLPDEAR SLPPPCLTDPRLLYIGFLGYCSGLIDNVIR RRPIATAGLHRQLLYINGLFLLGYL VKREDYLYAVRDREMFYGNLHPEDF FLKEDKKTGEIFLKNSHPHTLKVLQKC LAPSFH |
| 2777 | 10828 | A | 371 | 2 | 1309 | EQQDLQDPLEVFHPTVEAAEALHIQEP GGEPSQPTQLPGGAPNTRPPHOGALWS V*RAPEQELHQDGRQPTG*QWLRTCSLG WPEAQLPAHLIGQADWPSQRPP*DPE*TP PRPQQNPGPSNWRCTFATPSTGWA*AT TQIRMIENGKPELPGPPSGEVPLGQQQVG PGVPSGFPQPAPPGLILHSNNIHSQGV FNEFLFPWFGGGEAGPYNGHSASSTTP CPTGRCKPATFRRRH*PPGHPVWATTKS RGM/TAATAGPQWGLGNTARHPDGEA EPGS*ARAQLASNPAPHLRVP*PQLRLPH SPPFPWVPKGRWTQRPEGMTCYAWAH ELRPALPPQPPRGTP*SFFLVHSPACPAQ ALPPNLYCPGGGWEVEAQHPAQMTVPF LEAPHPHWPTGG*VSPYPSGPAQGGGAAS EVGGCLSIKETPCNV |
| 2778 | 10829 | A | 3714 | 1 | 948 | |
| 2779 | 10830 | A | 3715 | 644 | 2034 | AIETQAITDNCSEERKTFNLNVQMNSMD IRCSDIHQDGTQGPSVIAFISYSSLGNIINA TFFEEMDKKQVYLNQVVSAAIGPKR NVSLSKSVTLTFQHVKMTPTKKVFCVY WKSTGAG/CSQWSRDGCFLIHVNKSH MCNCSHLSSFAVLMAITSQEEDPVLTVI TYVGLSVSLCLLALALTFLLCKAIQNT STSLHLQLSLCLFLAHLFLVAIDQTGHK VLCIIAGTLHYLYLATLTWMLLEALYL FLTARNLTVVNYSSINRFMKLMFPVGY GVPVAVTVAISAASRPHLYGTADRCWLH LDQGFMSWFLGPVCAIFSANLVLFILVF WILKRKLSSLNSEVSTIQNTRMLAFKAT AQLFILGCTWCLGLLQVGPAQVMAYL FTIINSLQGFIFLIVYCL/LSAQQVQKQY QKWFREIVKSKSESETYTLSSKMGPDSK PSEGDFVPRTSEEKIL |
| 2780 | 10831 | A | 3716 | 1 | 451 | FFFFFVRQDLALSPRLECNGIIFAHCNLC LPDSSDPP/TSAFQVARTTGRNYYAQLNL YFFVETEFAMLTRAGLNLSSRGPLASA SQSVG DYRN SHHAQLIFCIGRDRIVSL WCPEWSQTPEFKRSACLPCWDYRGEP PHPVPSAL |
| 2781 | 10832 | A | 3717 | 1 | 5898 | |
| 2782 | 10833 | A | 3718 | 1 | 333 | |

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| 2783 | 10834 | A | 3719 | 1 | 5699 | VNDNTNTAGSPGEVLSRRRCVNLLKTALR PDMWPKSELKLQWFDKLLMTVEQPNQV NYGNICTGLEVLSFLLTVLQSPAILSSFKP LQRGIAACMTCGNTKVLRAVHSLLSRL MSIFPTEPSTSSVASKYEELECLYAAVGK VIYEGLTNYEKATNANPSQLFGDQGSW VTLAPGTLMLKSACSNPSYIDRLISVF MRS LQKMVREHLNPQAASGSTEATSGT SELVMLSLELVKTRLAVMSMEMRKNFI QAIL |
| 2784 | 10835 | A | 372 | 475 | 928 | NLVACSLPISPETLSPVPLATPKPSGLLALS LGLAFLSCPGLATPSPLPTKPGGTAGPPQ PCPCSGLAPQTLYL SRRRLGGWRPSIPAQ MTPINRPESQTPVFLEAPHWPTGG*VS PYPSGPAQGGAAASEVGGCLSIKETPCNV KKKKKK |
| 2785 | 10836 | A | 3720 | 109 | 11749 | ARRGERRLVELMDPILFSGEANQPKRKM AFVATQGATEVDQTTLMKKYLQFVAAL TDVNTPDETKLMMHEVSENFENGTSPP QYSTFLEHIIPRVLTFLQDGEVQLQKEP AQQLRKL VLEIHRIPTEHRLRPHTKNVL SVMFRFLETENEENVLICRLIIEHLHKQFR PPITQEIHHFLDFVKQIYKELPKVVRNYF ENPQVIPENTVPPPEMVGMITTIAVKVNP EREDSETRTHSIIPRGSLSLKVLAEAL |
| 2786 | 10837 | A | 3721 | 106 | 11708 | |
| 2787 | 10838 | A | 3722 | 2 | 581 | RRFERRMPRPHEVYTPPLVLQPLSLVSP WKSSQHIFARVLNTNIDGRRKNSPLPITA HLRVWARRYAHVVLRKADIDLTKRAG ELTVEDEV E RVIT/ISMQNPRQYKDPKTG FFEQDKKDVKDWKITARVLAQVWWTTS SRERPGSRLEERFRAHKKGLARHFLGGLS CSEGOAHPRTWPAVGRHRGASAGARR |
| 2788 | 10839 | A | 3723 | 6 | 297 | GIRPRKREQAASEADKGPKEPLEYGKA KLSFQSCCEGKAFQRHDLARHRSHLH LKDKARPFQCRYCVKSFTQNYDLLRHE RLHMKRRSKQALNSY |
| 2789 | 10840 | A | 3724 | 201 | 403 | |
| 2790 | 10841 | C | 3725 | 78 | 422 | |
| 2791 | 10842 | A | 3726 | 591 | 966 | EVLVTMALTRPSAASSKPQSPSPWQCPL DSSHWPPSV A HLPTSYSGREYGDKHTLSK RELKELIQKGAPPLASKLQDAEIARLM EDLDRNKDQAEVNFPRKYVTFPGGAF ESTIEGLKRVEK |
| 2792 | 10843 | A | 3728 | 165 | 828 | KEKARGRPKPLLLL PITSATTAMGLTISS LFSRLFGKKQMRILMVGLDAAGKATIL YKLKLG EIVTTIPATIGFVKTIGYRNICF HSMGMLGGPDRIRPLWKHYFQNTQGLI FVVDSNDRERIQEVADELHKMLLVDEL RDPVLLLFANKQDLPNAMAISEMTDK LWLQSLRNRTWYVQATCATQGTGLYEG LDWLSNELSKQLNEIGYLTQGPWFG |
| 2793 | 10844 | A | 3729 | 191 | 1574 | GVSQRDLTRLFGFSSPQLKKLD AWLS EDMNYARFITAASARRNPSPIRTMTDILS RGPKSMISLAGGLPNPNMFPKTAVITVE NGKTIQFGEEMMKRALIQSPSAGIPELL SWALKQLQIKLHNPTTIHYPPSQGMDLC VTSQSQQGLCKVFEMIINPGDNVLLDEP AYSGTLQSLHPLGCNIINVASDESGIVPD SLRDILSRWKPEDAKNPQKNTPKFLYYC FQMGNNPTGNSLTSEKKEIYELARKYD FLIIEDDPYYFLQFNKFRVPTFLSMDVDG RVIRADSFSKIISSGLRIGFLTGPKPLIERV ILHIQVSTLHPSTFNQLMISQLLHEWGEE GFMAHVDRVIDFYSNQKDAILAAADKW LTLGLAEWHVPAAGMFLWIKVKGINVK VELIERKRPLKMGVLMPLGN AFLRRIAQ LPSPYLRASFSSASPEQMDVAFQVLAQ LIKESL |

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| 2794 | 10845 | A | 373 | 2 | 643 | PICLFSRPTLRPSRSKVSLEIEGRGANMAA RWRFWCVSVMVVALIVCDVPSASAQ RKKEMVLSEKVSQLEWTKRPIVIRM NGDKFRRLVKAPPARNYSVIVMFTAILQ LHRQICVVCQADEEFQILANSWRYS SAFTNKDIFFAMVDFDEGS/DMYFQML KH*ISAPNFPSTFLQKGKPKRGWDTYELQ VRGFFQLRQISPWIADRTDVQY |
| 2795 | 10846 | A | 3730 | 2 | 454 | RSFFFFCEVGSWVGSMRVVMARLLSEG EQCIPTACAAFAQQPGRRRLAGVGE GGPQCSWVNYRCTLEFLVSLGTDLAR GRGNSATGPATAPADSKQLSCKTFIAVLS LSKEAGFCNVVQGWVSTSWGSSSPVPQ FFPKLLEFTGQ |
| 2796 | 10847 | A | 3731 | 379 | 640 | DGVSLCYPGWNTVAQSQLTVGSISWAQ VILQTPPRVAVAPGRITVYRDRVSLCC PGWSGLIVLGLKPPRVLGITGMGSPQPRP GI |
| 2797 | 10848 | A | 3732 | 373 | 598 | YPCPE/RCAQRHGQACLLPSLERKCVIS LPPSPHQTFAGPKGLGHGDALSGLIWP QTPSCEPTQPKQSNQLVN |
| 2798 | 10849 | A | 3733 | 2 | 444 | |
| 2799 | 10850 | A | 3734 | 151 | 485 | SPRGHYQLLLSGRALADRYRRIYTAALN DRDQGGGSAGHPAS/RSENLENTVIIPDI KLHSNPSAFNIYCNVRHCVLEWQKKEIS LAAASKNSVQSGESDSDEEESKEPPIN |
| 2800 | 10851 | A | 3735 | 1 | 176 | |
| 2801 | 10852 | A | 3736 | 1 | 6570 | |
| 2802 | 10853 | A | 3737 | 114 | 14222 | AAPVAAPGALFMPVPDGSVAAAAGLGLG LPAADSPGHYQLLLSGRALADRYRRIYT AALNDRDQGGGSAGHPASRNKKILNKK KLKRKQKSKSVKTRSKSENLENTVIIPD IKLHSNPSAFNIYCNVRHCVLEWQKKEIS LAAASKNSVQSGESDSDEEESKEPPIKL PKIEVGLCEVFELIKETRFSHPSLCLRS QALLNVLQGGQPEVLQSEPPEVLESFQ LLEITVRSTGMNDSTGQSLTALSCACL |
| 2803 | 10854 | A | 3738 | 373 | 662 | CRKNSCYQAQNFNLRIFFSTTKLNLHFH *NDSQKST*/SDSHLARSSQFCSLN*NY*I *TAKSHDVVCTRQHFPSPLESYIWHVKE KKYNPTAAAI |
| 2804 | 10855 | A | 3739 | 29 | 658 | LSVASLSFLPNASAEDTMSRLSRSLWA ATCLGVLCVLSADKNTTQHPNVTTLAPI SNVTSAPVTSPLVTTAPETCEGRNSCV SCFNVSVVNTTCFWIDCKDESYCSHNS TVSD/CQVGNTTDFCSVSTATPVPTANS VTAKTHSSPPLLQLPRQLLHQGTTNNTV NSVTSQPVKSTFDAASFIGGIVLVLEIRC HTRNYIPDLKK |
| 2805 | 10856 | A | 374 | 562 | 766 | GKSISRYPYFPVIFYFYFLETESCSSAQ GVQWRNLGSLQSPSGASSNPASAS*VA ETTGERHHAQ |
| 2806 | 10857 | A | 3740 | 1 | 183 | KKGLSPEQDIKFGHVSWSVGKTSMEVK MQMFQPAFVNPLIPESPEEEELFRQGE TLICL |

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| 2807 | 10858 | A | 3741 | 185 | 1548 | LNQGPQNPKKQGNFHIHETSSSIHANHV RDKLREIVKASTNWRDHVKAMEERKLL HSFLAKSQDGLPPRRMKDSYIEVLLPLGS EPELREKYLTVQNTVRFGRILEDLSLGR FLFCYMHNKIHSKMSPLSIVTALVDKID MCKKSLSPEQDIKFSGHVSWVGKTSME VKMQMFQLHGDEFPCVLDATFVMVAR DSENKGPFAVNPLIPESPEEEELFRQGE NKGRRIAFSSTSLKMAPSAEERTTIHE MFLSTLADPKTISFRSRVLPNGSVGWEN SKLKEFWEL/CAHPSGSRNIFNRILVGFLM RKAYELAWATACSFVGSRPFGAVDDA IMFQNPVEVGSLLFLSSQVCFQNNYI QVRVHSEVALPLQEKPAIQPHMPSFHH RFHVGGKESAPL/VFPKTYGESPCCTLD GQRAFPTMSGPATLEKGPTLVEPLRTP TIC |
| 2808 | 10859 | A | 3743 | 2 | 286 | TALQRHSEPSKLTfVgELAHGRFSAK/M GTLALGVYHGLPASHMELAQELMETCY QMNRMETGLSPEIVHFNLYPQGRRDV EVKPADRHNLRLP |
| 2809 | 10860 | A | 3744 | 1 | 287 | |
| 2810 | 10861 | A | 3745 | 1 | 339 | RPLLAFRLEEEQKMRPEIAGLKPANPPVL PAPQKADTDPENLPGMG*PSGQPRVQL CPGS*SLRCPQSKGLEGLP*LQRPEAPGL ALVFTSWTQGSWPERRGLGLDGKSV |
| 2811 | 10862 | A | 3746 | 2 | 991 | |
| 2812 | 10863 | A | 3747 | 1 | 2296 | FRVDGAAMAACEGRRSGALGSSQSDFL TPPVGGAPWAVATTVMYPPPPPPPHRD FISVTLFSGESYDNSKSWRRRSCWKKWK QLSRLQRNMILFLLAFLLFCGLLFYINLA DHWKALAFRLEEEQKMRPEFAGLKPAN PPVLPAPQKADTDPENLPEISSQKTQRHI QRGPPHLQIRPPSQDLKDGTEQEEATKRQ EAPVDPREPQDPQRTVISWRGAVIEPEQ GTELPSSRAEVPKPLPARTQGTVPVH LNYRQKGVIDVLLHAWKGYRKFAWGH DDLKPVSRSFSEWFGGLTLIDALDTMW ILGLRKEFEARKWVSKKLHFEKDVDVN LFESTIRILGGLLSAYHLSGDSLFLRKA DFGNRLMPAFRTPSKIPYSDVNIGTGVA HPPRWTSdstVAEVTsiQLEFRELSRLTG DKKFQEA VEKVTQHIHGLSGKKDGLVP LFHQLPVGLFTHLGVFTLGARADSYYE YLLKQWIQGGKQETQLLEDYVEAIEGVR THLLRHSEPSKLTfVgELAHGRFSAKMD HLVCFPLGTLALGVYHGLPASHMELAQE LMETCYQMNRMETGLSPEIVHFNLYP QGRRDVEVKPADRHNLRLPETVESLFY LYRVTGDRKYQDWGWEILQSFSTRFV PSGGYSSINNVDQPKPEPRDKMESFFL GETLKYLFLLFSDDPNLLSLDAYVFNTE AHPLPIWTPGLGWMAAGVGTSGGQRHL AGSVAFSKGPRRRHQPPSGPGSELGLGF LLVSALIRTP |
| 2813 | 10864 | A | 375 | 23 | 483 | NGVLLSSRLKCSGAISAHCSLCLGSSNS PTSASQVAGITGAHHHTWANFCI/YFF*V EMGFHHVGQAGLELLTSDDPALASQS AGITG/GEHLRLAVTYLNKHERGSFLSS CLPSAWWKWCLCSCFWVPKCLALCHF KHYGRRKQVGHSTK |
| 2814 | 10865 | C | 3753 | 150 | 584 | MHPSCCPCICKPFSTLVKSHVTASASSVP DSTCLRRGQQSCEVVLWQDRVSFQARE LKAVINSAVQTSSCFIRHLPRSVSSAIAEG VTSVAIHSSSPSAGGALLWSAPFFETQQT AVAPPASLETLGFLHQLPHLLHTAGSFG** |
| 2815 | 10866 | A | 3754 | 292 | 483 | |

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| 2816 | 10867 | A | 3755 | 84 | 316 | GGKLINIKYLFYTSY*FLSFPWHFLAAS RAQQGEVMRLACRLDPKTSFQMAGEW LKYQLSTFLDVAGSVNWKFFSLL |
| 2817 | 10868 | A | 3756 | 423 | 1186 | |
| 2818 | 10869 | A | 3757 | 222 | 435 | PCFLALAVCCVSKKGADHSSAPPADGD DEEMMATEVTPSAMAELTDLGKCLMKH EDVCTALLITAFHSLAW |
| 2819 | 10870 | A | 3758 | 1 | 936 | MAEPFTKALDMLDAEKSAILGLPQPLLE LNDSPVFKTVLERMQRFFSTLYEN/CECP WVGLFI*CTEHYEALVSPILGPLFTYLHC GEDEAADENPESQEMLEEQVRLTRE VMDLITVCCVSKKGADHSSAPPADGDD EEMMATEVTPSAMAELTDLGKCLMKHE VLSGTLADAVTWLFTSVLKGQLQMHGQ HDGCMASLVHLAFQIYEALRPRYLEIRA VMEQIPEIQKDSLDQFDCKLLNPSLQKV ADKRRKDQFKRLIAGCIGKPLGEQFRKE VHIKNLPSLFKKTTPMLETEVLDNDGGG LATIFEP |
| 2820 | 10871 | A | 3759 | 30 | 3498 | VAIVRHFGQLQLEHVVKFRWNGMSRLEK VYLKNSVMELIANGTLNILEENHIKDAL SRIVVEMIKREWPHWPDMLIELDTLSK QGETQTELVMFILLRLAEDVVTFTLPPQ RRRDIQQTLTQNMERIFSLLNTLQENVN KYQQVKTDTSQESKAQANCRVGAALN TLAGYIDWVSMSHITAENCKLEILCLLL NEQELQLGAAECLLIAVSRKGKLEDRKP LMVLFGDVAMHYILSAAQTADGGGLVE K |
| 2821 | 10872 | A | 376 | 129 | 365 | NYYTHLYANIFDTLEERGKFL/DKQNL SK LEQTGKAQGFYDLLKKLN**L*SLLTKK ASGRGPLLGNSFQF*RKKMTPTL |
| 2822 | 10873 | A | 3760 | 1 | 168 | PLKRS DGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPVERVCRYCPVGQKPG |
| 2823 | 10874 | A | 3765 | 1 | 234 | |
| 2824 | 10875 | A | 3766 | 1 | 1697 | LRAAGGGRTMPSFDEALQRVGEFGRFQ RRVFLLLCLTGVTF AFLFVG VVFLGTQP DHYWCRGPSAAALAERCGWSPEEWN RTAPASRGPEPPERGRRCQRYLLEAAND SASATSALSCADPLA AFPNRSAPLVPCRG GWRYAQAHSIVSEFDLVCVNAWMLDL TQAILNLGFLTGAFTLGYAADRYGRIVY LLSCLGVGVTVGVVAFAPNFPVFVIFRFL QGVFFSLTWMTCYVIVTEIVGSKQRRIV GIVIQMFFTLGHIILPGIAYFIPNWQGIQLA ITLPSFLFLYYWEVPESPRWLITRKKGD KALQILRRIAKCNGKYLSSNYSEITVTDE EASNPSFLDLVRTPQMRKCTILMFAWF TSAVVYQGLVMRLGIIGGNLYIDFFISGV VELPGALLILTIERLGRRLPFAASNIVAG VACLVT AFLPEGIAWLRTTVATLGRLGIT MAFEIVYLVNSELYPTTLRNFGVSLCSSL CDFGGIAPFLFRLA AVWLELPLIIFGILA SICGGLVMLLPETKGIALPETVDDVEKLG SPHSCKCGRNKKTPVSRSHL |
| 2825 | 10876 | A | 3767 | 103 | 370 | IGVPGAISASGRLAVALGTILSFSFSISE FFRFWLRVVGQVDSGDVVYCTYPLFI LSALSLEDYSPETKVFK*LKTKHDSHMT GN |

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| 2826 | 10877 | A | 3768 | 97 | 1639 | CPLQWICAINNISRQIYLTDNPEAVAIKL NQTALQAGTPITSFGKKQESSCPSQNLK NSEMENENDKIVPKATASLPEAEELIAPG TPIQFDIVLPATEFLDQNRGSRRTNPFGE TEDESFEAEDQQQEVNEILSGKCCLPD SLLQQMFIVRFLGSMVKTDTSTTEVIYE AMRQVLAARAIHNIFRMTESHLMVTSQS LRAPGGRGGCGRSFSRLKCSCLPALKRA AGLPAQRLSSAKGQTASSESLTLVVPD GETPPSRNRQTPHTGEFQLASGHQHQR KVDKSTKMRKKQHRKAENSKNQNASPP PKDHNSLPAREQNWTENEFEEFTERGFR SDRENGTKLENTLQDIIQENFHNLARQA NIQIQEIQRTPQRYSSRRATPRHIIIRFTKV EMKEKMLRAAREKGQVVTHKGKSIRLT ADLSAETLQVRREWGPIFNLKEKNFQP RISYPAKLSFISKGEIKFDTKQMLKDVV TTRPALKELLKEALNMERKNQYQPLQK HTKM |
| 2827 | 10878 | A | 3769 | 159 | 277 | |
| 2828 | 10879 | A | 377 | 67 | 224 | |
| 2829 | 10880 | A | 3770 | 1 | 474 | HPPPTMALKRIHKELNDLARDPPAQCSA GPVGDDMFHWQA\TIMGPNDGPLYQG GVFFLTIPFPQQITPFKPKVAFTTRIYHP NINHN\G\SICLDILRSQWSPALTISKVLLS\ ICSLLCDPNPDDPLVPEIARIYKT\DRWKY NRIAR\EWTKYAM |
| 2830 | 10881 | A | 3771 | 153 | 291 | |
| 2831 | 10882 | A | 3772 | 1 | 336 | |
| 2832 | 10883 | A | 3773 | 1 | 2336 | MVRSWLTATSASQVQAILLPQPKTQLN FTVAIDFTASNGETRMSEKVGGNLPQPT SLHYMSPYQLSAYAMALKAVGEIHDY DSDKLPAYGFGAKLPPEGRISHQFPLNN NDEDPNCAGIEGVLESYFQSLRTVQLYG PTYFAPVINQVASNSWSSVTLGTDSEPA VEVPQYVGIRLLVEGFTIKKPMAMCHRR MGVRPAVPLLTQRSGEGKDSGTPTHSL HTKAQLPSPHVLRHQGVLRQHSKLV GTKALSTTGKALRTLPTAKVFISLP*GPW HRR*AGRDCSAGR*AAEDSLRLFHSSV SHHWKP*SQWLL*SSAVSWAEAEAGELLE PGRRRLQ |
| 2833 | 10884 | A | 3774 | 1015 | 1292 | AGRAWWRMPYNPQHFRPRRVDHLRS GVQDQPGQVHGETPSLLKGPKIGWAWW RTPVIPATWEAEPAGELLEPRRQRLQVSQ DRTTALQPGQE |
| 2834 | 10885 | A | 3775 | 183 | 511 | SQHFGRRLRWADCLRSGIQDQPGQHGETL SLLKIQKLARSGGTCLQSOLLARLRQEN HFSLGEGGCSEPRSGHCTPAWARV/GHS VLKTNEQKNSSTLHTKSHWIFQFPFH |
| 2835 | 10886 | A | 3779 | 60 | 361 | |
| 2836 | 10887 | A | 378 | 436 | 829 | NLREFPWAPCPVLHYKFSSKLNWIPVT L*GGSHILPSATLKKQIYGEKKLKAADC DLQITNAQTKEEYDDNALIPKNSSVIVR RIPIGGVKSTSKTYVISRTEPAMATTKAV CKNTISHFFYTLLLPL |
| 2837 | 10888 | A | 3780 | 2 | 616 | ERTEKSDRAVRSGAPHADGSREAVFCAC IWRWRVGGGRGRSCCTGRPSWGASSAVT RGPHVTRSCRATQPSLQSSLASGYQLPA ALSSARSAFGPGKSGAGSATAKCSGAP RGENPEEKETARIGPGTKKMEQPYAR MEEEDR/HLWGGGEGPPSPARKIERGKA RPTCPLNFRMGYPNRPESMDGDGWKM EMDMGKYSMGGRR |

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| 2838 | 10889 | A | 3781 | 2 | 888 | RQRQRPRAGPAGRTGGQKAPGARVPPG PAMEGASFGAGRAGAALDPVSFARRPQ TLLRVASWVFSIAVFGPIVNEGYVNTDS GPELRCVFNGNAGACRFVGLGLGAFL ACAAFLLLDVRFQIQISSVRDRRAVLLD LGFSGLWSFLWFVGFCLTNQWQRTAP GPFTHAGDAARAAIAFNFFSILSWVAL TVKALQRFRLGTDMSLFATEQLSTGASQ AYPGYPVGSVEGTETYQSPFTETLDT PKGYQVPAYYRLAGTDQGSKATPTQA PGSPGPPLGPSSSVPRTE |
| 2839 | 10890 | A | 3782 | 1 | 1944 | MADRTKELESIPDSNRNGSIMGNSRDF DFGTTIKQDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGQDFADFG TTIKQDFRLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQTASPRAL ADSLMQLARQVSRLESGQWTLVPNWNT TQPLSGDILLIYKGFRCFRNHHQTGFSLA GANQRGPLAATLSGPGGEGQSAVARLT GEKKN |
| 2840 | 10891 | A | 3783 | 1 | 578 | MGVEGRYPVSLSSDLEWRPDRCDASE VQRDPRAGSAPLAEDVQVDPKDSHSSS ERFLEQSHSSMERAFAEADYGRSCDYKVG SPSYLDKLLWRDNKPHHYSEPKLILDLS HWKQAAGAPPTATGLADTGAREDEPAS LFLENPQGVKSTQGAQNTPARPPTPSA AWLPRPPPPGPTLADSCSVTKWQV |
| 2841 | 10892 | A | 3784 | 861 | 2636 | GARGRPLAETWFFLTAPVLPQQLQITEPT MAEKGDCIASVYGYDLGGRFVDFQPLG FGVNGLVLSAVDSRACRVAVKKIALS DARSMKHALREIKIIRLDHNDIVKVYE VLGPKGTDLQGELEKFSVAYIVQEYMET DLARLLEQGTAEHAKLFMYQLLRGL KYIHSANVLHRDLKPANIFISTEDLVKI GDFGLAKESLNQHYSHKGYLSEGLVT KWYRSPRLLSPNNYTKAIDMWAAGCIL AEMLTGRMLFAGAHELEQMQLILETIPVI REEDKDELLRVMPFSVSSTWEVKRPLRK LLPEVNSEAFLEKILTFNPMDRLLTAEM GLQHPYMSPYSCPEDEPTSQHPFRIEDEI DDIVLMAANQSQSLNWDTCSSRYPVSL SSDLEWRPDRCDASEVQRDPRAGSAPL AENVQKDPRKDSHSSSERFLEQSHSSME RAFEADYGRSCDYKVGSPSYLDKLLWR DNKPHHYSEPKLILDLSHWKQAAGAPPT ATGLADTGAREDEPASLFLEIAQWVKS TQGAQSTPTTRPPTPSAACLP PPPPPGP GRRRQPPVRPGRVHLRPEALHQARG PAGQ |
| 2842 | 10893 | A | 3788 | 1 | 167 | |
| 2843 | 10894 | A | 3789 | 1 | 1685 | NTIHDTELYLSRCWVCCAUSAIRARA ALPNIIVGEKGGAGSARSSPRAAAECA QIPQPRRSPAVQAEPARRSRFPFTLQGA FSSAIIGAGIGGTSAAYYLRQKFGKDVKI DLFEREEVGGRLATMMVQGGQYEAGGS VIHPLNLHMKRFVKDLGLSAVQASGL LGIYNGETLVFEESNWFIVIKLVWRY GFQSLRMHMMWVEDVVDKFMRIYRYS HDYAFSSVEKLLHALGGDDFLGMLNRT LLETIAQKPGCEKLLNEMIGPVMRVNY GQSTDINAFVGAGSLSCSDSGLWAVEGG NKLVCSGLLQASKSNLISGSVMYIEKT KTKYTGNPTKMYEVVYQIGTETRSDFYA DIVLVATPLNRKMSNITFLNFDPPNEEF HQYYQHIVTTLVKGELNTSIFSSRPIDKF GLNTVLTTDNSDLFINSIGIVPSVREKEDP EPSTDGTYYWKIFSQETLTKAQILKFLS YDYAVKKPWLAYPHYK/PPPEKCPLLSF SUDDI VVJLNGIECAASAIMEMSAIAAII |

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| | | | | | | SHDRLYYLNIECAASAWEMSAIAAH NAALLAYHRWNGHTDMIDQDGLYEKL KTEL |
| 2844 | 10895 | A | 379 | 74 | 378 | GCTKDSNIYFIKEHFQSVNNHIKRCISFL IRVM*LKPQQVTIINTPIRMAKI*KAENSK CWQECGAAVTLMH***V*LPLKSWHFL KLSTCLFYDLAIPL |
| 2845 | 10896 | A | 3790 | 52 | 264 | QSFAPGPPPFIPPPWGGRRAGGFPGPGMG/ PPPGPPGGTSSSSKIPKFGRRGGPPFPPL PKRVRPGDFFYP |
| 2846 | 10897 | A | 3791 | 627 | 1524 | SHGENCKCPSTGDYRKLIIHLKGCQGLR NKGSSPFTSIVSAAKVCGAASESPSVKSL CLLVADQDFSFKAGQWVDFIPGVSVVG GFSICSSPRLLEQERVIELAVKYTNHPPA LWVHNTCTLDCEVAVRVGGEFFDPOQ ADASRNVLVIAGGVGINPLLSILRHAAD LLREQANKRNGYEIGTIKILQCKKYPAE LLFKKNILDLVNEFFEKIACSLHVTKTDY TNPMRNSKPYTEGRITEKEIRDHISKETL FYICGPPPMTDFFSKQLENNHVPKEHICF EEVVVGGRQRQKK |
| 2847 | 10898 | A | 3792 | 331 | 756 | WKRSCLKYLWLLRSHNSHPSSSLTPSLSPS AEAEDGDLQCLCVKTTSQVRPRHITS EVIKAGPHCPTAQLIVSPRTASVSAPAPC LLCPSLPLMPFANPRTESHVSSLFPARA TLKNGRKICLDLQALLYKKIIEHLES |
| 2848 | 10899 | A | 3793 | 3 | 402 | HEETQPEFPALSTEILLEALPQHELRSRV LR/AORPGLLFLGLLLPLVVAFRRAEA EEDGDLQCLCVKTTSQVRPRHIHQGR* SKAGPHCPTCPT**PR*KNGRKIWLGTW QAPLLQK*FKETFWESLAN |
| 2849 | 10900 | A | 3794 | 2 | 146 | |
| 2850 | 10901 | A | 3795 | 3 | 1034 | SEFPARTPRRCPRPSPGPAMGLTVSALFS RIFGKKQMPILMVGLDAAGK/TSHILYKL KLGEIVTTIPTIGFNVETVEYKNICFTVW DVGGQDKIRPLWRHYFQNTQGLIFVVD SNDIRERVQESA/DLQKMLQEDELDA VLLVFSWKQDMPNAMPVSELTDKLGL QHLRSRTWYVIAHLLPTQGTGFTMV LDWLSHELKALNQPWGRPLDARKSRC VQSPTMSQNSPTPRGKCPFPPTFSLPHSP QASASAPCSCLHVLVVGAVEPLLSGHR GVPLFLPAGTYGRGFAGPRPPSSRGAGI WVSFFFFCFGCTLGGQVGRGKVRAFGW CYNVALDLE |
| 2851 | 10902 | A | 3796 | 1536 | 1838 | GLPQQLTKRIQQVLIKCCLAFLFLFFF LRWSLALLPILECSGVISAHCNLRPLGLG DSLASASRVAGMTTGTCHHAQLIFCIFS RDGVSVLARTVWIS |

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| 2852 | 10903 | A | 3797 | 2 | 740 | GRVQGQSTSKVPKEGLLSLHLLCSTAHYQ KTAEMKSIYFVAGLFVMLVQGSWQORS QDTEKSRFSASQADPLSDPDQMNED KRHSQGTFTSDYSKYLDSTRRAQDFLQ WLMNTKRNRRNIAKRHDEFERHAEGTF TSDVSSYLEGQAAKEFIWLVKGRGRR DFPGEGRPLLKNLAGRHADGFSFDEM TILDNLPAVARDFINWLRTKINTREITYIT YSEIIFTNITLLAHVGCLEMFKSW |
| 2853 | 10904 | C | 3798 | 204 | 272 | |
| 2854 | 10905 | A | 3799 | 1 | 350 | |
| 2855 | 10906 | A | 38 | 3 | 203 | HASDKMADKEKKKKESILDLSKYIDKTI RVKFQGGREGE\GLPLSVPL*KFQINPA TEMMRTHAEA |
| 2856 | 10907 | B | 380 | 1 | 483 | MGQARWLTPVIPALWEAEAGGSRGPSA AGLLEFARGPLQTLFAWVSAVAEQRI FVNRECCCLIVPLEVLSQRSTRPCEVSVC PYWENAFQLGCSGTVTVGSTTVTLAECL KWLTTFQLVLSIGLAAMVDVLTGDDVV WLLNVAAEWSFNIPNDSLS* |
| 2857 | 10908 | A | 3800 | 1 | 397 | QRPI*PTKPIGQVSKGHQPTRHDFQTQF LAAHETISRLVGFSAGQVQYLDLIKK\DP SKLFNEERLIDKTKVTYKWLPESESLFL ASHASGHLYLYNVSHPCASAPPQYSLK QGEFVSVAAYKYNDFL |
| 2858 | 10909 | A | 3801 | 1 | 2066 | MAAGGAEGGSGPGAAMGDCAEIKSQFR TREGFYKLLPGDGAARRSGPASAQTPVP PQPPQPPPGPASASGPGAAGPASSPPAG PGPGPALPAVRLSLVRLGEPDSAGAGEP PATPAGLGSGGDRVCNLRGELYFYPGC CRRGSQRWHTPLTPFLPLKSIDLNKPID KRIYKGTQPTCHDFNQFTAATETISLLVG FSAGQVQYLDLIKKDTSKLFNEERLIDKT KVITYLKWLPESESLFLASHASGHLYLYN VSHPCASAPPQYSLKQAWGFSFYAAK SKAPRNPLAKWAVGEGPLNEFAFSPDGR HLACVSQDGLRVFHFDSMLLRGLMKS YFGGLLCVCWSPDGRYVVTGGEDDLVT VWSFTEGRVVARGHGHKS WVNVAFD SLYTTRAEEAATAAGADGERSGEEEEEE PEAAGTGSAGGAPLSPLPKAGSITYRFGS AGQDTQFCLWDLTEDVLYPHPLARTRT LPGTPGTTPPAASSRGGEPPGGLPRSL RSNSLPHPAGGGKAGGPGVAAEPGTPFS IGRFATLTLQERRDRGAKEHKRYHSLG NISRGSGSGSGSGGEGKPSGPVPRSLDPA KVLGTALCPRIHEVPLLEPLVCKKIAQER LTVLLFLEDCIITACQGLICTWPRPGKA FTDEETEAQTGEGSWPRSPSKSVVEGISS QPGNSPSGTVV |
| 2859 | 10910 | A | 3802 | 1 | 1155 | |
| 2860 | 10911 | A | 3803 | 285 | 1444 | LLISPGPRLGAPSFPMAGHLASDFAFSPPP GGGGDGPGGPEPGWVDPRTWLSFQRP GGPGIGPGVGPGEVWGIPPCPPPYEFC GGMAYCGPQVGVGLVPQGGLETSQPEG EAGVGVESNSDGPSEPCTVTPGAIVKL EKEKLEQNPEK\SDIKALQKELEQFAKL \LKQKRITLGYTQADVGLTLGVLFQKVFS QTTICRFEALQLSFKNMCKLRPLLQKWV EEADNNENLQEICKAETLVQARKRKRTS IENRVRGNLENLFLQCPETPHWQQ\SHIA QQLGLKKHVVRVVRVWFCNRRQKGA RSSSDFA\QREDFAAGSPFSGGPVSLFP \LPPGPHFGTPGYGSPHFTA\LYSSVPFPE GEAFPPVSVTILG\SPMHSN |
| 2861 | 10912 | A | 3806 | 3 | 225 | GQTSQHHVALRTTQHHWALGQHRVAL HTVEYYLALKRKEMDTGCK\WMELEYI VLSGISQSQEDMHCMIPFVSGP |

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| 2862 | 10913 | A | 3807 | 874 | 1444 | CQARPMPLRAFNPVSSFRWARGMTIVA ALMTVFFIMQLVGQVPAALWVIFGEDRF RWSATMIGLSLALFGILHALAQAFVTGP ATKRFGEKQAIHAGMGPNALGYVLLAFA TRGWMAFPIMILLASGGIGMPALQAMW LAE*ITDTRANVKRLLLQNVCDLSNNMN GLRFPFCFVKSCGTPTSVLTKRWH |
| 2863 | 10914 | B | 3808 | 1 | 1917 | MIGLSLAVFGILHALAQAFVTGPATKRF GEKQAIHAGGRRAGLRLAGVPTRGWM AFPIMILLASGASGCRVAGHAVQAALRA QGLLKEAEHVESQSAETVLTPECCQLLG YLDKGKRKRKEKAGSLQWAYMAIARL GGFMSKRTGIASWGALCAGAAVLFVK TDLSGALNELQDEAARLSWLATTGVPC AAVLDVVTEAGRDWLLGEVPGQDILLS SHLAPAEKVSIMADAMRRLHTLDPATCP FDHQAHRIRERARTRMEAGLKDLMRRD QDLIKRQDEDRSHDEQDDARRSPA RAYSAIAATTDNSSGRPVLFVKTDLGAL NELQDEAARLSWLATTGVPCAAVLDVV TEAGRDWLLGEVPGQDILLSHAPAEK VSIMADAMRRLHTLDPATCPFDHQA RIERARTRMEAGLVDQDDLDEEHQGLA PAELFARLKARMPDGEDLVVTHGDAAC RISWWKMAAFLDSSTVAGWDIALATRDI AEELGGEWADRFLVLYVLLSGTLGFEM TDQATPNLPSRDFDSTAIFYERLGFIVF RDAGWMILQRGDLMLEFFAHPGLDPLA SWFSCCLRLDDLAIFYRQCKSVGIQETS SGYPRIHAPELQEWGGTMAALVRIFVKE PYFCGVT* |
| 2864 | 10915 | A | 3809 | 1057 | 1905 | |
| 2865 | 10916 | B | 381 | 119 | 955 | MVSISRPRDPPASASQSAGITGPALGAEG ERAFHRHRVMIVTEGAPGGLSSGHLRDA MDSEAGTDDGASHVRVVRDLKPSNI LYVDESGNPECLRICDFGAKQLRAENG LLMTPCYTANFVAPEVLKRQGYDEGCDI WSLGILLYTMLAGYTPFANGPSDTPPEIL TRIGSGKFTLSGGNWNVTSETAKDLVSK MLHVDPHQRLTAKQVLQHPWVTQDK LPQSQSLSHQDLQLVKGAMAATYSALNS SKPTPOLKPIESSILAQRRVRKLPSTTL* |
| 2866 | 10917 | A | 3810 | 1 | 2928 | |
| 2867 | 10918 | A | 3811 | 630 | 1159 | GAPWGQVPAALWVIFGEDRFRWSATMI GLSLAVFGILHALAQAFVTGPATKRFGE KQAIHAGMAADALGYVLLAFATRGWMA FPIMILLASGGIGMPALQAMLSRQVDDD HQGQLQGSALALTSLSIIGPLIVTAIYAA SASTWNGLAWIVGAALYLVLPAVLRG AWSRATST |
| 2868 | 10919 | A | 3812 | 1 | 3525 | |
| 2869 | 10920 | A | 3813 | 1 | 1606 | MLMKAHKGVLGEQEKVPRRLMKVLKG VPGEQEKVLWEAREEGVSSRWGTSPMG CEQRVWMGDEQAMEPLGLADGKLWRT FMGAADAERKEGRGMKVAPAPAVVKK QEAKKVNNPLFEKRPKNFGVGQDIQPKR DLTRFVKWPRYIKLQHQRFLYKRLKVP PAINQFTQALDRQTATQLELAHKYRPE TKQEKQRLLAQAEETAGKGDISTKRL PVLQAGVNWEDKSALAKLVEGIRTNYN ERYNEIHHHWGNNVLGPESVARIKLLK ADGSLRLDFTVCKKAWIVSHPVSRKLP QQRQNRKKRQEVQAWGSGPCLSLVV GSEPATGGSSCSETSGFGKSCKVKETNP QPMATPTLEQGEAAHAEIPACSHG QVPAALWVIFGEDRFRWSATMIGLSLAV FGILHALAQAFVTGPATKRFGEKQAIHAG MAADALGYVLLAFATRGWMAFPIMILL ASGGIGMPALQAMLSRQVLTSHIGPLIVTA |

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| | | | | | | IYAASASTWNGLA WIVGAAL YLVCLPAL RRGAWSRATST |
| 2870 | 10921 | A | 3814 | 1701 | 1904 | |
| 2871 | 10922 | A | 3815 | 1 | 427 | MAKMKNQIIPSVGEKLEQQKPSYDARAF VTGPATKRFGEKQAIHAGMATDALGYVL LAFATRGWMAFFPIMILLASGGIGMPALQ AMLSRQLTSIIGPLIVTAIYAASASTWNG LA WIVGAAL YLVCLPALRRGAWSRATS T |
| 2872 | 10923 | A | 3816 | 1 | 1629 | |
| 2873 | 10924 | A | 3817 | 1 | 1013 | MMGLRNSYDVKERLKHQVRGGKAPKA VNSGKLLPFPRLKELAGVEGMGNCYL RTQPGTRMQWSPMKLSVELRAGQSRLL RESKGKEIPEPRCAAVGGKEPEAKPPKV PRPMPPLRAFNPVSSFRWARGMTIVAAL MTVFFIMQLVGQVPAALWVIFGEDRFR WSATMIGLSLAVFGILHALAQAFVTGPA TKRFGKQAIHAGMAADALGYVLLAFAT RGWMAFFPIMILLASGGIGMPALQAMLSR QVDDDHQQLQGSLAALTSLTSIIGPLIV TAIYAASASTWNGLAWI*PGMFHISNPY REHPLSFHRYHYHPHEQKSPLHGGISDQT GKNRP |
| 2874 | 10925 | A | 3818 | 1 | 2634 | |
| 2875 | 10926 | A | 3819 | 1328 | 2536 | |
| 2876 | 10927 | A | 382 | 1 | 662 | LGSTVTQTGVQWCGHSSLRPQTQAQAI LLPCLSNCDYKHEPLHLAYVTQCFLS FFFGGGGWSLALSPMLECGGVILAQCKL RLLGFTPFSCSLPSSWDHRHPPCLANF LNF/SVETGFHFLAQDGLDLTS/S/PPAS A/FPKCWDYRRDHRAQPM*CNSDVNSL MLPQMPQVK/AHQSPIGCPFRHTCRLG CPQTTCTSHQLAANLEVPTMPSSSITH |
| 2877 | 10928 | A | 3820 | 1 | 1594 | MSAAPCSTVPSPIDHPRAEECGHTARDW QVAPPAAQSHDDDEEEDEKEEEEEEE ELLLAGSPYSPTVPCFPLECPCLENGSRQ KQDKHTPGFKHKFQHAFFSFPLATITHS FWVAEHSRLLEGKQGAQISPHLQVGPGL VWQGYLWQNREAGSSRDShlNMPCGM AAGHSHSGTLFSDQGLWEQCQLLKSTSV FARCHPLVDPEPFVALCEKTLCECAGGL ECACPALLEYARTCAQEGMVLYGWTDH SACSPVCPAGMEYRQCVSPCARTCQSLH INEMCQERCVDGCSCEGQLLDEGLCVE STECPCVHSGKRYPPGTSLSRDCNTCICR NSQWICSNEECPDREGHNSRQREVALSA QVGCNHVTPALVSGQVPAALWVIFGED RFRWSATMIGLSLAVFGILHALAQAFVT GPATKRFGEKQAIHAGMAADALGYVLLA FATRGWMAFFPIMILLASGGIGMPALQAM LSRQLTSIIGPLIVTAIYAASASTWNGLA WIVGAAL YLVCLPALRRGAWSRATST |

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| 2878 | 10929 | A | 3821 | 3 | 995 | TSPTATGPALVCYRASLVALREEDTRSQ EYVPFRGNRDFAHVKKMGGLGLLAMD VPEELGGAGLDYLAYAIAMEEISRGAS TGVIMSVNNSLYLGPILKFGSKEQKQAW VTPFTSGDKIGCFALSGTRAFNPVSSFRW ARGMTIVAALMTVFFIMQLVGQVPAAL WVIFGEDRFRWSATMIGLSLAVFGILHA LAQAFVTGPATKRFGEKQAIAGMAADA LGYVLLAFATRGWMAFFIMILLASGGIG MPALQAMLSRQVDDDDHQQQLQGSAA LTSLSIIGPLIVTAIYAASASTWNGLAWI VGAALYLCLPALRRGAWSRATST |
| 2879 | 10930 | A | 3822 | 1 | 619 | MPLRAFNPVSSFRWARGMTIVAALMTV FFIMQLVGQVPAALWVIFGEDRFRWSAT MIGLSLAVFGILHALAQAFVTGPATKRF GEKQAIAGMAADALGYVLLAFATRGW MAFFIMILLASGGIGMPALQAMLSRQVD DDHQQQLQGSAAALTSLSIIGPLIVTAIY AASASTWNGLAWIVGAALYLCLPALR RGAWSRATST |
| 2880 | 10931 | A | 3823 | 1 | 565 | MPLRAFNPVSSFRWARGMTIVAALMTV FFIMQLVGQVPAALWVIFGEDRFRWSAT MIGLSLAVFGILHALAQAFVTGPATKRF GEKQAIAGMAADALGYVLLAFATRGW MAFFIMILLASGGIGMPALQAMLSRQLT SIIGPLIVTAIYAASASTWNGLAWIVGAA LYLVCLPALRRGAWSRATST |
| 2881 | 10932 | A | 3824 | 1 | 934 | MTMWVLHCFTYFVSAWSKHGYAHAV TAKILYAGRIVAGITGATGAVAGAYADI TDGEDRARHFGLMSACFGVGMVAGPV AGGLLGAISLHAPFLAAAVLNLNLLG CFLMQESHKGERRPMPLRAFNPVSSFRW ARGMTIVAALMTVFFIMQLVGQVPAAL WVIFGEDRFRWSATMIGLSLAVFGILHA LAQAFVTGPATKRFGEKQAIAGMAADA LGYVLLAFATRGWMAFFIMILLASGGIG MPALQAMLSRQLT SIIGPLIVTAIYAASA STWNGLAWIVGAALYLCLPALRRGAW SRATST |
| 2882 | 10933 | A | 3825 | 657 | 7035 | LRTCWHSDCQNTAADHSAQGSRRHRK PCNRCAPGSQNWAVPLLPDISCRTGCAV RKDRLIAGPIQ*N/LKTAVVGRQPYLTKL CLMLGCLGRMRWRCSTGWRLRLRTSSVQ CS*RISNRMSCTGSMLTTWL*MKLQQVN GLGQGLIQSAGKDCDVQGLEHDMEEIN ARWNTLNKKVAQRIQLQEALLHCGKF QDALEPLLSWLADTEELIANQKPPSAEY KVVKAQIQEQKLLQRLDDRKATVDML QAEGGRI |

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| 2883 | 10934 | A | 3826 | 140 | 2298 | LFPRLLSFLTTPPHCSFSJCFVICSRILTILK GSSLITG/CTQFRLSETKEITNPYAMRLYE SLCQYRKPDGSGIVSLKIDWIERYQLPQ SYQRMPPDFLPLPAGALSLISKVTDRA DSMEQGAETSQGALGTLANVVTSLANL SESLNNGDTSEIQPEDQSASEITRAFDTL AKALNTTDSSSPSLADGIDTSGGGSIHVI SRDQSTPIIEVEGPLLSDTHVTFKSIREDR NGRSQKTVHTEGDMNMNIKKIVKQATV LTFTTALLAGGATQAFKENNQKAYKE TYGVSHITRHDMLQIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWDSWPLQNADG TVAEYNGYHVVFALAGSPKDADDTSIY MFYQKVGDNIDSWKNAGRVFKDSKDF DANDPILKDQTQEWSGSATFTSDGKIRL FYTDYSGKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKTIFDGDGKTYQNVQQFI DEGNYTSGDNHTLRDPHYVEDKGHKYL VFEANTGTENGYQGEESLFNKAYYGGG TNFRKESQKLQSSAKKRDAELANGAL GHIELNNDYTLKKVMKPLITSNTVTDEIE RANVFKMNGKWYLFTDSRGSKMTIDGI NSNDIYMLGYVNSLTGPYKPLNKTGLV LQMGLDPNDVTFTYSHFAVPQAKGNV VITSYMTNRGFFEDKATFAPSFLMNIK GNKTSVVKNSILEQQQLTVN |
| 2884 | 10935 | A | 3827 | 1 | 2604 | |
| 2885 | 10936 | C | 3828 | 1 | 2076 | MNMNIKKIVKQATVLTFTTALLAGGAT QAFKENNQKAYKETTYGVSHITRHDML QIPKQQQNEKYQVPQFDQSTIKNIESAKG LDVWDSWPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKVGDNIDS WKNAGRVFKDSKDFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSGKHYGKQ SLTTAQSIREDRNGRSQKTVHTERDMIM NIKKIVKQATVLTFTTALLAGGATHAFA KENNQKAYKETTYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHVVFALAGS PKDADDTSIYMFYQKVGDNIDSWKNA GRVFKDSKDFDANDPILKDQTQEWSGS ATFTSDGKIRLFYTDYSGKHYGKQSLTT AQVNVSKSDDTLKINGVEDHKTIFDGDG KTYQNVQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENGYQGEES LFNKAYYGGGTNFRKESQKLQSSAKK RDAELANGALGHIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKMNGKWYLFTDS RGSKMTIDGINSNDIYMLGYVNSLTGP YKPLNKTGLVLQMGLDPNDVTFTYSHF AVPQAKGNVITSYMTNRGFFEDKKA TFAPSFLMNIKGNKTSVVKNSILEQQQLT VN* |
| 2886 | 10937 | A | 3829 | 1 | 3603 | |
| 2887 | 10938 | A | 383 | 110 | 784 | AAAAASKVLM*TGGAAPQEQP*TGGVQ A*APGSVA/AEGASVEGPGFDTAPAHQ GLSPTRSHGQGGAGRASAHSRDPPGGTG GWGFLKCGPGALCPRGKDGASASVPR GPYAEAEKGGWALRGLGGVAAPGPPSR AGQAPSGLHTGPNARPAPWPIPGQGGGL RRDQAG*VSSWTGSTEPGAHTAHRAPG HGGKGGSPQQPHPGQGPQIPTTHTRMHS CRITAA |

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| 2888 | 10939 | A | 3830 | 2455 | 3151 | DRRCPIFCLLPFGIRFILLFGSSQLRGPFIL FFFLIFFPPFIFLLSILGSFFFFLLSPVLLLL HHFFLSLFPACLLHLLLLLLQVLGAQLG RCLHA/SSPTWCRGRGR/VLAGSRGPGAE TEGPWTAEGGRGRNLARWRRRRRQRQ RRPLGKLGWKRQRRAAGWGGGGSGA ETRRAAAVRRAGGRAVQAVAGALGRG SSIPGSPPHQQAADQPCRPREGNPLIRR RLP |
| 2889 | 10940 | A | 3831 | 1 | 2376 | MKLMETLNQCINAGHEMTKAIAIAQFND DSPEARKITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQRVGYTIE QINHMRDVFGLRLRAEDVFPVIGVAA HKGGVYKTSVSVHLAQDLALKGLRVLL VEGNDPQGTASMYHGWVVDLHIHAEDT LLPFYLGKDDVTYAIKPTCWPGLDIIPS CLALHRIETELMGKFDEGKLPTDPLML RLAIETVAHDYD*FVQLYNQHVAPVL/ GISISGCGSRPAFSASLIA*EETPTKSAASP ILQRRVIFLASGLSSLNCAMIAFVIS |
| 2890 | 10941 | A | 3832 | 1289 | 3109 | ETPVVSLYAFWLFSAKA*VAPPSGFSPT VVSSDSWLGSLVPTYLIART/PELIFVVRQ QVLDVERGAAACG*FLPRLVG*VPDLDA VGLYSTAPII*GAIPGQGG*GLRMSEAQG VPAGGSGLSTTVRLTWACLLPSLFSTSSV *QPQCSWRAARMVSLLPFLSFSTFMCSL SWICFRNFIQVQVMG*VPVTLNPSSTDSP ARTFWSSGNWMI*GGIAAFGGVLGAGFF FTVAS/PLSS*HGRKRALGPPGFHLWGLG VLTGWSIIHGDLAGALRLASVILGYTLV* ASVLRQCLLDGDGQSEPSWERMMNLV VLMVFPFSVQMMVAGGSEDTWHWSSSF LPSAT*TSCSFCLKAGAVPWLSLFLSV VPAWPLLQFTSFLTSFLSSLLADFRSSG LALPMGFRVSAGLALPIGFRVSAGLALP TGFKGPEGCALLRGLSTALAFRVSA LLPFSAGNFFLPSTERKSGVAGFGGGTF SGTGVLVPFLARTEKSTCWGLCTFLS SSDTVFGFTCRCLARKSICSAGISFRSSS DRVFLVTFFPRSRKSSCSTSCWRIASSV CCLVSTRLFSTPRTSSPSSSSQPCPLAQ PGLRDP |
| 2891 | 10942 | A | 3833 | 1 | 2968 | MTIVAALMTVFFIMQLVGQVPAALWVIF GEDRFRWSATMIGLSLAVFGILHALAQA FVTGPATKRFGEKQAIHAGMAADALGYV LLAFATRGMMAFPIMILLASGGIGMPAL QAMLSRQPNFDHWTADRHGDLCLGEH MERVGMDCRRRPIPCLPPRVASRCMEPG HLDMNCSRRLHANGFTTPRIGANQFLRR TVNAQTNPWQNISIASAISSSRTRRISGSV GSWPRSGNAEVSALHHYVPDLHRRMLL ATL |
| 2892 | 10943 | A | 3834 | 1 | 563 | MPLRAFNPVSSFRWARGMTIVAALMTV FFIMQLVGQVPAALWVIFGEDRFRWSAT MIGLSLAVFGILHALAQAFTGPATKRF GEKQAIHAGMAADALGYVLLAFATRGM MAFPIMILLASGGIGMPALQAMLSRQLT SIIGPLIVTAIYAASASTWNLAWIVGAA LYLVCLPALRRGAWSRATST |
| 2893 | 10944 | A | 3835 | 850 | 1280 | |
| 2894 | 10945 | A | 3836 | 3 | 3971 | VCTGSSTRHIVTFDGGQNFKLTGSCSYVLF QNKEQDLEVILHNGACSPGARQGCMSI EVKHSALSVELHSDMEAFRLVHGHPYS ITTACFLVKLCKVKLCFLVKLFFILEELPT NIKVTVNGRLVSPYVGGNMEVNVYGA IMHEVRFNHLGHIFTFTPNNEFQLQLSP KTFASKTYGLCGICDENGANDFMLRDG TVTTDWKTLVQEWTVQRPQGTCPILEE QCLVPDSSHQVLLPLFAECHKVLAPA |

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| 2895 | 10946 | A | 3837 | 1838 | 4062 | KRHKKPFKKSTNPGAGFEKINKIDRLLA RLIKKKREKNQIDAIKNDKGDITTDPTM QTTVREYYKHLVYNKPENLEEMDKFLD TYTLPRLNQEELESLNKPITGSEIEAIINSL PTKKSPGPDGFTAIFYQRYKEELLPFLK LFQSIEKEGILPNSFYEASILIPKPRDIT KKENFRPISLMNIDANILNNILANQIQHI KKLIHHDEVGFIPGMQGWFNIRKSINLIP HVNRTKDKNHMVISVDAEKAFDKIQQH FMLKTLNKLIGDGYLKIIRPIFDKPTADI ILNRQKLEALPLKTGTQRCSLSPLLFNI VLEVLARAIQEKEIKGIQLGKEEVKLSL FADDMIVYLENPIVSAQNLLKLIGNFSKV SEYTINVQKSQSFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTREVKDFFKENYK PLLDEIKENTNKWKNIPWSWVGRIDIVK MAILPKQMPDVNVSWDGEGPKQLPFIDI SVAVATDKGLLTPIIKDAAAKGIQEADS VRSNIVLQCQARPMPLRAFNPVSSFRWA RGMATIVAALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLAVFGILHALA QAFVTGPATKRFGEKQAIHAGMAADALG YVLLAFATRGMMAFFPIMILLASGGIGMP ALQAMLSRQVDDDHQGGQLQGSALALTS LTSIIGPLIVTAIYAASASTWNGLAWVG AALYLVCLPALRRGAWSRATST |
| 2896 | 10947 | A | 3838 | 346 | 777 | GELYFQVCGQFVNRRCGVVMKKMYILLF LSGEFCRCL*YSLMVVCISVGSVVISPLSF FIVSI*FFSLFFFISLASSLSILLILSKNQLLD SLIF |
| 2897 | 10948 | A | 3839 | 1 | 564 | MPLRAFNPVSSFRWARGMTIVAALMTV FFIMQLVGQVPAALWVIFGEDRFRWSAT MIGLSLAVFGILHALAQAFVTGPATKRF GEKQAIHAGMAADALGYVLLAFATRGM MAFFPIMILLASGGIGMPALQAMLSRQPN FDHWTADRHGDLCLRGHEMERVGMDC RRRPIPLPPRVASRCMEPHGLDLNGSRR HLANGFTTPRIGANQFLRTVNAQTNPW QNISIASAISSSRTRISGVSWSRSGNA EVSA |
| 2898 | 10949 | A | 384 | 244 | 315 | NPKGQKDREAPLSRSVFLKIKIKRAFAL LLHGRF*PSTPAASASPASKSPRGSGKAL ASALFYIVQLTK |
| 2899 | 10950 | A | 3840 | 3 | 1049 | GSLQGCAASCARAFLRTCCARSESLAV RGTKGVAFGENPRAAGTCSQSPFFVPAP PPGVRLWVLCPRFTGAFLLRTTLALNV RAGDEGPRLLRAPRVPSRPSAPLAPAP ASTPARRLPVPMQAPGRGPLGLRLMMP GRRGALREPGGCGSCLGVALALLLLLP ACCPVRAQNDTEPIVLEGKCLVVCDSPP SADGAVTSSLGISVRSKSAKVAFSATRST NHEPSEMSNRTMTIYIDQVFSNIGHHFDL ASSIFVAPRKGIYSFSFHVVKVYNRQTIQ VSLLLNGYPVISAWAGYQDVTGEAASN GVLLLMEREDKVHLKLERGNLMGGWK YSTFSGLVFPL |
| 2900 | 10951 | A | 3841 | 1 | 401 | KGASSPVQVPGPVAASTEALLQEAQCSG LSWVVALPQVKQEKADTQDEWTPGTAV LTSPVLVPGCPSKAVDPGLPSVKQEPDP EEDKEENKDDSAKLAPEEEITEIFSLGGP RFRDTAV*LPRSKDLKKPR |

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| 2901 | 10952 | C | 3842 | 108 | 293 | MNMACLGCFVVALIILPFSNPAPPLKSN FLYSGSWEEKMHQLSTLSLFPPLTSSRSS KYS* |
| 2902 | 10953 | A | 3843 | 1 | 1490 | MIREQKIYHKYLAQRREEKAQEKEFDR ILEEDKAKKLAEKDKELRLEKEARRQLV DEVMCTRKLQVQEKSYVKLLAAHPT GDIRSKVELTRYLGPACDLTLFDFKQGI LCYPAPKAHPVAVASKRKRKPSRPAKTR KRQVGPOSGEVRKEAPRDETKADTDTA PASFPAPGCCENCISFSGDGTQRQLKT LCKDCRAQRIAFNREQRMFKQPYTNRR QNRKCGACAACLRMDGRCDFCCDKP KFGGSNQKQKCRWRQCLQFAMKRLLP SVWSEEDGAGSPPPYRRRKRPSSARRH HLGPTLKPTLATRTAQPDHTQAPTKEA GGGFVLPPTGDLVFLREGASSPVQVPG PVAASTEALLQEAQCSGLSWVVALPQV KQEKADTQDEWTPGTAVLTSPVLVPGCP SKAVDPGLPSVKQEPDPPEEDKEENKDD SASKLAPEEEAGGAGTPV/VTSVDSIYPE RQL*VSSWSYLHSCGTERYPGCSI |
| 2903 | 10954 | A | 3844 | 1 | 1758 | MAEDWLDPCALGPGWKRREVFRKSGA TCGRSDTYQSPGDIRSKVELTRYLG PACDLTLFDFKQGILCYPAPKAHPVAVA SKKRKKPSRPAKTRKRQVGPOSGEVRKE APRDETKADTDAPASFPAPGCCENCIS FSGDGTQRQLKTLCCKDCRAQRIAFNRE QRMFKRVGCGEACQVTEDCGACSTC LLQLPHDVASGLFCKCERRRCLRIVERSR GCGVCRGCQTQEDCGHCPICLRPPRGL RRQWKCVQRRCLRGKHARRKGGCDK MAARRRPGAQPLPPPPPSQSPEPTEPQY T/IPPAEPQVRGLCSLPTAEWMWPLRVC CDKPKFGGSNQKQKCRWRQCLQFAM KRLLPVWSEEDGAGSPPPYRRRKRPSS ARRHHLGPTLKPTLATRTAQPDHTQAPT KQEAGGGFVLPPTGDLVFLREGASSPV QVPGPVAASTEALLQAVDPGLPSVKQEP PDPEEDKEENKDDASASKLAPEEEAGGAG TPVITEIFSLGGTRFRDTAVWLPSLQGRH SGREDGCKVWETEDTVEPTSTSWNPRG WPGTHVLSPPPASMMWVSCRRSWCPS SQS |
| 2904 | 10955 | A | 3845 | 1 | 1647 | |
| 2905 | 10956 | A | 3846 | 1 | 1821 | MAEDWLDPCALGPGWKRREVFRKSGA TCGRSDTYQSPGDIRSKVELTRYLG PACDLTLFDFKQGILCYPAPKAHPVAVA SKKRKKPSRPAKTRKRQVGPOSGEVRKE APRDETKADTDAPASFPAPGCCENCIS FSGDGTQRQLKTLCCKDCRAQRIAFNRE EQRMFKRVGCGEACQVTEDCGACST CLLQLPHDVASGLFCKCERRRCLRIVER SRGCGVCRGFQVTEQED/CLGHCPICLRPP RPGLRQWKCVQRRCLRGKHARRKGG CDKMAARRRPGAQPLPPPPPSQSPEPTE PHPRALAPSPPAEFIYYCVDEDELQYTN RRQNRKCGACAACLRNCGRCDFCCD KPKFGGSNQKQKCRWRQCLQFAMKR LLPSVWSEEDGAGSPPPYRRRKRPSSAR RHHLGPTLKPTLATRTAQPDHTQAPTKEA EAGGGFVLPPTGDLVFLREGASSPVQV PGPVAASTEALLQEAQCSGLSWVVALPQ VKQEKADTQDEWTPGTAVLTSPVLVPG CPSKAVDPGLPSVKQEPDPPEEDKEENK DDASASKLAPEEEAGGAGTPVITEIFSLGG TRFRDTAVWLPRSKDLKKPGARKQ |
| 2906 | 10957 | A | 3847 | 1 | 1723 | |

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| 2907 | 10958 | A | 3848 | 1 | 1949 | MAEDWLDCPALGPGWKRRVFRKSGA TCGRSDTYYSPTGDRJRSKVELTRYLG PACDLTLDFKQILCYPAPKAHPVAVA SKKRKKPSRPAKTRKRQVGPQSGEVRKE APRDETKADTDTAPASFPAPGCCENCIS FSGDGTQRQLKTLCKDCRAQRIAFNRE QRMFKRVGCGECAACQVTEDCGACSTC LLQLPHDVASGLFCKCERRRCLRIVERSR GCGVCRGCQTQEDCGHCPICLRPPRGL RRQWKCVQRRCLRHLAHLRRRHQRC QRRTPLA VAPPTGKHARRKGGCD SKMA ARRRPGAQPLPPPPSQSPEPTPHPRAL APSPPAEFIYYCVDEDELQPYTNRRQNR KCGACAACLRMDCGRCDFCCDKPKFG GSNQKRQKCRWRQCLQFAMKRLPSV WSESDGAGSPPPYRRRKRPSARRHHL GPTLKPTLATRTAQPDHTQAPTKEAGG GFVLPPPGH*TL CFLREGASSPVQVGP VAASTEALLQEAQCSGLSWVVALPQVK QEKADTQDEWTPGTAVLTSPVLVPGCPS KAVDPGLPSVKQEPDPPEEDKEENKDDS ASKLAPEEEAGGAGTPVITEIFSLGGTRF RDTAVWLPSLQGRHSGREDGCKVWETE DTVEPTSTSWNP |
| 2908 | 10959 | A | 3849 | 2 | 1682 | LCDTPPGRGGGGRRGGRLQEGPSF MGPRGLEWRKIPAWLPNWL LLLPVASM AEDWLYCPALGPGWKREFFRKS RATC GRLNTYYQSPTGDRILSKVELTRYLGP CDLTLDFKQILCYPSPQRPIPLGGLPG KKRKKPSRPAKTRKRQVGPQSGEVRKE APRDETKADTDTAPASFPAPGCCENCIS FSGDGTQRQLKTLCKDCRAQRIAFNRE QRMFKRVGCGECAACQVTEDCGACSTC LLQLPHDVASGLFCKCERRRCLRIVERSR GCGVCRGCQTQEDCGHCPICLRPPRGL RRQWKCVQRRCLRGLKHARRKGGCD SK MAARRRPGAQPLPPPPSQSPEPTPHPR ALAPSPPAEFIYYCVDEDELKRLPSVWS ESEDGAGSPPPYRRRKRPSARRHHLGP TLKPTLATRTAQPDHTQAPTKEAGGGF VLPPPGTDLVFLREGASSPVQVGPVAA STEALLQAVDPGLPSVKQEPDPPEEDKE ENKDDSAASKLAPEEEAGGAGTPVITEIFS LGGTRFRDTAVWLPRSKDLKKPGARKQ |
| 2909 | 10960 | A | 385 | 933 | 1511 | QVYRPSQTPHLALSPERVAPGRLAGGRL APPEARAPRGSP/LPPHRVSEKTIRVMVFH PGARRAGGTPPRAPRGDTGGAPGAPTY STPLMSLHRARLESSSTGSSFPADSAKPV PLAVVSLDSR*GQWESRSSIHA VTN*AS SSSSSSSSSF SR/VYPRFIEFLHFDIQSTG Q/RITSRQHPPR/DFRDALF*LNS |
| 2910 | 10961 | A | 3850 | 1 | 391 | SPLNKVQLINELNEREVQLGVANKVSW HSEYKDSAWIFLGGLPYDLTKGDIICVF SQQRSTIVAVDNFNIGIKIGRTIRVDHVS NYRAPKDSEEIDDVTRQLQEKGCCARTP SPSLSESEDEKPTKKP |
| 2911 | 10962 | A | 3851 | 1 | 135 | |
| 2912 | 10963 | A | 3852 | 18 | 238 | |
| 2913 | 10964 | A | 3853 | 254 | 1424 | |

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| 2914 | 10965 | A | 3854 | 8 | 1015 | FLSAEREPEEMNPLTKVKLINELNEREVQ LGVADKVSWHSEYKDSA\WISLG\GLPY ELTEGDIICVFSQYGEIVNINLVRDKKT GKSKGFCFLCYEDQQRSTILAVDNFNNGIKI KGRITRVDHVS\NYRAPKDSIEDDDVTR QLQEKGGSGARPPSPTLSESEDEKPTKKH KKDKK\EEKKKKKEKEKADREVQAEQP SSSSPRRKT\VEKDDTGPKKHSSKNSER AQKSEPREGQKLPKSR\TAYSGGAEDLER ELKKEKPKHEHKSSSRREAREEKTRIRD RGRSSDAHSSWYYWRS\EGRSYRSRSRS RDKSHRHKRARRSREREASSNP\SDRW RH |
| 2915 | 10966 | A | 3855 | 299 | 374 | |
| 2916 | 10967 | A | 3856 | 1 | 993 | |
| 2917 | 10968 | A | 3857 | 3009 | 3583 | LFCLFFHILQPSHCWISSEM\VVQLSDSLTD LLDKFSNISEGLSNYSIIDKL\NVIVDDLVE CVKENSSKDLKKSFKSPEPRLFTPEEFFRI FNRSIDAFKDFV\VASETSDCVVSS\TLSPE KGKAKNPPGDSSLHWAAMALPALFSLII GFAFGALY\WKKRQPSLTRA\VENIQINEE DNEISMLQEKEREFEV |
| 2918 | 10969 | A | 3859 | 880 | 1196 | SPTTRRGTPGTCLKPTACAGAA*PGCSA RRTCASAAPLSTCPPSSCAAPPAPAAVP STPRPTSPSPWAAPASPSRRRTQTASTPA STNRAPSSCWAPTTRPLAP |
| 2919 | 10970 | A | 386 | 15 | 466 | GVPNNFIINKNKTPSGWLQPLPRWL*AP VGGACHYPGLEARTEERAPCPSKYTGEP EVLRIKNQGGTPRPGGGPGPSAPRGSFL WST/PGSCPSITPHSLPAAR/PLPPTPRHPA PSSPPCTE/SAPSGPSSSQAPGITVAPGISQ VQRAAALR |
| 2920 | 10971 | A | 3860 | 305 | 631 | IEKISLEPKNRSPQIPNLVGP/RLFLVPGD FQSQVPNFLPFKPPSSGPHPAAGKGQPPFSF LP\AWRSTGPERATPGPRPAACSALEAP SLRGPSGYSAQEP\RRRISARI |
| 2921 | 10972 | A | 3868 | 980 | 1498 | VSLINLQVLRQSLEQVTETFTSYFKPSCQ/ PPTSPIRAMKWTELRLSCLPAGRQHLY LPATPPCSVRGVHGKPS\TVPPAAPSPTS QSHQPASHPLSSPTFLFEPIKDAGTHASLF SRDRHLPFP\TCHIRPPQCLSPPHCSQGS RTGRAVTAALRMAAAAAMTGNQSPTRI |
| 2922 | 10973 | A | 3869 | 94 | 484 | AAAALAAALLRRREDPGPGAGPSMAE TEALSKLREDFRM\QNKS\VFILGASGETG RIVLLKEILEVQGLFSK\VTLIGRRKLT\DE EAYKNVNQEVGGLLKSLDDYASAFQGH DLGFC\CLGYHQEGKAGGG |
| 2923 | 10974 | A | 387 | 50 | 481 | FMEYLTLSFIHVLLQ*FIHCFVHLFIHSFF YALMKS\LIQ*FIHLYSCF/CIDLLISSCIYS FIYALVKSLANSLTHSFIHTFLQ*FVHLFT PLLICSFTHSSIH*PSHSLTFIQLHLFFHAL VSGFIWSFIYLFCKINVFLIDK |
| 2924 | 10975 | A | 3870 | 302 | 1187 | TALVPRDKDWQSPDTLKTGICRCYFPSM AETEALSKLREDFRM\QNKS\VFILGATVE TGRVLLKEILEQGLFSK\VTLIGRRKLT\FD EEAYKNVNQEVVD\FEKLDDYASAFQG HDVGFCCLG\TTRGKAGAE\GFVRVDRD YV\LSAELEKAGGCKHFNLSSKGADK SSNFLYLQVKGEVEAKVEELKFDRYSV FRPGVLLCDRQESRPGEWLVRKFFGSLP DSWAIRGHSPVVT\TVVRAMLNNVVRPR DKQMELENKAIHGPGGKRHGSSQGH HTGRNGFYLFNLNTHDQIG |
| 2925 | 10976 | A | 3871 | 71 | 335 | PTRSTSSGSYMKRRSGSCSP\MISDTSVV LSMDNSRSSRAVVVKKIETRDGKLVSES SDVLPK*TAAAAPP\SLPLLRCPRAWEGG RYAW |

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| 2926 | 10977 | A | 3872 | 35 | 450 | DIEECESMH*DDIRKHTEMENEFALIKKD MDEAYKNKVELESHLEGLTEEISFLTQL YEEEIRELHVDPDLGHICGAVH*QQSLPGH EQHHR*GQGTVRGDRQPQPG*G*EHEIK YEELQTLAWKHGMTRGAQRLRSR |
| 2927 | 10978 | A | 3873 | 2121 | 2371 | LENQSPRHVYSLSLKSKNDVMLL/DTAI FCPEATSEALDVVTWASEAGTEELAFG FGLVLSYCKLSTSLSVASSFVGGDWL |
| 2928 | 10979 | A | 3874 | 29 | 3977 | AEVAHARWERCFFSPTFLWGCFRDRLL PGRRACFRRAGRLKRGSYNCSQLWLCV EKALAMDRSGFGEISSPVIREAEVTRTAR KQSAQKR VLLQASQDENFGNTTPRNQVI PRTSPSFRQPFTPKSRLLRQPDISCILGT GGKSPRLTQSSGFFGNLSMVTNLDDSN WAAAFSSQRSGLFTNTEPHSITEDVTISA VMLREDDPGEAASMSMFSDFLQSFLKHS SSTVFDLVEEYENICGSQVNLKIV |
| 2929 | 10980 | A | 3875 | 597 | 1088 | GCQRQVVPSPWRPPLQRAKQDMAWQLL EYQELMNIKLALDIEIATYRKLEGEESQ LDSGMQNMSIHTKTGGYAGGLSSAYG DLTDPGLSYSLGSSFGSGAGSSSFRTSS RAVVVKKIETRDGKLVSESSDVLPK*TA AAAPPSLPLLRCPRAWEGGRYAG |
| 2930 | 10981 | A | 3878 | 1 | 2474 | MPGYSALSNNKPMLETTQMSITRGMGKL LVVRCGTEKAGPAVPGGMEGPRSSTHV PLVLP LLVLLLAPARQAAAQRCPQACI CDNSRRHVACRYQNLTEVPDAIPELTQR LDLQGNLLKVIPAAAFQGVPHLTHDLR HCEVELVAEGA FRGLRLLLLNLASNHL REL PQEALDGLGSLRRLEEGNALEELRP GTFGALGALATLNLAHNALVYLPAMAF QGLLRVRWRLRSHNALSVAPEALAGLP ALRRLSLHHNELQALPGPVLSQARGLAR LELGHNPLTYAGEEDGLALPGLRELLLD GGALQALGPRAFAHCPRHLTDLRGNQ LDTLPPLQGPQQLRRLRLQGNPLWCGCQ ARPLEWLARARVRSDGACQGPRLRG EALDALRPWDLRCPGDAAQEEEELEERA VAGPRAPRGPGRGPGEERAVAPCPRAC VCVPESRHSSCEGCGLQAVPRGFPSDTQ LLDLRRNHFPSPVRAAFPGHLVSLHL QHCGIAELEAGALAGLRLLIYLYLSDNQ LAGLSAAALEGAPRLGYLYLERNRFLQV PGAALRALPSLSLHLQDNAVDR LAPGD LGRTRALRWGL/HLSGNRITEVSLGALGP ARELEKLHLDRNQLREVPTGALEGLPAL LELQLSGNPLRALRDGAFQPVGRSLQHL FLNSSGLEQVGTGHLAGLVQEAAGHR QRAFTQAFASPLVPGLGPGQLSLHLQK NQLRALPALPSLSQLELIDLSSNPFHCDC QLLPLHRWLTGLNLRVGATCATPPNAR GQVRKAAA VFEDCPGWAARKAKRTP ASRPSARRTPIQKTVWTR |
| 2931 | 10982 | A | 3879 | 1 | 531 | ETPSSEPMEEEDDDLELFGGYDSFRSYN SSVGSESSYLEESSEAEENEDREAGEL/H DLPAFAAQPWDSSLLGWQWF*ASCL/LR CVVSWVQGKPSSPRPRGSAASPAPGATP PTRPKPVSWLGYRENHRPKPKSCTRLP GLPKLEPSSTLKGQDSWQMGHQDCTL WSWASTGGSS |

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| 2932 | 10983 | A | 388 | 119 | 1533 | KKMNLAEICDNAKKGREYALLGNYDSS MVYYQGVMMQQDSRDIAQSVQSRQLSK GKWPTRFGQELLAEYEQVKSIVKHFKK VFKIDKPSQISPVLSR*THLEIPAVWPTP VPAEHRAPPQIRR/RQSRKTSEERNGRS RSPGTCRPSTSYIKE*/NSLLQVGTRTIEPE GGDDKGRKNMQDGASDGEMPKFDGAG YDKDLVEALERDIVSRNPSIHWDIADL EEAKKLLREAGVLPWWMPDFFKGIRRP WKNDSONLGKPYSAQDDIGMNIVGPL THGFSSASAAPETTRQPLFLLLSLSKV KTFKGVLMMVGPPTGKTMLAKAVATEC GTTFFNVSSSTLTSKYRGESEKLVRLFE MARFYSPTTIFIDEIDSICSRRTSDEHEA SRRVKSELLIQMDGVGGALENDPDKM VMVLAATNFPWDIDEALRRRCFIWVG FPDVPQEKDTSVPESCLLTDWWWGL |
| 2933 | 10984 | A | 3880 | 143 | 606 | NKYTDYCQLLKSKGVDKKGKTASSLP EGSQSISREHLPAQSWLPWACLLWLPA LL/HDEMOMRKQLPGLRSRAHSARQVR W/PCEAAAAGCRMQRQASHLKSPEGKFH GHFLNTRVGRAGGNPHRPGKKWLLPSS VYVCNTEHCLWGAWCPKPNG |
| 2934 | 10985 | A | 3881 | 253 | 514 | |
| 2935 | 10986 | A | 3882 | 950 | 1612 | IIPIASVTQPKQPAWKTGTGKGPQVS ISITEKVKSMQYDKQGIADTWQVVGTV TCKCDLEGIMPVNTISLSLPTNGSPLQDIL VHPCVTSLSAILTSSSIDAMDDSAFSGP YKFPPTPLESFNLCFYTSQSVIDDQPSKL LLNDGIGELMGFNWSNRSCGQVGSNQY AYCMPYAADQRTWRRGAWTSKYRNKN ALYTFVKRFSHLRKQREKNPYP |
| 2936 | 10987 | B | 3886 | 146 | 326 | MDESAPFLCRTLGRVDSDDPGLPGCAS GPLAVPESEQKVHERKSLHWDGLTVSL VRAQX* |
| 2937 | 10988 | A | 3887 | 575 | 828 | CYPKVGRKPIKGEAPGAREKKNFAAE KRGLIPHGRKCLPISPCTGTRGPWCPCSS SGCASADTCTPRGALGAQKPIRESNF |
| 2938 | 10989 | A | 3888 | 3 | 267 | AMVGGGGVGGGLENANPLIYQSRGER PVTAGEEDEQVPDSIDAREIFDLIRS*AW PLTPQPAYWYPGPSSCQGCYRCFLES LTMRN |
| 2939 | 10990 | A | 3889 | 1 | 942 | |
| 2940 | 10991 | A | 389 | 293 | 805 | KARDKSPFLGDLCLKDTGQSSLLQCRFF PFLGTKISCFQNVHSWQTITSDGLSAGDG GFGPKYQ/RSRGQIPSGLNSLPLNSSEDL LPTPHFPLQSQGLGSQVAQIDDVKAPPPF PAEPQPKRLRSPRPLGAIESVAVSRSLP SGPTGTDAL*WLSVQKPPTRIHGNE |
| 2941 | 10992 | A | 3890 | 3 | 470 | AMVGGGGVGGGLENANPLIYQSRGER PVTAGEEDEQVPDSIDAREIFDIRRCWAR AGSGGLRWGEQ*YRAAGGAASQQGVP GRGF*VGKGAESLFLHFPQLIRFLNDP EHSLEELNVVEQVRVQVSDPESTVAVA FTPTISHWSMGTIGVC |
| 2942 | 10993 | A | 3891 | 2 | 604 | ARSHRISGGGSAMVGGGGVGGGLEN ANPLIYQRFGE/RPVTAGEEDEQVPDSIDA REVFDLIRSHQMTPEHPALTLEELNVVE QVRVQVSDPESTVAVGFPKPTHSGTCR HGPPILGLSNKVKLLRSLPSAFSRWDVA HLLPGDPLPQEHAVEQATLQIKEAGWAT ALGRTHHLLVVNQCLSSPAPGTWAFV PLSLA |
| 2943 | 10994 | A | 3892 | 73 | 204 | |

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| 2944 | 10995 | A | 3893 | 1 | 846 | QGANMPRYAQLVMGPAGIVKSTYCAT MVQHCEALNRSVQVNLDPAAQHFNYS VMADIRELIEVDDVMEDDSLRFGPNGL VFCMEYFANNFDWLENC LGHVEDDYIL FDCPGQIGVVTLTWPVMKQLVPALEQ WEFRVCGVFLVDSQFMVDHSRFSGHL AALSAWISLEIPQVNIMTKMDLLSKKA KKEIEKFLDPDMSLLEDSTDLRKAKN SRKLDLKAJMWDLIGWTYSLVRIF/IPYD QSDEESMNIVLQHIGFAIQYGEDLEFKR NPKEREE |
| 2945 | 10996 | A | 3896 | 1 | 1319 | MDYGLLCGQQLVPQVEPVIORGHESLV HHILLYQCSNNFNDSVLESHECYHPNM PDAFLTCTVIFAWAIGGEGFSYPHVGL SLGTPLDPHYVLEEVHYDNPTYEEVLD EKYKYKVLASDEGLLTGHNMAVGFTW WKGLIDNSGLRLFYTM DIRKYDAGVIEA GLWVSLFHTIPPMPPEFQSEGHCTLECLE EALAEKPSGIHVFAVLLHAHLAAGR GIRL RHFRKGKEMKLLAYDDDFDNFQEFQY LKEEQTILPGDNLITECRYNTKDRAEMT WGGLSTRSEMCLSYLLYPINLTRCASI PDIMEQLQFIGVKEIYRPVTTWPFIIKSPK QYKNLSFMDAMNKFKWTKEGLSFNK LVLSLPVNVRCSTDNAEWSIQGMTAL PPDIERPYKAEPLVCGTSSSSSLHRDFSIN LLVCLLLSCTLASTKSL |
| 2946 | 10997 | A | 3897 | 1 | 394 | |
| 2947 | 10998 | A | 3898 | 1 | 150 | |
| 2948 | 10999 | A | 3899 | 708 | 911 | |
| 2949 | 11000 | A | 39 | 132 | 370 | SNSPA*PSGEPGTMG/CRPPCPVNFILRK NGVPPCGPGGPKSPDLRTHPLGPPKG/RG IPGGTHCPGPPLGFKKPWPPGRV |
| 2950 | 11001 | A | 390 | 2 | 428 | GLPGSTTASAAAASAASSDAPSFQLG KPRLQQTSTFYGRFRHFLDHDPTLFTVTE RRLKEAVQLLEDYKHGTLRPGVTNEQL WSAQKIK/SGYIPFGTPIVVGLLLPNQTLA STVFWQWLNHSHNACVNYANRNATKP SPA |
| 2951 | 11002 | A | 3900 | 1 | 1349 | MAAGQRRSSLSRLGSQFINCDPECQLSC LVGLEVQKEEVIRAAEGWKRAAPAGLR PTNYSNRQASEGRVVIAGNQSYQSRASP RPLARWKASANGRAPIAEPAAVAGLG AGSGKRRRGWKMPVHSRGDKKETNHH DEMEVDYAENEGSSSEDEDTSSSVSED GDSSEMDDDCERRRMECLDEMSNLEK QFTDLKDQLYKERLSQVDAKLQEVIVAE RAPEHLEPAGNLQENMQIRTKVAGIYR ELCLESVKNKYECEIQASRQHCESEKLLL YDTVQSELEEKIRRLIEDRHSIDITSELW NDELQSRKKRKDPFWDKPKPGVVSGP YIVYMLQDLILEDWTTIKNAMATLGPH RVKTDPPVKLEKHLHSAISEEGRLYYDG EWYIRGQTICIDKKDECPTSAVITTINHDE VWFKRPDGSKSKLYISQLQKGKYSITFII MI |
| 2952 | 11003 | A | 3901 | 38 | 383 | |
| 2953 | 11004 | A | 3902 | 252 | 526 | |

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| 2954 | 11005 | A | 3903 | 777 | 1719 | LLTLTFPRCSVAQPLPFTGGTSVSWALL ALHVAVVFLFAGAAGCVATLLHDAAM NPAEVVKQRMQMYNSPYHRVTDCVRA VWQNEGAGAFYRSYPTQLDHDVPFQAI HFMDLWNSCRSTLTPKRSYNPDSHFFSG LCAGAVAAAATTPLADVCKTLLNTPGVL GFELTHYRTYQGMASAFRTVYQVGGV TAYFRGVQARVIYQIPSTAIAWSVYEFF KYLIHLKGQEEWRAGKVKLALNESPGV QDDTDASWSHSLSPGMLPPQVELKGKE KGLSPTDFGVLNTSSCQPLPPPPFLPGP KHVQQSTPQHL |
| 2955 | 11006 | A | 3904 | 1 | 1788 | MLQQGAILEAETKPSDITKYTSALIFNFP ASTADLGKTKRPAVEEKETPNKTRAQSL FLLAKERRQDPFRPGLSALPLVKMAAIG GAAHSEGRRLPCRPRPFTSPRPSRLDA LQVQRDQSDGAALFGQPLQGRAGLSER PCQTERGKKPQQRQLSNRLQTAFRRGPL GSGFQLRWSCRGCNVNAARSPPGSAQR SRSREPLLGPRWPGSRGWQLCESLKKIA KGWVSQDPSPRQLKECGQSASTSPRTPY SQDLLQHPKLEVAADPRTRGTREPAAL VERLEMLSGAGSVVDVPLLVVRRRRR RRRRHSAQRALAAAAAAASEPLDCQM RLCASLGVFSTAPSSACRADITDCVSGL AGGEMVPRRVLADQLTEEQIAEFKEAFS LFDKDGWDTITTKELGTVMRSLGQTQT EGVELQDMINEVYADNGTIDFPVFLTM MARKMKDSDSEENRESFRVFAKDNGN YISAAELRHVMTNLGEKTTDLEVDemi READIDGDGQVNYEEFVQMMTGKMED LTFQLPFPSPLESNWNLLLTLLQKKEKK KKVHLFHSCFLYSKTECQKYLIVHTHQ NLHVLVGGPVP |
| 2956 | 11007 | A | 3905 | 1 | 351 | GPPRPPTPPLLKPIRGATARPPRSRF*PRS DIPPLSRVLVARPPSPPLGKPLWIMGRP RPPIAPLARAPMGRPNRAWMLLLPRRCF KLFEGNRRQCSSRGCHHGSGRRAGDRP NLS |
| 2957 | 11008 | A | 3906 | 3 | 345 | SCRCKRKAGKGRPGEQTDRTROPTSNN ELSSHTTAYASNQPI*LTRAPPSTQVRP VPGPPAGAVVAVPGGALASVSFDSRDSK TAAQSSEVGALPPHQDVTICAVRAAT |
| 2958 | 11009 | A | 3907 | 3 | 387 | RPLQTKGRKGQAGFGRSPARLPEPWWQ PREEH/WASVSFDSRDSKMAAQSAKVV LKSTTKMSLNERFTNMLKNKQPTPVNIR ASMQQQQQLASARNRRLAQQMENRPSV QAALKLKQSLKQRLGKSN |
| 2959 | 11010 | A | 3908 | 565 | 719 | GRDVTPRSKPAPRWTSRSSPGLKKRW CSRSWRSWERGPR*SSALGKSNIQAR/ WPTHGPGQGSNRRTRPTPYSREALPRE GLRGGRATENPT*GRDVTPRSKPAPRW SRSSPGLKKRWCSRSWRSWERGPRW SYGSWRNRW |
| 2960 | 11011 | A | 3909 | 299 | 557 | ADGSADLDSQRSSNELSHTTAYASNQP/ LHLANPSPSTSQLRFRPVPVAVPGAVG GSPREEHLASVSFDSRDSKMAAQVSSEK LC |
| 2961 | 11012 | A | 391 | 3 | 297 | |
| 2962 | 11013 | A | 3910 | 1 | 420 | |
| 2963 | 11014 | A | 3911 | 2 | 437 | |
| 2964 | 11015 | A | 3912 | 10 | 250 | |
| 2965 | 11016 | A | 3913 | 2824 | 3156 | SNEGVKGLSRQKAWTADYNFCLGNGCH FSGFYFDSDCYSSYRRCRTCCDFCNSG RNCSGFWFLCCTILCSD*SSFLISRSTW TPGLAIIPTRRLIT*TLISWSTV |
| 2966 | 11017 | A | 3914 | 1 | 70 | |
| 2967 | 11018 | A | 3915 | 42 | 140 | |

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| 2968 | 11019 | A | 3916 | 4594 | 4848 | HIYCE*SLYLFRE*DLDDGDLDLECELAR LRDLVYDLE |
| 2969 | 11020 | B | 3917 | 565 | 1161 | MYHGWVVDLHIHAEDTLPPFYLGEKDD VTYAIKPTCWPGLDIIPSCALHRIETELM GKFDEGKLPDPLMLRLAIETVAHDYD VVIDSAPNLGIGTINVVCAADVLIVPTPA ELFDYTSALQFFDMLRDLKNDLKGFE PDVRILLTKYSNSNGSQSPWMEEQIRDA WGSMVLKNVRETDEVGKDLHALLVR L* |
| 2970 | 11021 | A | 3918 | 3 | 226 | LSVLFCFCFVGSNFNFYVYSCCVFMATS QTDICMHTYSLIEMIVIHYNLEFF*ISKM ATIAVLGFLRLDIYHV |
| 2971 | 11022 | A | 3919 | 1469 | 2806 | CGSPPFATSSFFALS GHVLF AKLCTMVAP KLRSWMYAVYGALAVMTMGWPWYLL LLGHCVGLYVASLLGQPWLCLGLGLAS LASFKMDPLISWQSGFVTGTFDLQEVLF HGGSSFTVLRCTSFALSCAHPDRHYSL ADLLKYNFYLPFFFFGPMITDRFHAQVS QVEPVRREGELWHIRAQAGLSVVAIMA VDIFFHFFYILTIPSDLKFANRLPDSALAG LAYSNLVYDWWKAAVLFVGVNTVACL DHLDPQPPKCITALYVFAETHFRGIND WLCKYVYNHIGGEHSAVIPELAATVAT FAINTTLWGPCDIVYLWSFLNCFGPQTL KLWVVPKTGQKWGPKEIEGLLCQVQ MSRRVRALFGAHELSPHMYNLVSLN SLAKFTELVARRLLTGFPQTLSILFVTY CGVQLVKERERTLALEEEQKQDKKKPE |
| 2972 | 11023 | A | 392 | 1 | 885 | |
| 2973 | 11024 | B | 3920 | 54 | 316 | TIWDGEETVYCFKERSRAALKACYRGN RYPTPDEKRRLATLTGLSLTQVSNWFKN RRQRDRTGAGGGAPCKRKLPPGQPCVW QPHRDG* |
| 2974 | 11025 | A | 3921 | 1 | 2219 | MATLPAEPSAGPAAGGEAVAAAAATEE EEEEARQLLQTLQAAEGEAAAAAGAGA GAAAAAGAEGPSGPGVSPPEAASEPPT GLRFSPEQVACVCEALLQAGHAGRLSR FLGALPPAERLRGSDPVLRARALVAFQR GEYAELYRLLESRPFAAHHAFLQDLYL RARYHEAERARGRALGAVDKYRLRKKF PLPKTIWDGEETVYCFKERSRAALKACY RGNRYPTPDEKRRLATLTGLSLTQVSNW FKNRRQRDRTGAGGGAPCKSES DGNPT TEDESSRSPEDLERGAAPVSAEAAAQGS FLAGTGPPAPCPASSILVNGSFLAASGSP AVLLNGGPVIINGLALGEASSLGPLLLTG GGGAPPPQSPQGASETKTSLVLDPQTG EVRLEEAQSEAPETKGAQVAAPGPALGE EVLGPLAQVVPGPPTAATFPLPGVPVAV AAPQVVPLSPPPGYPTGLSPTSPLNLQP VVPTSQVVTLQAVGPLQLLAAGPGSPV KVAAAAGPANVHLINSGVGTALQLPS ATAPGNFLANPVSGSPIVTGVALQQGKI ILTATFPTSMLVSQVLPAPGLALPLKPE TAISVPEGGLPVAPSPALPEAHALGTLSA QPPPPAAATTSSLSLFPSPDSPGLLPNFA PPPEGLMLSPAAPVWSAGLELSAGTEG LLEAEKGLGTQAPHTVLRLPDPDPEGLL LGATAGGEVDEGLEAEAKVLTQLQSV VEEPLEL |
| 2975 | 11026 | A | 3922 | 185 | 478 | VSDTLWALAGLAAGRWAGGCQTGLQ GVVQGLGLLINGPRAGAAPLSLGNLHPP SAARWHPS*AASHTGTGQSLVGIVEPHN PTSSGG*RPGTAGRSQ |

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| 2976 | 11027 | A | 3923 | 74 | 593 | RGWVMWVDEFQPALVLSPYERQLNLDA SVQHLEDGDGKRKRSSSSPRSSINKKAKA LDNSLQPKSLAASSPPPCSQSPQCPPEKP QGVKPHGPRGPLSASGVPGPQPWPQG GG/WWGAAGRVAEPRTESREPVSGAGT SSRSPSPTGFRQPPHPSARPSRAAPGQR GWAGDRR |
| 2977 | 11028 | A | 3927 | 1 | 2936 | MALMFTGHLLFLALLMFAFSTFEESVSN YSEWAVFTDDIDQFKTQKVQDFRPNQK LKKSMHLPSLYFDAGEIQAMRQKSRASH LHLFRAIRSAVTVMLSNPTYLPPPKHA DFAAKWNEIYGNNLPLALYCLLCPEDK VAFEFVLEYMDRMVGYKDWLVENAPG DEVPIGHSLTGAFATAFDLYNLLDNHRR QKYLEKIWWITEEMYEYSKVRSWGKQL LHNHQATNMIALLTGALVTGVDKGSKA NIWKQAVV |
| 2978 | 11029 | A | 3928 | 2 | 512 | |
| 2979 | 11030 | A | 3929 | 1 | 399 | |
| 2980 | 11031 | A | 393 | 2 | 674 | SCPLSCTSAATGLWVKEGLRIVSSVLLGL SCPWGSPLAELDLGEG/RLWRTSFYGR FRHFLDIIDPRTLFTVTERRLREAVQLED YKHGTLRPGVTNEQL*SAQKISQAIYHP DTNEKIFMPFRMSGYIPFGTPIVVGLLP NQTLASTVFWQWLNQSHNACVNYANR NATKPSPASKFIQGYLGAVISAVSIAGL NVLVQKANKFTPATRLLIQRFVPPFAV |
| 2981 | 11032 | A | 3930 | 1 | 1812 | NRRTRP GCGVVTCTYRREFIQRLEAAL NVHDGCVNTICWNDTGEYILSGSDDTKL VISNPYSRKVLTTIRSGHRANIFSAKFLPC TNDKQIVSCSGDGVIFYTNVEQDAETN RQCQFTCHYGTTYEIMTVNDPYTFLSC GEDGTVRWFDTRIKTSCTKEDCKDDILIN CRRATSVaicPIPIYLAvgCSDSSVRU YDRVRLGHLKELQGNyAGRGTTGIGLP RFISLPHLNNKSCRVTSLCYSEDGQEILV SYSSDYTYLFDPKDDTARELKTPSAEVER REELRQPPVKRLRLRGDWSDTGPRARPE USERERDGEPESPMCPMLQRMSDMLSR WFEEASEVAQSNRGRGRSRPRGGTSQSD ISTLPTVPSSPDLEVSETAMEVDTPAEQF LQPSTSTMSAQAHSTSSPKESPHSYFSC YFLPDSQDRQSVEASGHHTHQSEFLR GPEIALLRKRLQQLRLKKAQQRQQLA AHTQQPSTSDQSSHEGSSQDPHASDSPS SVVNKQLGSMSLDEQDNNNEKLSPKP GTGEPVLSLHYSTEGTTTSTIKLNFDEW SSIASSSRGIGSHCKSEGQEEFVPQSSVQ PPEGDS |
| 2982 | 11033 | A | 3931 | 1 | 1878 | |
| 2983 | 11034 | A | 3932 | 2 | 202 | |
| 2984 | 11035 | A | 3933 | 9 | 111 | SRQAWHEASNYGPMKSGNFGGI/RNMG GPYGGGNL |
| 2985 | 11036 | A | 3934 | 297 | 611 | QWGLRFMNGVLSGGLSVQTASPPSASR RHFP SLGVGDGELSHGGRCPAGVKVGR GGGNSYSLSKARCFGGHGVSSASVSAGS RSS*ARLSFPSPSLTGTGFGR |

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| 2986 | 11037 | A | 3935 | 14 | 1276 | KSGGTALAAVAAAPGVRRCSSQSCFSS SGSSHYSARTSPVRVRPRRLSSRSAAGN RAEATESAMEKTLETVPLERKKREKEQF RKLFIGGLSFETTEESLRNYYEQWGKLT DCVVMRDLASKRSRGFCFVTFHSIGLE VDAAIASRPHSINGEVVEQKRAVAREE SGKPGAHVTVKKLFVGGIKEDTEEHHLR DYFEEYGKIDTIEIITDRQSGKKRGFGFVT FDDHDPVDKIVLQKYHTINGHNAEVRK ALSRQEMQEVQSSRSRGGNFGFGDSR GGGNGFGPGPSNFRGSDGYGSGRGF GDGYNGYGGGPGGNGFGSPGYGGGR GGYGGGPGYGNQGGYGGGYDNYGG GNYGSGNYNDFGNYNQPSNYGPMKS GNFGGSRNMGGPYGGGNYGPGGSGGSG GYGGRSRY |
| 2987 | 11038 | A | 3936 | 827 | 2064 | QRRVPCGAPRRVVSRAAAVLTAPG RVRVFVVRGDLSHLARLREIGLKRLSPR WREKKKQFRKLFIGGLSFETTEESLRNY YEQWGKLTDCVVMRDPASKRSRGFGFV TLSSMAEVDAAAMAARPHSIDGRVVEPK RAVAREESGKPGAHVTVKKLLVGGIKE DTEEHHLRDYFEEYGKIDTIEIITDRQSG KKRGFGFVTFDDHDPVDKLDLRKYHTI NGHNAEVRKALSRQEMQEVQSSRSRGR GNFGFGDSRGGGNGFGPGPSNFRGSD GYGSGRGFGDGYNGYGGGPGGNGFGGS PGYGGGRGGYGGGPGYGNQGGGYGG GYDNYGGGNYGSGNYNDFGNYNQGS SYGPMKSGNFGCWRNMGGPYGGGNY GPVGGSGSGGYGGRSPILKLLPICHGAS LV |
| 2988 | 11039 | A | 3937 | 36 | 320 | GPGRWVVVDEVTMWLELEQYPVSFLKQ PFEIGRHLDLPKGTYGICVNMCPGNKSC/ PRGKRCQSNCGHVCKVVPETSKSQPLR CSQGMTHWSSL |
| 2989 | 11040 | A | 3938 | 3 | 713 | |
| 2990 | 11041 | A | 3939 | 1 | 519 | |
| 2991 | 11042 | A | 394 | 485 | 1044 | HLVPLCPCNLKAGRCTVQERLLVICCS RSWRWRNLM*RWLNYPVSSGHRH*SS LARETSVDPDMRKGPAGAEGKGKAVGC KGVSQETAAYWKRTSSSLEPTWTLTN KPMFFGFRNLFAPTFRHTPEALWLPTPC HRGSPALHIEAFMPAALPSGTASCELPGH WPYQLSGVLCCAPWVIKEA |
| 2992 | 11043 | A | 3940 | 1 | 966 | MGHHLMDKLVALGGLYYAIQRHYATK CSVLKNDQILVIGLFMIQNVIYRKHFANP LSALFLQQGIELFAAIAEIHITVAERNHA ITQIRLEAQTFDSLKEWHNAIRKSLDYE ALQAFEFVRGATDRGFALSSSEALVRVL VLDANDNSPFVLYPLQNGSAPCTELVPR AAEPGYLVTKVVAVDGDSGQNAWLSY QLLKATEPGLFGVWAHNGEVRTARLLS ERDVAKHRLVVLVKDNGEPPRSATATL QVLLVDGFSQPYLPLPRAAPAQAQADSL TVYLVVALASVSSLFLFSVLLFVAVRLC RRSRAAPVGRCSVL |
| 2993 | 11044 | A | 3941 | 1 | 2783 | RILSVDDFVELNVSSLVAVAEGIGYRDL DSNMKKLGRIHPNRQVLAFLMVFLSQV RLEPIRYSVLEETESGSFVAHLAKDLGLG IGELASRSARVLSDDDKQRLQDRQTGD LLLREKLDREELCGPIEPCVLHLQVVLE MPVQFFQGELLIQDINDHSPIFPEREVLL KILENSQPGTLFPLLIAEDLDVGSNGLQK YTISPNSHFILTRNHSEKKYPDLVQDK PLDREEQPEFSLTLVALDGGSPRSGT |
| 2994 | 11045 | A | 3942 | 383 | 703 | NRITPTSARINLSJLVPSAINNGSMTEIN RTVISGTPRQNSIKMTDKIRTIGIWERRPG VVVLTTCIMV*HLTSAIANRLNLLRKL |

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| | | | | | | RMVIFSHRLKVSSMKSA |
| 2995 | 11046 | A | 3943 | 1887 | 3072 | NFVMCHGEPWLAGRTVVPVSTLSGPEL ALQKLGKTPLGRLFTSSTLTRDFIEIGR DAGLWGRRSRLRLSGKPLLLTELFYRRH RCTKRKKICDCISANVWAVLKTVEAAGS DRPVQCLTITAVQREERDTQSLSVITAELE PVSSPHFIREAGQYGTGRSSKEREVQPVV QRSFSNWIRNNGDICELSPSTSGDHPPPS GPGLYSARKAIMQHYQARGMRDVTVED IYIGNGVSELIVQAMQALLNSGDEMLVP APDYPLWTAASVLSGKAVHYLCDESS DWFPDLDDIRAKITPRTRGIVINPNNTG AVYSKELLMEIVEIARQHNLIIFADEIYD KILYDDAEHHSIAPLAPDLLTTTFNGLSKT YRVAGFRQGWVHRFFTPRLTVQAI |
| 2996 | 11047 | A | 3944 | 623 | 2587 | SPRKGKKGKKANRVLLTGAPLDPIDLS QSAVSHSVKEL/ENHTGVRLLDRTTREV VLTDAGQQLALRLERLLD/ELNSTLRDT GRMGQQLSGKVRVAASQTISAHLIPQCI AESHRRYPDIQFVLHDPQQWVMESIRQ GDVDFGIVIDPGVGDLCQCEAILSEPFLL CHRDSALAVEDYVPWQALQGAKLVLO DYASGSRPLIDAALARNGIQANIVQEIGH PATLFPMAAGIGISILPALALPLPEGSPL VVKRITPVVERQMLVRRKNRSLSTAAE ALWDVCNCAIQPFFTAITRCIGSVTVKLV LVPVGKSEFLAAQHKVVTCPNAGDIAV VASVIGLICITLSKERFEPPTAAGEIVADT VQEHIVVEIHAIRRTVGAIQRMQVEIKSGV TQAYLQLGINEKLGLSGRPDRPIGCLGTS KIYRILGKTVVCYPIIFDLSDFYMSQDVF LLIDDIKNALQFIKQYWKMHGRPLFLVLI REDNIRGSRFNPILDMLAALKKGIGGVK VHVDRLQGPLENDLVHVALIAESQRLQ VFLNTYGIQTQTPQQVEPIQIWPQQLVK VTLGAFGHEEEVISNPLSPRVIQNIYYKC NTHDEREAVIQELVIHIGWISNPNELFS GMLKIRIGLQNECSLVIQVSTIIPAT |
| 2997 | 11048 | A | 3945 | 102 | 2392 | RKQMNYSKQLKVFVTVAQEKSFSTRAG ERIGLSQSAVSHSVKELENHTGVRLLDLDR TTRAVVLTADAGQPLALRLERLLDELNST LRDTGRMGQQLSGKVRVAASQTISAHLI PQCIAESHRRYPNIQFVLHDPQQWVME SIRQGDVDFGIVIDPGVGDLCQCEAILSEP FLLCHRDSALAVEDYVPWQALQGAKL VLQDYASGSRPLIDAALARNGIQANIVQ EIGHPATLFPMAAGIGISILPALALPLPE GSPLVVKRITPVVERQMLRVDLRFAQK FQIGDRKILRSGNNVAVNVLPAATCGFPFP VCCWRFAYGCCSALLRIPRLYSVFIIISL LYGFSRAHSSPGACWVFIHERFGQFMY GLYPHDQRWRINLALLIGLVSIAPMFWKI LPHRGRYIAAWAVIYPLIVWWLMYGGF FALERVETRQWGGLTLTLIIASVGIAGAL PWGILLALGRRSHMPIVRILSVIFIEFWRG VPLITVLFMSSVMLPLFMAEGTSIDKLIR ALVGVLFSAYVAEVVRGGLQALPKG QYEAESLALGYWKTQGLVILPQALKLE TVRQPOTLAMEEINCHHNYVQKEQHFG EEIYVTRKGAVSARAGQYGIIPGSMGAK SFIVRGLGNEESFCSCSHGAGRVMSTRK AKKLFSVEDQIRATAHVECRKDAEVIDEI PMA YKDIDAVMAAQSDLVEVIYTLRQV HSCRAGETGAVAPASDRGKGGDGNLRS NRGRRGAGVAASALPARHRARGRLPLC YR |
| 2998 | 11049 | A | 3946 | 2 | 331 | |

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| 2999 | 11050 | A | 3947 | 3 | 116 | |
| 3000 | 11051 | A | 3948 | 3 | 162 | |
| 3001 | 11052 | A | 3949 | 181 | 804 | RPLPRIGCCGPGAGQVGEARSPRVS LCF APCRLLRAGGGRALRRRGPGTPGPVARP SYSSFTQGD SWGEVDEEEGCDQVAR DLRAEFIMGQWSEPRKLSVLPDRNGS PVL PDKRNGIFPSGRGQQEPLRRWPFQ VLSILCSLLFAILLAFLLAIAYLIVKELHA ENLKNEDD VDTGLLGFWTLLIISLTAGIL LLQLFLGQ |
| 3002 | 11053 | A | 395 | 901 | 1213 | SQHFRPRWADHLRSGV*DQPGQHDET PSLLKIQKLAGYSGEHL*SQLLRRLRHEN CLNPGSGGCSEPRLHHCTPAW/VAEPDS VGGGVGGKEKNNTSNMLQTRP |
| 3003 | 11054 | A | 3950 | 1 | 149 | |
| 3004 | 11055 | A | 3951 | 1 | 1896 | |
| 3005 | 11056 | A | 3952 | 3 | 275 | |
| 3006 | 11057 | A | 3953 | 2 | 395 | |
| 3007 | 11058 | A | 3954 | 1 | 209 | |
| 3008 | 11059 | A | 3955 | 466 | 3315 | EMVPRWAIYQGFQDCLVHHASSRASGL WKL NPCRGLRCPDTRLPTSRWPNRDTR SASTQLLGKQSLPPAPEADPVFLPQEENE PPSPLVSGIIDYNMPLTSTYLKQMKLRV MNSQEQAGSSPTPIQTERHTAQLLLTAD QTLVLPATQHYVVLK KFRPGAEDIMSG GPTLEAAEFDDLIGKCLPDRPIAGSVRLG DRIWNPRGSPRRRCRLHGQCVPGSGLER RPRDYPITLQLWLARRQDPARCGLAEHN DR |
| 3009 | 11060 | A | 3956 | 11 | 755 | ETHAPPSGVWGLERPSHPADQEIAGGQG QTAPAWEKPHSHPTPKSCGDQTKTTLHT ERREDKPSFTRAGWG WENLKGPVTEG AGSPGGSSHGAGLNRDHPLQSQPGRRAI PWPQRAPTHMLFSMTRGQSPGAAPGAQ PEISKLAGYKQKQKQKRSCLRKKCHP/QE AGHRQRVASAGPGLQGEAAGEGRGEG AFWLKARN SKYSSLGINIPNKG AQGSC LGKVGCRRHDPHSGLSAPFPRMSQAL |
| 3010 | 11061 | A | 3957 | 175 | 559 | VKRQLRRLRRSPWPDEKPKEGVKTE NN DHINLKVAGQDGSVEQFKIKRHTPLSKL MKAYCERQGLSMKQIKIPDFDGPVINE TDTPATVGKWKDERYQLMVFQARPG GVYLKRELCFLYSQNSVSF |
| 3011 | 11062 | A | 3958 | 140 | 380 | |
| 3012 | 11063 | A | 3959 | 98 | 426 | LLTPSSSAALKGESVQWHLREAGQSLPR RLTCAGWNKRFLHWIDQLSG* TQTCLLL VVFVWIATE*LGESLPL*APIGGTQPW*F LIGAMKKHQETGENDHFNSPGPSH |
| 3013 | 11064 | A | 396 | 110 | 1012 | KTTRGYTLLHCAAAWGRLETLKALVEL DVDIEALNFRERARDVAARYSQTECVE FLDWAGLNP GTATHDSDEEAAFLTRVW STGHND SGVKQRMGQKEIQNATSSNH TCPSSITLQRKKG V*FVGLLW*FRNVSTL LMKTFLPQARNSPPETPSGTTITQITGKIC RMYFWSYMESEGPPESEAEFFSQEEEE NEEEEAQEPEETGPKNPLLQPALTDGVE GLQKIFEDPENPHHEQAMQLLEEDIVG RNLLYACMAGQSDVIRALAKYGVN LN EKTTRGDTLLHCAAAWGRLETL |

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| 3014 | 11065 | A | 3960 | 234 | 1050 | ARTLKRRWKVRKTVIGRKVQTMKILETL RISALLWEEVLLLGLKDKEYTSFWND CISSGLRGGILIELAMRGRIYLEPRTMRK KRLLDRRVLLKSDSPTGDVYWDETLKH IKATEPTETVQTWIELLTGETWNPFLQY QLRNVREERIAKNLVEKGILTTEKQNFLLF DMTHPVTNTTEKQRLVKKLQDSVLER WVNDPQRMCKRTLALLVLAHSSDVLEN VFSSLTDDKYDVAMNRAKDLVELDPEV EGTKPSATEMIWAVLAFAFNKS |
| 3015 | 11066 | A | 3961 | 1 | 1074 | MEPIGARLSLEAPGPAPFREAPPAEELPA PVVPCVQGGGDDGGGASETSPDAQLGD RPLSPKEE/CRPPGAGGAAGMPPPLPRAL LFLARRPHL/VRRPSSCSSSSNRNRHWA A/SGAEDAQLGPGGCCAKCKKRVQFAD TLGLSLASVKHFSEAEPPQVPPAVLSRLR SFFPMRAEDLEQLGGLLAAAAVAAPLSAP PSRLRPLFQLPGPSAAAERLQRQVCLER VQCSTASGAEVKSGRVLSCPGPRAVTV RYTFTEWRSFLDVPaelQPEPLEPQQPEA PSGASEPGSGDAKKEPGAECFHSLCLPP GLQPEDEEDADERGVAHVFAVCYRCAQ GEYWDNNAGANYTLRYARPADAL |
| 3016 | 11067 | A | 3962 | 42 | 424 | |
| 3017 | 11068 | A | 3963 | 3 | 899 | PPNVFSPASLPFFPAEGGPGRSRWREGG YLSQSRSGRLSQEEAASRSAGGMAGAPD ERRRGPAAGEQLQQHVSCQVFERLA QGNPQQGFFSFFTSNQQCLRLKLTLET NPYVKLLLDAMKHSGCAVNKDRHFSCE DCNGNVSGGFDASTSQIVLCQNNIHQA HMNRVVTHELIAFDHCRAHVDWFTNI RHLACSEVRAANLSGDCSLVNEIFRVQ FGLKHPPQTCVRDRATLSILAVRNIKE VAKKAVDEVFESCFNDHEPFGRIPHNKT YARYAHRDFENRGRIYYNSI |
| 3018 | 11069 | C | 3964 | 165 | 347 | |
| 3019 | 11070 | A | 3965 | 871 | 1194 | EFVFFFETESFSVTQLECSGHNGLHCN LHLPSSNAPASASRVARITGAHHHARLI FVFLVEMGFHQTGWAMLVLKLPDIQVIC PPWPPQSAGIYRHEPQHPGRK |
| 3020 | 11071 | C | 3966 | 54 | 197 | MVLSSFNQKAIKLALLKYFKISFQLPFF YVHKIGCRHSHFAMNVS** |
| 3021 | 11072 | A | 3967 | 263 | 742 | SRSHDHLTYVYVSPWNFFRALRISNSK NEMFMSFLFREMKKKKLPSDSDGLEAL EGKDKEKESTVHIETHQNTSKNVAAVQP MKRAGQKSKMKMKMEKY*DQDEEDREL IMKLLGSAGSNKEEKGKKGKGTCKDE PVKKQPOKPRGGQVRVSDNIKKE |
| 3022 | 11073 | A | 3968 | 189 | 1393 | SHTDFPYDNSTDGGDTSSDEDKEEHETP VEVELMTQVDQEDITLQSGRDELNEELI QEESSEDEGEYEEV/REKDQDSVGEMKD EGEETLNYPDTITIDLSHLQPQRSIQKLA SKEESSNSSDSKSQSRRLSAKERREMK KKKLPSDSDGLEALEGKDKEKESTVHIE THQNTSKNVAAVQPMKRQKSKMKMKM KEYKDQDEEDRELIMKLLGSAGSNKEE KGKKGKKGKTKDEPVKKQPOKPRGGQ RVSDNIKKETPFLEVITHELQDFC/AVDD P/HLIDQKPEPDLDDQGNENLFDSDQ GQPHPEDVL/LGFAIPICAPYTTMTNYKY KVKLTPGVQKKGKAATAKALNSFMHSKE ATAREKDLFRSVKDTDLRNIPGVKSV CTQSSERKKEIAEMKF |
| 3023 | 11074 | A | 3969 | 192 | 1510 | |
| 3024 | 11075 | A | 397 | 247 | 496 | |
| 3025 | 11076 | A | 3970 | 68 | 382 | MSVPDEEERLLRLTQRWPRASKFLLSGC AATVAELGTRLPTGPPGPVARAALGEE TAGAASRPGSAQSKRSPPSHARLAEVAV |

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| | | | | | | EARPRGGRRRDLEVSTAFSF |
| 3026 | 11077 | A | 3971 | 3 | 1451 | GAVRTWGRGFQTEKCOASLLNFWNPPT TAQVTIEAEPKVSCKGKDVLLLVHNLPO NLAGYIWKYGQMKDLYHYITSYVVDGQ IIYGPAYSGRET VYSNASLLIQNVTRDA GSYTLHIVKRGDGRGETGHFTFLYRH SLDSALSLEVTGSSQPL*DTWENCPTLW LHCLMTELTSGLDVLPVISAEPSPRS GFPVSKGKDNWKFHHPSLGCPWQGKL QRKHTSGGKVRLLKRRFQHCLMQVRTT SIEPKPSISSSNLYPREDMEAVSLTCDPE TPDASYLWWMNGQSLPMTHSLQLSKNK RTLFLFGVTKYTAGPYECEIRNPVSASRS DPVTLLNLLPKLPKPYITNNLNPRENKDV LAFTCEPKSENYTYIWWLNGQSLPVSPR VKRIENRILILPSVTRNETGPYQCEIQDR YGGIRSYPTLVNLYITTKHSGLYACSVR NSATGMESSKSMTVKVSAPSGTGHLPLG NPL |
| 3027 | 11078 | A | 3972 | 1 | 1008 | |
| 3028 | 11079 | A | 3973 | 3 | 1374 | |
| 3029 | 11080 | A | 3974 | 1 | 1854 | |
| 3030 | 11081 | A | 3975 | 1 | 1319 | |
| 3031 | 11082 | A | 3976 | 1 | 2247 | |
| 3032 | 11083 | A | 3977 | 1 | 1993 | |
| 3033 | 11084 | A | 3978 | 1 | 1006 | |
| 3034 | 11085 | A | 3979 | 3 | 1095 | AQLTAVLRKFLDPRLISTEENTQAAETM GPLSAPPCTEHIKWKGLLVASLLNFWN LPPTAQVTIEAQPPKVSEKDVLLLVHN LPQNLTYIWKYGQIRDLYHYITSYVVD GQIIYGPAYSGRETAYSNASLLIQNVTR DAGSYTLHIKRGDGRGVGTGYFTFLYL ETPKPSISSSNLNPREAMETVILTCDPETP DTSYQWWMNGQSLPMTHRFQLSETNRT LFLFGVTKYTAGPYECEIWEVSGSASRS PVTLESP/RMGPDLPRIFFSSPLNYFRER NLGFVPGLGDF*TPPAQYSWTINGKFQL SGQKLFIPQITPKHNGLYACSRNSATGE ESSTSLTIRVIAPPGLGTFCFQ |
| 3035 | 11086 | A | 398 | 653 | 1139 | RPFFPPHSESQNPQRQ/PDSSPTGTST*PA DTHCPRPVSAQGGTAEG**PRVHGSP PLPHSIGSAPPQCQEGAPAGEWAREPGE DGVVPGAPGQN*GKMEFSGAG/GQVPSR VVEGVQSHLRSEGPPACPAVPCAEGP DGRPGNTGRGGPGLRNQRRWEEW |
| 3036 | 11087 | A | 3980 | 3 | 1442 | IRADPAHELENCSCPGKRLSTERGRTAQ LTAVLREFLDPRLISTEENTQAAETMGTL SAPPCTQRIKWKGLLLTASLLNFWNLPT TAQVTIEAQPPKVSEKDVLLLVHNLPO NLTYIWKYGQMRDLYHYITSYVVDGEI IIYGPAYSGRETAYSNASLLIQNVTRDA GSYTLHIKGGDDGRGVGTGRFTTLHLET PKPSISSSNLNPRETMEAVSLTCDPETPD ASYLWWMNGQSLPMTHSLKLSETNRTL FLLGVTKYYLQDPIECEIRNPVSASRSDP VHPGISCPKLPKPYITNNLNPRENKDVL NFTCEPKSENYTYIWWLNGQSLPVSPRV KRPIENRILILPSVTRNETGPYQCEIRDY GGVRSDPVTLVNLYGPDLPRIYPSFTYY RSGEVLYLSCSADSNNPPAQYSWTINEKF QLPGQKLFIRHITTKHSGLYVCSVRNSAT GKESSKSMTVEVSGKVDPKHRWQ |

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| 3037 | 11088 | A | 3981 | 79 | 1565 | EASLLEDDDDGMVYLRPLTSHQYRTAQL RAMLRKFLDPRLSSTEENTQAAETMGPL SAPPCTQRITWKGLLLTASLLNFWNPPTT AQVTIEAEPTKVSKGKDVLVHNLQPN LAGYIWYKGQMKDLYHYITSYVVDGQII IYGPAYSGRETVYSNASLLIQNVTRDA GSYTLHIVKRGDGTGETGHFTFTLYLE TPKPSISSNLYPREDMEAVSLTCDPETP DASYLWWMNGQSLPMTHSLQLSKNKR TLFLFGVTKYTAGPYECEIRNPVSASRSD PVTLNLLPKLPKYITNNLNPRENKDVL AFTCEPKSENYTYIWWLNGQSLPGSVP RVKRPIENRVLIFTCSRGIETGPYQCEI VRDRLWVGLRSLPSPWNVPLMGPDLPRI YYPYFTYLPFQGGKPSDLSWLSRES*PHR AGVFFWGFNGGSFSGIQGQKLFIPQITT KHSGLYACSVRNSATGMESSKSMTVKV SAPSGTGHLPLNPL |
| 3038 | 11089 | A | 3982 | 1 | 2045 | MLEAAVHAPGNSDVTRTRCATQVLKPL VSYGQAETGFSVPQLKYPPWDGLLHRDI PPGTLPVEHSPCSLAALQFLNATSTHGE SAFARRKLESSFSQHSLOEGHRHGSRLSP SGAPVKDSGSRAPGSRGGQHPSQLLL CGRDDLQASSGHGPFLLLPPELPSRDA LQLLREASKFPTDKRQGRSWVAITNTA ATSLEWVPFHAFAPRSTLVSQQLSTER GRTAQLTAVLREFLDPRLISTEENTQAAE TMGTLSAPPCTQRIKWKGLLLTASLLNF WNLPTTAQVTIEAEPTKVSEKDVLLLV HNLQNLGTGYIWYKGQMRDLYHYITSY VVDGEIHYGPAYSGRETAYSNASLLIQNA VTQEDAGSYTLWHIKRRDGTGGVTGHF TFTLHLETPKPSISSNLPREAMEAVILT CDPATPAAGYQWWMNGQR/LSPMTHR LQLSKTNRTLFIKGVTKYIAGPYECEIRNP VSAISRSDPVTLNLLPKLPKYITNNLN RENKDVNLNFTCEPKSENYTYIWWLNGQ SLPVSPRIVKRPIENRILIPSVTRNETGPY QCEIRDRYGGIRSDPVTNLVLYGPDLPRI YPSFTYYRSGEVLVLSCFADSNPPAQYS WATNGKVFSLAQQGKLSIPQITTKHSGLY ACSVRNSATGKESKSITVKVSDWILP |
| 3039 | 11090 | A | 3986 | 212 | 461 | TEEHLYSPHWKGCGRKVKRLFQVRRGR GWIQTRQPGSMVKEPPLSEAGAESHVSC /RQGDCSRPPSPPLSPERVTPWLPDSHTW |

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| 3040 | 11091 | A | 3987 | 1 | 2353 | MRPPRAPVVPDLGGPRLCPVPAAGGAR SPSSPYSVETPYGFHLDLDFLKYIEELER GPAARRAPGPPTSRRPRAPRPLAGARS PGAWTSSSESLASDDGGAPGILSQGAPSG LLMQPLSPRAPVRNPRVEHTLRETSRRL ELAQTHERAPSPGRGLVREQMAAALRR LRELEDQARTLPELQEQVRALRAEKARL LAGRAQPEPDGEAETRPDKLAQLRRLTE RLATSERGGRARASPRADSPDGLAAGRS EGALQVLDGEVGSLDGTPQTREVAAEA VPETREAGAAQAVPETREAGVEAAPETVE ADAWVTEALLGLPAAAERELELLRASLE HQRGVSELLRGRLRELEEAREAAEEAAA GARAQLREATTQTPWSCAEKAAQTESP AEAPSLTQESSPGSMDGDRAPAGILK SIMKKRDGTPGAQPSSGPKSLQFVGVNL GEYESSSEDTNDSGDSENGGAEPGGS SSGSGDDSGGSDSGTPGPPSGGDIRDPE PEAAEAPQQAQGRCELSPLREACVAL QRQLSRPRGVASDGGAVRLVAQEWFRV SSQRRSQAEPVARMLEGVRRGLPELLAH VVNLADGNGNTALHYSVSHGNLAIASLL LDTGACEVNRQNRAGYSALMLAALTSV RQEEEDMAVVQRLFCMGDVNAKASQT GQTALMLAISHGRQDMVATLLACGAD VNAQDADGATALMCASEYGRLDIVRL LLTQPGCDPSILDNEGPSALAVALEAET GMKVAALLHAHLSSGHPDTQSGVTPLA PQTANTW |
| 3041 | 11092 | A | 399 | 2 | 510 | FLANFLCFIRD/GFHHVGDGLHLLTS*S ACGLPKCWDYRREPLRPTSPLSRPHQ ALCCLAFGHSAATCTCVN/SALAWAGF WNPQAPGF/SVAPAHLLTHTVSLSPMPL WATCSPGAGHEAPGLMLQDPFGPPWCS CGPVFHEKTAGCKARAFSGRVCRCQAQ ALPETGR |
| 3042 | 11093 | A | 3990 | 53 | 364 | RSKVEAGLAPEPGPLGARVGS/PGTRAR HGRPG/PA/GASIGPGCGPNEQVDEQAGP AQLQGPQGPAPRAIGFPHRLGGCKI KGDGPGVRRPGSDRLSSSSPT |
| 3043 | 11094 | C | 3991 | 408 | 620 | |
| 3044 | 11095 | C | 3992 | 64 | 300 | MDSSHSTTLXPTANPNTGLVEDLDRTGP LSMTTQQSNSQSFSSTSHGLEEDKDHP TSTLTSSNRNDGHRWKKRPKSF* |
| 3045 | 11096 | A | 3993 | 1 | 530 | |
| 3046 | 11097 | A | 3994 | 1 | 436 | |
| 3047 | 11098 | A | 3995 | 3 | 1009 | |
| 3048 | 11099 | A | 3996 | 1 | 2226 | |
| 3049 | 11100 | A | 3997 | 2 | 1599 | QPLPGSVRHRPVLRRPLPRAQSSSSFR PRPPFAPDTMDKFWWWAAWGLCLVPLS LAQIDLNITCRFAGVFHVEKNGRYSISRT EAADLCKAFNSTLPTMAQMEKALSIGFE TCRYGFIEGHVVIPRIHPNSICAANNTGV YILTSNTS QYDTYCFNASAPPEEDCTSVT DLPNAFDGPITITIVNRDGTTRYVQKGEYR TNPEDIYPSNPTDDDVS SSGSSSERISSTSG GYIFYTFSTVHPIDEDSPWITDSTDRIPA TNMDSSHSTTLQPTANPNTGLVEDLDRT GPLSMITTQQSNSQSFSSTSHGLEEDKDH PTTSTLTSSNRNDVTGGRDPNHSEGST LLEGYTSHPHTKESRTFIPVTS AKTGSF GVTAVTVGDSNSNVNRSLSGDQDTFHPS GGSHTHGSESDGSHSGSQEGGANTTSG PIRTPQIPEWLILASLLALALILAVCIAVN SRRRCGQKKKLVINSNGGAVEDRKPSGL NGEASKSQEMVHLVNKESSETPDQFMT ADETRNLQNVDMKIGV |

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| 3050 | 11101 | A | 3998 | 245 | 1148 | FPGSTPTPFAPDTMDKFWWHAAWGLCL VPLSLAQIDLNITCRFAGVFHVEKNGRYS ISRTEAADLCKAFNSTLPTMAIQMEKALS IGFETCRYGFIEGHVVIPRIHPNSICAANN TGVYILTYNTSQYDYTCFNASAPPEEDC TSVTDLPNAFDGPITITIVNRDGRTRYVQK GEYRTNPEDIYPSNPTDDDVSSGSSSER ESTSGGYIFYTFSTVHPIPEDDSPWITDS TDRIPATRDQDTFPPQWGFLPLHGSEFR WDTMGSQGRWEQTQPLGPIRDTFNSQ NGLIHLGHPLLALGL |
| 3051 | 11102 | A | 3999 | 3 | 327 | AGPGEVAGDGRDSGGPAGGRRRCWLNW SGSGKSLRKGNPSVSIYCFCLPNHYLFDR N/SCLRSSAGTKSGSYPPQISSLMILVPP CVPQQTHPGLDLKTQKLSLLSALI |
| 3052 | 11103 | B | 4 | 3508 | 3762 | MTPGVVHASPPQSQRVPRQAPCEWAIRN IGQKPKEPNCHNCGTHIGLRSKTLRGTPN YLPIRQDTHPPSVIFCLAGVGVPGLPV* |
| 3053 | 11104 | A | 40 | 25 | 412 | IQARKKQQSVLGIKTEDQGTFNLLRKGI MDIEAYLERIGYKKFTSKLDFETLTDILS HQIPAVSFDNLTVLCGDAMDGLGLEAIFD QAVR*NRIGGWILQVNHLLYWALTTIG YETTKIGRYGYQTPAEK |
| 3054 | 11105 | A | 400 | 249 | 434 | IVEYRGMWDYRLLFFFPETESCSVAQVG TQWHDLSLQPLSPGSSNSPASAS*VAGI TGIH |
| 3055 | 11106 | A | 4000 | 8 | 280 | SAQMAVTTADPRVRPRVRTTVFTSIAHT DTMVHLTPVEKSAVTALWAKVNVNEV GGEAPGQGCWVVLPLGPPKGPLKPFGGI CPNSLNAG |
| 3056 | 11107 | A | 4001 | 405 | 647 | |
| 3057 | 11108 | A | 4002 | 405 | 606 | |
| 3058 | 11109 | A | 4003 | 1 | 849 | |
| 3059 | 11110 | A | 4004 | 2 | 1173 | PQQSPECVPLPVSVCSHWSIPTSHRLLR VLVTVCELYVRWPRCNADLTCTKAVQ NGWDLKVPCTCLHLLAVPGVGLFIDEG VKQGFVETFRDTRGVLVHGCIMSCLCN NRVRPYLKKKQKSKKTTDVGVEVEESG RGCAAGAEVFCMQQGSASHAAEQES SSKVESGRHSYNLYLVVISPRTPASLQN LQILKCIRFWTWHEERFLYMLMEYVPGG ELFSYLRNRGHFSSTTGLFYSAEIIAIEY LHSKEIVYRDLKPENILLDRDGHIKLTD GFACKLAAYRLMWKSLSEKRWVWRCG GEAKER*Q*QFGWVPASRKVRS*SQDT CPHHRKQGRRLRTWTLCTGPEYLAPEVIQ SKGHGRAVDWWALGILIFEMLSGWVL |
| 3060 | 11111 | A | 4005 | 149 | 1358 | APPSHCLCVSVSRAEPRTQRRRAWGAS VDAAAAAAPPSEAASRGVRLPERSGLAR RGPPECLPMEAPGAQAAAAESNSREVT EDAADWAPALCPSPEARSPEAPAYRLQD CDALVTMGTFGRVHLVKEKTAKHFF ALKVMSPDVIRRKQEQHVHNEKSVLKE VSHPLIRLFWTWHEERFLYMLMEYVPG GELFSYLRNRGHFSSTTGLFYSAEIIAIE YLHSKEIVYRDLKPENILLDRDGHIKLTD FGFACKLVDRTWTLCTGPEYLAPEVIQS KGHGRAVDWWALGILIFEMLSGFPPFFD DNPFGIYQKILAGKLYFPRHLDHFVK/DG ANDVNHHRWFRSVDWKA VPQRKLKPI VPTIAGNGDTSNFETYPEHDWDTAAPVP QKDLEIFKNF |
| 3061 | 11112 | A | 4006 | 1 | 683 | |

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| 3062 | 11113 | A | 4007 | 521 | 1163 | SQDTCPHHRKQGRRLRTWTLCTGPEYLAP EVIQSKGHGRAVDWWALGILIFEMLSG AFPKHVSSNASPGLQNWGRFPFFDDNP FGIYQKILAGKLYFPRHLDFHVKCQTPK EKQKTKNKVIFLHARHQKQNKTNNNNN SNNKMKFIKNGANDVKHHRWFRSVDW KAVPQRKLKPPIVPTIAGNGDTSNFETYP EHDWDTAAPVPQKDLEIFKNF |
| 3063 | 11114 | A | 4008 | 181 | 1448 | APPSHCPRRSVSRAQPRTRRRERAWGAS VDAAPPPSEASREARLPERSGLARCP GPECVPMAPGLAQAAAAESDRKVAE ETPDGAPALCPSPEALSPPEPPVSLQDFD TLATVGTGTGFRVHLVKEKTAKHFFALK VMSIPDVIRLQEQHVHNEKSVLKEVSH PFLIRLFWTWHDERFLYMLMEYVPGGEL FSYLRNRGRFSSTTGLFYSAEIIICAEYLH SKEIVYRDLKPENILLDRDGHKLTDFGF AKKLVDRTWTLCTGPEYLAPEVIQSKGH GRAVDWWALGILIFEMLSGFPFFDDN PFGIYQKILAGKVDPRHLDFHVKDILK KLLVVDRTRLGNMKNKNGANDVKHHRW FRSVDWEAVPQRKLKPPIVPKIAGDGD TSNFETYPENDWDTAAPVPQKDLKIFKNF |
| 3064 | 11115 | C | 4009 | 3 | 167 | MPMXAQIEEPQPIQVKTRTNLRLTQLRE QDQTKCLCPLYNQQAAPRKFFLLWA* |
| 3065 | 11116 | A | 401 | 532 | 986 | PWAKLGLSCVPAWQVQVLAICRWKEVG ILDFLFFVFFFLR*SL/SDSTQAGVQWC DLGSLQTLPLPGFKWFSCPSLPSSWDYRH APPRSADFCIF/M*RWGFTMLAKLVSNS* PQ/CDLPASASQSAGITGVSQCTRNLGIF IDGTSVSDSSRT |
| 3066 | 11117 | A | 4010 | 1 | 2195 | MDPGTLQASQGPTAINPCDYVLKRRNI QTSWQRLTPIIKWHVYILMIGPGEKEAG RNLGIFGKWTPFKIPAKRLRESNCPVDA QEIWLPQAFREYLGRRGNFGPGRRTCEF WEVESICSVESWELWLRQADSGDSGKC SPDACGIIDTSLRAGHCYLTRLWHVSG RIPPSFKLHHPGVCKFPKVGGKMTTFKE AVTFKDVAVVFTEELGLLDPAQRKLYR DVMLNFRNLLSVGHQPFHQDTCHFLRE EKFWMMGATQREGNSGGKIQTELESV PEAGAHEEWSCQIWEQIAKDLTRSQDS IINNSQFFENGDVPSQVEAGLPTIHTGQK PSQGGKCKQSFSDVPIFDLPQQLYSEKS YTCDECGKSICYISALHIVHQRVHMGEKC YKCDVCGKEFSQSSHLQTHQRVHTGAEK PFKCGIQCCKGFSRRSALNVHKLHTGE KPYICEACGKAFIHDSQLKEHKRIHTGEK PFKCDICGKTFYFRSLKSHSMVHTGEK PFRCDTCDKSFHQSALNRHCMVHTGE KPYRICEQCGKGFGRDLDFYKHQVVTG EKPYNCKEKGKSFWRSSCLLNHQRVHS GEKSFKCEECKGFYTNSQLSSHQRSHS GEKPYKCEECKGYVTKFNLADLHQRVH TGERPYNCKEKGKNSFRASISILNHKRL H/SPEKNPFKCEDCGKRLVHRTYRKDQP RDYSGENPSKCEDCGRRYKRLNLDILL SLFLNDT |
| 3067 | 11118 | A | 4011 | 1 | 4559 | MDGAKAFFSAVAAGFVILTCQLQWQW QHGGVHAHLWQLASGYRDACFCVST YSSGPSEFFGPTLGTNLALDLEERKHR RKAKVWKEGGGGLRSRQSLAFAVL ASRGTRSCHVSPYLGVSALSSPNPHST TGAGPIPPVQRWGLPQINQKNREIAIPLT LGMSTHLRRGCKNMSRFSPLHCCTPIS TNFTDPGSHCKGAHGDICLLIQNLKGAL PMSINRSYFNAHPLLQISEAVTFKDVAV VFT |

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| 3068 | 11119 | A | 4014 | 1 | 1387 | FRAASGRETRAALGASQCLTPHPLPRVG GGGASGGGLRGAGQAWSAMSSPDAGY ASDDQSQTSQALPAVMAGLGPCPWAES LSPIGDMKVKGAPANSAPAGAAGRA KGESRIRPMNAFMVWAKDERKRLAQQ NPDLHNAELSKMLGKSWNALTLAEKRP LVEEAERLRVQHMQDHPNYKYRPRRRK QVKRLKRVEGGFMHGMDEPQAAAMGP EGGRVAMDGLGLQFPEQGFAGPPLLP HMGGHYRDCQSLGAPPLDGYPLTPDTS PLDGVDPDPAFFAAPMPGDCPAAGTYSY AQVSDYAGPEPPAGPMHPRLGPEPAGP SIPGLLAPPSALHVYYGAMGSPGAGGGR GFQMOPQHQQHQQHQQHPPGPGQPSPP PEALPCRDTGTPSQPAELLGEVDRTEFE QYLHFACKPEMGLPYQGHDSGVNLPDS HGAISSEVSASSAVYYCNPYDV |
| 3069 | 11120 | A | 4019 | 77 | 407 | ESDGGKRKKKSRGDPSQLEEKISKGCPO RRKKPRLYRPSNYNRAFRMRRL/ARLPT RTSPETRTPOPHSPHS/PERTPTPPGRPP FLGAGQLQRLFMGIPQVGDCCPPSS |
| 3070 | 11121 | A | 402 | 2 | 992 | FVDAAGCPLRCSVVTGIVVLQKSGNRPE DLRAAQLPGRLELLNNFCSAMSPAPDA APAPASISLFDLSADAPVFQGLSLVSHAP GEALARAPRTSCSGSGERESPERKLLQG VLWTISEKLFCTCDQTFQNHQEQREHY KLDWHRFNLKQRLQGQPLLSALGL*KA ELHRRSFPAFSGIRRIQDSASEEDLQTL RERATFEKLSRPPGFYPHRVLFQNAQGO FSLCLPLCPR/LLIRIPQKRQNLTLRTLQS RGPRDCVVLMAAAGHFAGAIQGREVV THKTFHRYTVRAK/QGHSQGAFG/NARG GPSHSAGANLRWYNEATLYKVS |
| 3071 | 11122 | A | 4020 | 20 | 463 | |
| 3072 | 11123 | A | 4021 | 572 | 1594 | SSDWKRTMSWIKEGELSLWERFCANIHK AGPMPKHIAFIMDGNRRYAKKCQVERQ EGHFTGFKQLAETLRWCLNLGILEVTYV AFSIENFKRSKSEVDGLMDLARQKFSRL MEEKEKLQKHGVCIRVLGDLHLLPLDLQ ELIAQAVQATKNYNKCFNLVCFAYTSRH EISNAVREMAWGVEQGLLDPSDISESL DKCLYTNRSPHPDILIRTSGEVRLSDFLL WQTSWSCLVFQPVLPWEYTFWNLFMAIL QFQMNHSLVQKARDMYAEERKRQQL RDQATVTEQLLREGLQASGDAQLRRL HKLSARREERVQGFQALELKRADWLA RLGTASA |
| 3073 | 11124 | A | 4022 | 2 | 365 | |
| 3074 | 11125 | A | 4023 | 1 | 464 | RRWRICSTWTRSFATAWLPPAPSANFPR TDRSQGDRGAPAGFALAPILEFFLWDT SQKFLQKPHCFMHGRERAKMGRRAQOE SAQAENHLNGKNSSLTLTGETSSAKLPR CR/QGGWAGDSVKASKFRRKASEEIEDF RLRPQSLNGSDYGGDIP |
| 3075 | 11126 | A | 4024 | 254 | 662 | |
| 3076 | 11127 | A | 4025 | 3 | 392 | MKYSAIQTLDEIDLKLLTKVLAPEHEV R*VQWWQQFPGLSTLAIPINPAELPGLAL CLP*RPWNGREKVSQLEKALSLSYPA KPFLVEDDVGWDWDHLFTEVSSEVLTE WDPLQTEKEDPAGQARHT |
| 3077 | 11128 | A | 4026 | 63 | 779 | GPIRGPWGPGFGGWGGATPPAPTSRLRL RAAGLAPRRRAKMGRRAQQAQSAQEN HLNGKNSSLTLTGETSSAKLPRCRQGGW AGDSVKASKFRRKASEEIEDFRRLRPQSL NGSDYGGDIPNPDLEEVEEDFVLQVVA APPSIQIKRVMTYRDL/DNDLMKYSAI QTLDEGID/LDKLL/TPKVLAPHEVRER NPSWQDDVGWDWTHLFTEVSSE/VSFT EWDPLQTEKEDPAGQARHT |

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| | | | | | | EWDPLQTEKEDPGGQARHT |
| 3078 | 11129 | A | 4027 | 2 | 311 | |
| 3079 | 11130 | A | 4028 | 1 | 136 | |
| 3080 | 11131 | A | 4029 | 2 | 170 | |
| 3081 | 11132 | A | 403 | 2583 | 3827 | DRVSLLLPRLECNGAJLAHCNLC/SGFK *FSCSLPSNWDYREVPPHQLIFVFLVE MGFHHIAQAGLELLTS/SI/PPTLA/FPKC WDYRR/DHHAWLFFFCSENSFTLLPRLE *GGLISDHCNLRLLGSSDLPASASQEPRL QACATTPR*FLYFW*RRGFTMLARLVN S*PQV/HPPASASQSAEIGVSHHTWPQEV FLFLNLFYLRWSLALSPRECSDBGSAH CKLRPPGSSVLLPQPPE*LGLQAPATTPG* FFCIFSRDGFSPC*PGGS*SPDLVICLPRPP KVLGLQV*ATTPGYFFETGTHSVTWA AVQWYTIAHCSLELLSSDPPTSSSQVIG TTGAPHHALHLYLFYLFIFIEMRVPCVV QAGLELLSRDPFAWASQSAEITGMSHR AQLGIIFKAPRMSV |
| 3082 | 11133 | C | 4030 | 64 | 276 | MCKALGTPYSPQQRLGTEASSVHRTC WHLLGQGSAAARXXXXXXXXXXXXXXXXX XXXXXXXXXVSIDPTTQG** |
| 3083 | 11134 | A | 4031 | 3 | 295 | |
| 3084 | 11135 | A | 4032 | 3 | 279 | |
| 3085 | 11136 | A | 4033 | 3 | 392 | RIRHEAAAKGAAAMSAHLQWMVVRNC SSFLIKRNKQTYSTEPNNLKARNSFRYN GLISPARLWGVEPAADGKGVVVVVKR RSGQR/KPA/TSYLRTTINKNARATLSSIR HMIRK/NKYRPLAHGHAGI |
| 3086 | 11137 | A | 4034 | 2 | 562 | VAAAKGSRROCLRHLQWMVVRNCSS LIKRNKQDPTALSPNNLKARNSFRVNG LIHRKDCGTWSRSADGK/GVVVVVVKRR SG/QRKLATSYVAGPPSTRNARSHASGR HQ/VHIDPARNKLPPPTCRMGPSPFRAQR PFLAQAGRLVDWLKEGRRDPAPRSSLK PLGPQKQLKSAGVFSKKKKKSR |
| 3087 | 11138 | A | 4035 | 1 | 139 | |
| 3088 | 11139 | A | 4036 | 1 | 299 | VGIW*PVTNFGVISGTAIEMD*G/TPYIH ALTNGLLTVEAPHK/ERIALKPGYGYLS INSDELVV/GRSDAIGPREQWEPVFQNDG HPVMRMNSLQKATI |
| 3089 | 11140 | A | 4037 | 796 | 911 | AMA*YSYVKSSKLVLKGTSSKKKSTDK KRKREDEETQLD/IVGIW*TVTNFGEISG TJAIWNGRKGTYIHALDNGLFTLGAPHK /ERIALKSGYGYLGINSDDL VVGRSDAI GPREQCEPVFQNGKMALLASNSCFIRC EAGDIEAKSKTAGEEEMIKIRSCAERETK KKDDIPEEDKGNVQCEINYVKKFQSFQ DHKLKISKEDSKILKKARKDGLHETLAL DRAKLEADRYCK |
| 3090 | 11141 | A | 4038 | 193 | 754 | EPSRGVWPHEARINGSKKKKKEKKR KREDEETQFD/IVGIW*TVTNFDEISGTI AIEMDEGTIHALDNGLFTLGAPHEGK MALLASNGCFIRCNEAGDIEAKSKTAGE EEMIKIRSCAERETKKKDDIPEEDIGNVK QCEINYVKKFQSFQEHKLKISKEDSKILK KAQKDGFLHETLLDRGP |

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| 3091 | 11142 | A | 4039 | 213 | 919 | YVQSLKQILS/GCI*ESIAIKKKKNKDKKR KREDEETQLDIVGIWWTVTNFGEISGTI AIEMDKGTIHALDNGLFTLGAPHKEVD EGPSPPEQFTA\VKLSDSRIALKSGYGKY LGINS DGLVVGRSDAIGPREQWEPVFK\ MGKMALSTSNSCFIRNHEAEDIEAKSKT AGEEEMIQQSP*SSVQPFHLLWTFAFILT QEHRSLLLKIRSCAERETKKKDDIPEEDK GNIKQCEI |
| 3092 | 11143 | B | 404 | 1 | 336 | MGRARWLT\VIPALWEAEAGGSREVEE YMGAEAVKSWTSSMFKEWDEKVRREK TSSRRARAAQCGGVFESPEYVHLLKVFL EDLDKQQQTNSKASRRQEIIRAELEIK T* |
| 3093 | 11144 | A | 4040 | 802 | 1463 | AEATALENPLEESRPHEARINGSKKKK SKDKKRRKREDEETQFD\IVGIWWTVIN GGISGTIAIEMDEGTIHALDNGLFTLGA PHK\ERIALKPGYGKYL\NSDELVV\GRS KAIGPREQWEPVFQNGACAAGFTVIGSE KQSECSLLRESRAKYHGCTHGQISSLK QHPRWMYSHQEDLKVWSLVEKKVTFE HIYLLKRNNSHSIAEAMYGRLSNYI |
| 3094 | 11145 | A | 4041 | 879 | 1051 | GGARYHFFFFFFFDGACSVTQAGVQWP ILGSLQPPPPRFKQFSCLSLPSSWDYRRD |
| 3095 | 11146 | A | 4042 | 125 | 1366 | RDSSSTLSHKSAKACGFFPSTHKS GTF RFTSVRCLKYKSAKSFHLHIGYREAAVWC CQRLVPCTRRTQESSLDFATNLQHSAWS RLCRRGASRTSSAARSRSRSPAVEGCNR SPGAPQAPRARRRPSRGAPGRAMVKV AFNSALAQEAKKDEPKSGEELIIPPD AVAVDCKDPDDVVPVGQRRWCWCM CFGLAF\MLAGVILAGGAYLYKYFALQPD DVYYCGIKYIK\DDVILN\ESPSADAPAA\ LYQTIEENIKIFEERRSLNFISVPVEFAD SDPAKIVQDFNQETYRYPYLD\FNLDKCY VIP\NTSMCYATPKTLELLINIKAGNLF ALSPYLD\SMRHMGYLLDRINENIDHPGF FIYRLCHDKETYKL\QRRETIGIKQKREAS NCFAIRHFENKFAVETLICS |
| 3096 | 11147 | A | 4043 | 42 | 557 | QAGKL RPGGLDSRSRSSAAGLDRDQGL HRVAF LPKRRTGGTRMDRSATAATAPP AAPAGEGGPPAPPPNLTSNRRLQQTAAQ VDDVDIMRVNV\DKVLERDQKQSELD RC\ADALQAGASQFETSAAKLKRKY\W WKNLKM\MIILGVICAILI\IIVYFQHLNP RGVCPA |
| 3097 | 11148 | A | 4044 | 178 | 731 | SSERCHQQVFIPMPALPPGF\SQAGSCVP TGSSLVL\CLLAASLLFVPTLALLTGATT CWCLHNKRLAV\RRPLAWAGAFGLVLS TRLIHGRT\SFYFNSLP\QTNSTC\QNH SWDSGGRGDLPWPLAAPRRVGLDLCS QAHTCQQGADWIHALLCLMGVTGVPTA LPAKHLEQNTSPFVVDAE |
| 3098 | 11149 | A | 4045 | 3 | 155 | |
| 3099 | 11150 | A | 4046 | 100 | 448 | WWEVKGM SHGQKNKQEGGAIFRACV CVMESHVTRLECSGAISAHCNRLQGS SNSPDSASRVAGTTSTRHEAQLIFVFLAE TGFHHVQAALELLTSSDPPTSASQSAD MLYK |
| 3100 | 11151 | A | 4047 | 151 | 461 | RLTAAATASLCPLRPVTRLPLSRGSKM KEGMSNNSTTSISKPRKAVEQLKMEAC MDRVKVSQAAADLLAYCEAHVREDPLI IPVPASENPFREKKFFCTIL |
| 3101 | 11152 | A | 4048 | 1 | 447 | |
| 3102 | 11153 | A | 4049 | 553 | 1938 | |
| 3103 | 11154 | A | 405 | 2 | 313 | FFFFLRRSLALSPRLECSGVISAHCKLR GSR\RFSCLSLSHSDYRRPPRPANFLY FLVEKGFHCVSQDGLHLLTS\AIPP\TSA\F |

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| | | | | | | PKCWDYRCDSMNFLMVSKD |
| 3104 | 11155 | A | 4050 | 303 | 478 | DCTSRPSLCPLSARCDVHGLSPGPVLVR* GLIVIEDALPKSHSGGRGEVRQPWDFCG A |
| 3105 | 11156 | A | 4051 | 458 | 964 | DPRTMNLAIISIALLLTVLQVSRGQKVTSL TACLVDQSLRLDCRHENT/SAVSPIQYEF SLTRETKKHVLFGTVGVEHTYRSRTNF TSKYNMKVLYLSAFTASKDEGTYTICALH HSGHSPPISSQNVFVRDHGVKCEGISL LAQNASWLLLLLLLSLLQATDFMSL |
| 3106 | 11157 | A | 4052 | 411 | 557 | YSTDELPNIKISTSGRLQWLMSPALWE A/EDQAGRSFEFRNLRLVWTT |
| 3107 | 11158 | A | 4053 | 508 | 1220 | PLPPAATPCPKQLGSQAWACRAARGA EQGVWGWKRHPAPSRGRVDKGSTQKQ DPSAHTTSTLNYQMHSCH/KHRRHTHT HTHTHTHTHTHTHQHNIPGGPSPDQE EAGQVVEKKAANPSHNPTLQDRRVSSIL SCCKRKLEAPSPEQISMVGPGRSNLWFP HWQRRQEPAKCSFGLKEQWGGDFSRM NRLMGPGVNPSTSPFWSRKLHKGKDV CWLHRHAKCLSARCPRIWRVW |
| 3108 | 11159 | A | 4054 | 1609 | 1807 | DRVWLLPRLEYSGMVSAHCNTHLLGSS QSPTSASQAAGTTGAHHYVQLVYIYIY JLGLFVETFR |
| 3109 | 11160 | C | 4055 | 169 | 297 | MILEFHXXXXXXXXGGGRFKEPLGGPNLP GAGKVLFFSLWGAD* |
| 3110 | 11161 | A | 4056 | 270 | 614 | PFKFILITQVIRDPFSSEPYLGEKANHPP GFHHVKGQASHVCKTHPAPSCPP/PDC CLPCPSLGPAPHFRGCCMEFPKGNFRC LDPFYLDNIFRFFCSLVTPGGKEIARTFF |
| 3111 | 11162 | A | 4057 | 637 | 890 | TKWAGSIVYLSFSFLHMFMSFLLV/STF LALCMLILVVLFLKLPPKLFSELPLKL TFLPCELLHLHLFQDLAYFFNGLRK |
| 3112 | 11163 | A | 4058 | 3 | 297 | ATAARPCPLGRRAGESRGPGHIGVRPG STLCQIIATCHMSVNDGGCKYVLCRWE KRLWPAKVLARTATSTKNKRRKEYFLA VQILSLEEKLSVVL |
| 3113 | 11164 | A | 4059 | 2 | 1940 | CPGLGRRAGESRGPGHIGVRPGSTLCQII ATCHMSVNDGGCKYVLCRWEKRLWPA KVLARTATSTKNKRRKEYFLAVQILSLE EKVKVKSTEVEILEKSQIEAIASSLASQNE VPAA/PLEELAYRRSLRVALDVLSECSI WSQESSAGTGRADRSRKGPMHVSPPC DSNSSSLPRGDVLGSSRPHRRRPCVQSSL SSSFTCEKDPECKVDHKKGLRKSENPRG PLVLPAGGGAQDESGSRIHKNWTLASK RGRNSAQKASLCLNGSSLEDDTERDM GSKGGSWAAPSLPSGVREDDPCANAEG HDPGLPLGSLTAPPAPEPSACSEPGECPA KKRPRLDGSQRPPAVQLEPMAAGAAPSP GPGPGPRESVTPRSTARLGPPPSHASADA TRCLPCPDSQKLEKECQSSEESMGNSM RSILEEDEEDEPPRVLLYHEPRSFVGM LVWHKHKKYPFWPAVVRSVRQRDKKA SVLYIEGHMNPMMKGFTVSLKSLKHFD KEKQTLNQAQREDFNQDIGWCVSLITDY RVRLGTWGAGEGWSWAAGVQPLKTPW TGWAGAAWRRGIFPWAAGIPCGWAGV LAWPDYFLNRDAGPAPGTHFLGLLGLH SALSPPPAGCGSFAGSFLEYAADISKS TGCI |

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| 3114 | 11165 | A | 406 | 4565 | 5027 | LIGYILFCFFFFFFFLRQSLVLLPGLECSG VILAHCNPR/LPGFK*FSCSLPSSWNYR HAPARPVSVFLAEMGFHHIGQAGLKL LT/SV/PPPTSA/FRKCWDYRREPPRTAF FVLNKFTVLGSNSGF*T*DRHNHFMRLY CNYTLEYSGSHL |
| 3115 | 11166 | A | 4060 | 1 | 2722 | MERPLRGSRHPRLFPVPPGVLGPSQGHIG VRPGSTLCQIIATCHMSVNDGGCKYVL CRWEKRLWPAKVTAII/RVTSGLRNDFR VTKTSVTGPSILKYLVFEPVTLNQRLLTK RQITDDQAAHCSAPIKVKSTEVEILEKSQI EAIASSLASQNEVPAAPLEELAYRRSLRV ALDVLSEGSISQESSAGTGRDNRSRLRG KPMEHVSSPCDSNSSSLPRGDVLGSSRPH RRRPCVQQSLSSSFTCEKDPECKVDHKK GLRKSSENPRGPLVLPAGGGAODESGSRI HHKNWTLASKRGGNSAQKASLCLNGSS LSEDDTERDMGSKGGSWAAPSLPSGVR EDDPCANAEGHDPGLPLGSLTAPPAPEPS ACSEPGCECPAKKRPRLDGSQRPPAVQLE PMAAGAAPSPGPGPGPRESVTPRSTARL GPPPSHASADATRCCLPCPDSQKLEKECQ SSEESMGSSNSMRSILEEDEEDEEPVLL YHEPRSFVGMVLVWHKHKKYFPWPAVS WDESTRGWISRLKAAFRTIALHIPKSNAQ NRCHLTSPSLRVPGAHLRSDQPKPSGPR CPPAFRPAQAIGSPVPTCVQISPSHRVPG AHLRSDQPKPSGPRCPPFEQLRAOTCAW CVSHLPEGPCARRLEPPLSGRNQAREDF NQDIGWCVSLITDYRVRGCGSFAGSFL EYAAADITSRACGALIPWATSSVLLW LVAHIRCCECRPGASFAGYPVRKSIQ QDVLGTLKLPQLSKGSPEEPVVGCPGQR QPCRKMLPDRSRAARDRANQKLVEYIV KAKGAESHLRAILKSRKPSRWLQTLSSS QYVTCVETYLEDEGLDLVVKYLQGVY QEVGAKVLQRTNGDRIRFILDVLLPEAII CAISAVDEVYKTAEEKYIKGPSLKLPG KRNI |
| 3116 | 11167 | A | 4061 | 57 | 235 | |
| 3117 | 11168 | A | 4062 | 754 | 1767 | WTSWWMSSVLITLLFSLQGNKMLNYS PSAGGCLDRKAVGTPAGGGFRRHSVT LPSSKFHQNLSSSLKGEPAPALSSRDSR FRDRSFSEGERLLPTQKQPGGGQVNSS RYKTTELCPFEENGACKYGDCKQFAHG IHELRLTRHPKYKTELCTFHTIGFCPY GPRCHFIHNAEERRALAGARDLSADRPR LQHSFSFAGFPSAAATAAATGLLDSPTSI TPPILSADDLLGSPTLPDGTNNPFAFSSQ ELASLFAPSMGLPGGGSPTTFLFRPMSES PHMFDSPPSPQDSLSDQEGYLSSSSSSHS GSDSPTLDNSRRLPIFSRLSISDD |
| 3118 | 11169 | A | 4063 | 568 | 715 | |
| 3119 | 11170 | A | 4064 | 65 | 347 | GLPAPLPPP/PPRSLPFPAPGLRSQRFSTSA PPRHARPPPVARARAAPHPQASGRKSQ VSAPLVERAPLRAPGLTATAVVTVLGDP ACAFPLEM |
| 3120 | 11171 | A | 4065 | 1648 | 1974 | KVFFCFYRJYVCICVCVCVCVC/TLQTL/C YSIANMLTSSQCLQSCGSQSWCQMHIKS SKAIMTIPCKFISRKPWEGDCSSLEPHGV SAFDIWWPQLCIKKVLNHFSPRKN |

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| 3121 | 11172 | A | 4066 | 12 | 1662 | FLRGGCCFCYMTQCQRPSLRPTALLPERS VPPLPPAAPPRPVRHPPVAAPPARRCPAP APPPPPPPDDWVMLDMGDRKEVKMIPK SSFSINSLVPEGLQNDNHHASHGHHNSH HPQHSHHHHHHHHHHPPPAPQPPPPRAA QQQQPPPPPLAPQAGGAAQSNDEKGPQL LLLPTDHHRPPSGAKAGGCCRPGEGLGP VGPDEKEKGAGAGGEEKKGAGEGGKD GEGGKEGEKKNGKYEKPPPSYNALIM MAIRQSPEKRLTLNGIYEFIMKNFPYYRE NKQGWHNISIRDNLNLKCFVKVPRHYD DPGKGNYWMLDPSSDDVFIGGTTGKLR RRS'TTSRAKLAFKRGAALTSTGLTFMD RAGSLYWPMSPFLSLHHPRASSTLSYNG TTSAYSPHPMPYSSVLTQNSLGNHNSFST ANGLEAWDRLVNGEIP/YTATHHLTAA ALAAISVPCGLSVPCSGTYSLNPCSVNLL AGQTSYFFPHVPHPSMTSQQSSTFMSARA ASSSTSPQAPSTLPCESLRPSLPSFTTGLS GGLSDYFTHQNQGSSSNPLIH |
| 3122 | 11173 | A | 407 | 187 | 741 | TRGTSAAARTGRSSGIASMASGILVNVE EVTCPICLELLTQPLSLDCGHSCQACLT ANHKKSMMLDKGESSCPVCRISYQENIRP NRHVANIVEKLREVKLSPEGQKVDHCA RHGEKLSNFCQEDGEGSFCWVC*AVFR EHRGSPHVSSQRRFAREYQVKLQAAL MLRQKQQAEELEADIR |
| 3123 | 11174 | A | 4070 | 1 | 507 | |
| 3124 | 11175 | A | 4071 | 259 | 1409 | FLLWRYFVFGIVTEEKEKVQPTVYLIQLL DLLKAIT/SPHLEAGSKPSKKTGEKSSGS SSHSESKKEHHRKKVSGSSGELPLEDGV SHKSKMKPLYVNTETLTLREPDGLKM KLILSPKEKGSSSVDEESFQYPSQQATV KKSSKKSARDEQGALLGHELQSFLLTA RKKHKSSSDAHSSVPGPLKGLGLDAISQ FRKSPHSANLDSLGLPILVESDSSSGGE LEAGELVIDDSSREIKKKKKSKSKKKK DKEKHKEKRHSKSKRSLGLSAVPVGEVT VTSGPPPSIPYAGAAAPPLPLPLHTDGH SEKKKKKEEKDKERERGERKMGPSWKK ISSGLPLILHDGPWKNCFPRNRYVPKRL RTADLVGLYLGSKHK |
| 3125 | 11176 | A | 4072 | 436 | 2063 | RRREVEGWYFGGFSHRRTVCICDTPDISS LESSQKKKKKSSPQSTDTAMDLLKAITSP LAAGSKPSKKTGEKSSGSFKAISGELKR EHRKKVSGSSGELPLEDGGSHKSKKM KPLYVNTETLTLREPDGLKMKLILSPKEK GSSSVDEESFQYPSQQATVKKSSKKSAR DEQGALLGHELQSFLLTARKKKHSSSD AHSSPGPEGCGSDASQFAESHSANLDSL GLEPILVESDSSSGGELEAGELVIDDSYR EIKKKKKSKSKKKKDKEKHKEKRHSK SKRSLGLSAVPVGEVTVTSGPPPSIPYAG AAAPPLPLPLHTDGHSEKKKKKEEKDK ERERGERKPKKNMSAYQVFCKEYRVTI VADHPGIDFGELSKKLAEVWKQLPEKD KLIWKQKAQYLQHKQNKAEATTVKKR ASSEGSMMKVKASSVGVLSPOKKSPPTT MLLPASPAKAPETEPIDVAHLQLLGESL SLIGHRLQETEGMVAVSGSLSVLLDSIIC ALGPLACLTTQLPELNGCPKQVLSNTLD NIAYIMPG |
| 3126 | 11177 | A | 4073 | 323 | 539 | PFMICLVHFCAPGNPPSARPRPSPSPRCH PCAPQEGKMTHPQFRVMPAPSCYNWLL ENVPFHQNSGVRIS |
| 3127 | 11178 | A | 4074 | 27 | 425 | GGGSGPRAPSATLLDTGESVAASGEGD KGIAASAAAAAVFACSCSPDPQSSTMN VYSPVQPGAPYGNPKNMAYTGYPATYAP AAAPAYNPSLYPTNPSYAPATLVMMKQ |

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| | | | | | | AWPQNSSSCGTEGTFHLPVDTG |
| 3128 | 11179 | A | 4075 | 1 | 434 | |
| 3129 | 11180 | C | 4076 | 117 | 251 | MVPGPSLQNSWQASFNIPWPALPKPDLG PSPSVSPVDIFCGACC* |
| 3130 | 11181 | A | 4077 | 58 | 313 | SSKQKNPKESKTTKQNQIYTSYTQARP WGFPIFTPGLCFENTYKFFDQTTWKTLLV KSSSSSSSSSSPILFLFKM*VPIKFKN |
| 3131 | 11182 | A | 4078 | 1 | 279 | |
| 3132 | 11183 | A | 4079 | 54 | 946 | GGGSGPRAPSATLLDTGESVAAVASGED KGIAASAAAAAVFACSCSPDQSSMTNP VYSPVQPGAPYGNPKNMAYTGYPATYP AAPAYNPPLYPTNSPSYAPEFQFLHSA YATLLMKQAWPQNSSSCGTEGTFHLPV DTGTENRTYQASSAFRYTAGTPYKVPP TQSNATAPPYSPSPNPYQTAMYPISAYP QQNLYAQGAYYTQPVYAAQPHVIHHTT VVQPNSIPSAIYPAPVAAPRTNGVAMGM VAGTTMAMSAGTLLTPQHTAIGAHVPS MPTYRAQGTPAYSYVPPHW |
| 3133 | 11184 | A | 408 | 1234 | 1337 | TRGPRGPADSCRKAWSEKAWQRGPWS WCPAAGASGGCGLHPWLW/PEPWVE RATPT*GPCSRTPAPGSPLPGFLRPLPA AVCRPPGSPCSETVLF*EAE/PT/P*APVRI GGTFQPCAVLLPARMKVVQSSTVR*/VT VTRLPVQKVEVAGGWPGSHEKTLF/AA/ PAWGLDRKPLQAPRSQKPPNPQGTAE GQRWAHRYKCCFVSLTPCSSQLPVP*DL ASKG*PSHT*ILGSF*DLCLPA*PMLQGPC PQPLSAP*VFLFPLS*VGALIGPFLARPF SRGQLP*AWATPPWPS*PLAK/SPPDVAC SLVPGPSFSPSHPSAPVVEPHL*APGALN VLSPLDLMCIPSPASYVAAKAPQAVNGG SCHTSLPELT*PPATSCIGILRAGPCSLM GPFRPVKPW*RLACLGLNSQCLTPQPK TGSVPYGPSPAVAWVP/ERLPPPGSPPPAP IKVLPLMQACVDHVFPWPEPPPATGGQL PF |
| 3134 | 11185 | A | 4080 | 1 | 502 | RHEGGMWRAGSMSAELGVGCALRAVN ERVQQAIVARRPRDLSPSQPRLVAV/SA KTKPADMVIEAYGHGQRTFGENYVQEL LEKASNPKILSLCPEIKWHFIGHLQKQNV NKLMDGKSEFLIKRENIMPTELNSPFGV IYTWETYPTSMFIIHWSFRKIKNCSF |
| 3135 | 11186 | A | 4081 | 171 | 1184 | IPILIMKLLCCHKSSGDPYHLFAKSKH STLPFSLGLGVGPRGMWRAGSMSAELG VGCALRAVNERVQQAIVARRP/RGDLPAI QPRLVAVSKTKPADMVIEAYGHGQRT FGENYVQELALEKASNPKILSLCPEIKWH FIGHLQKQNVNKLMAVPNLFMLAETVG FCECLADKVNSSWQRKIGSPERLKVMG PGFNTSREEIYLFVSLLLEGKHGLPPSETI AIVEHINAKCPNLAEFVGLAMTLGSFGHD LSQGPNDPQQLLSLPEE/ICGKKLNIPAE QVELIMGMSADFQHAVEVGSTNVRIGST IFGERDYSKKPTPDKCAADVKAPEVA QEH |
| 3136 | 11187 | A | 4086 | 1 | 265 | AGNRLRFQLELEFVQCLANPNYLN/WYP QCLHMLELLQYEHFRKELVNAQCAKFID EQQILHWQHYSRKRMRLQALAKQQQ QNNTSGK |
| 3137 | 11188 | A | 4087 | 1 | 987 | |

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| 3138 | 11189 | A | 4088 | 1 | 491 | RGFRNFARVSGLLLCQAGGVLVSSFVM AAAVAMETDDAGNRLRFQLELEFVQCY ANHNTLIFLPQRGYFKDKAFVNYLKYL LYWKDPEYAKYLYPQCLHMLGAAPN MEHFRKEAGWNAQCAKFIGWNRQVST LGKHYSRKRMRLLQQAELAEQQQNNTS GK |
| 3139 | 11190 | A | 4089 | 55 | 858 | EKGRARGRERRRKMQLTRCCFVFLVQG SLYLVICGQDDGPPGSEDPERDDHEGQP RPRVPRKRGHISPKSRPMANSTLLGLLAP PGEAWGILGQPPNRPNHSPPSAKGKKIF GWGDFYSNIKTVALNLLVTGKIVDHGN GTFSVHFQHNATGQGNISISLVPPSKAVE FHQEQQIFIEAKASKIFNCARMEWEKVER GRRTSLFTHDPAKICSRDHAQSSSTWSIC SQPFKVVVCVYIAFYSTDYRLVQKVCPCD YNYHSDTPYYPSG |
| 3140 | 11191 | A | 409 | 89 | 596 | IILKTGSSLCHPRLECSGVILVHRNLRLP GSSNSPASGSPVA*ITGARHHDRLIFVFL VEMGFCYVQGAGLELLTSSDPPTSASQS AGVTGVSHCARPSFAL*F*KSA*YNLELC LFYHH*YSKCIHFHFLDYNQNLITINIE SSLIFSILLISTFYCYLAEIPR |
| 3141 | 11192 | A | 4090 | 1 | 368 | MRARNLMTKLTVISRKEELQOEAAHR EVQSLPPGEMEERSSSKTCPQVCDGRILS CMIKVPP/VGREKH*RPGRSH*HEAGCG PFTPPKVDHHEHLPPRRVEAGSRQKST TEPFPQAAGW |
| 3142 | 11193 | A | 4091 | 253 | 536 | YLASLEIPQSKVPESRPSHQVPSSQSLDSE TPPSN/RHRQPPVDRKCVCR/LPLPPPTF RPPKVDHHEHLPPRRVEAGSRQKSTTE PFPQAAGC |
| 3143 | 11194 | A | 4096 | 318 | 543 | KSSWSRWAFGTVRSPCGRQHRDIGATD NSGRSGPAEQRPQSS/ASSAMSAAGGSRL TFHPRNLPPRTPTQDSAALT |
| 3144 | 11195 | A | 4097 | 42 | 342 | ENEILEVVQLGSRVCFVHFYHLHCCRHH CPENVHAG/CFGDCLG/HGRCSIQNCFFE R*I*VG*NNVAATAVMFGLVFPLVLSLK YQVYFFKVLALMNFCS |
| 3145 | 11196 | A | 4098 | 1 | 1289 | MYERVYVSTDIAIKLCKLLNRQFDRLY KKHSTGSASGEGLKALPLIVEGEGEPCV AEITRQEREEGA VHLFGLTWQLQPVGE LYANGVSKGNRGTESMDTTYSPIGGKVS DKSEKKVFQKGRAIDTGEVDIGAQVMQ TIPPGFLWRFQITHHPIYLKFNISLAKDSL LGIYGRNIPPHTHTQDFVKLMDGKQLV KQDSKGSDDTQHSRNLITSLQETGFIE YMDQGPWYLA FYNDGKKMEQVFLTT AIEIMDDCSTNCNGNGECISGHCHCFPGF LGPD CARDSCPVLCCGNGEYKGHCV RHGWKGPECDVPEEQCIDPTCFGHGT MGVCICVPGYKGEICEEEDCLDPMCSNH GICVKGECHCSTGWGGVNCETPLP/EQC SGHGTFLLDAGVCSDPKWTGSDCSTE H KGGSSRLFL |
| 3146 | 11197 | A | 4099 | 1 | 4509 | VRLEWPTDLAVNPMDNSLYVLDNNIVL QISENRRVRIIAGRPIHCQVPGIDHFLVSK VAIHSTLESARAI SVSHSGLLFIAETDERK VNRIQQVTTNGEIIAGAPTDCDCKIDP NCD CFSGDGGYAKDAKMKAPSSLAVSP DGTLYVADLGNVRIRTISRNOAHLNDM NIYEIASPADQELYQFTVNGTHLHTLNL TRDYVYNFTYNSEGDLGAITSSNGNSVH JRRDAGGMPLWLVPVGGQVYWLTISSN G |
| 3147 | 11198 | A | 41 | 319 | 1002 | |

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| 3148 | 11199 | A | 410 | 372 | 639 | RAFWQYFKSLNMFMSFDPAILLIGIYPKE KS*IQK/DTLCEPVSEILLMVVN*YIC HTRNDQAGLIY/HLYSGIYLALK*VCEFF TLKG |
| 3149 | 11200 | A | 4100 | 338 | 8522 | SEMEQTDCKPYQPLPKVKHEMDLAYTS SSDESEDGRKPRQSYNSRETLHEYNOEL RMNYSQSRKRKEVEKSTQEMEFCEETS HTLCSGYQTDHMSVSRHGYQLEMGS DV DTETEGAASPDHALRMWIRGMKSEHSS CLSSRANSALSLTDTDHERKSDGENGFK FSPVCCDMEAQAGSTQDVQSSPHNQTF RPLPPPPPPHACTCARKPPPAADSLQRR SMTTRSQPSAAPAPTSTQDSVHLHNS WVLNSN |
| 3150 | 11201 | A | 4101 | 139 | 520 | LSLPLSPRLECSGTLARC�LHPSPPRSKR FSCLSLPSSWDYRRAPPNLAIFFLLFLV EMGFHHVGQTGLELLASNYLPTSA/FPK CWDYRHEPPCPADKTNFLSLWFIGYNIF LESEVNFFLPWDA |
| 3151 | 11202 | A | 4102 | 7 | 497 | |
| 3152 | 11203 | B | 4103 | 93 | 182 | PPPKALRRELPEEAAAAEEERRKIEVPSEIE * |
| 3153 | 11204 | A | 4104 | 51 | 394 | WGGPGLKPLLMVLDPYRAVALELQANR EPDFSSLVSPSPRRMAARVFYLLLVSV CMCVCVCGAGTQRPEARTGTPPTCPLLA S*PVLSAQQILHVQKEKPYGRLLIQGPFR FH |
| 3154 | 11205 | A | 4105 | 427 | 499 | |
| 3155 | 11206 | A | 4106 | 796 | 2482 | KTRGNMFYYPNVLQRHNGCFATIWL ATRGSRLVKREYLRVNVVKTCCEILNYV LVRVQPPQGLPRFRSLYLAQLQIGVI RVYSQQCYLVEDIQHILAYRLHRAQLQ MRIDMETELPSLLPNHLAMMETLEDAP DPFFGMMSVDPRLPSFDIPQIRHLEAAI PERVEEIPPEVTEPREPERIPVTVLPPEAI TILAEAEPLRMLEIEGERELPEVSRRELADL LVAEEEEAILLEIPRLPPAPAEVEGIGEA LGPEELRLTGWEPGALLMEVTPPEELRL PAPPSPERRPPVPLRRRRRRRLLFWDK ETQISPEEFPRNNLQTRAHCWECMVQ PPERTIRGPAELFRTPTLSGWLPPELLGL WTHCAQPPPKALRRELPEEAAAAEEERR KIEVPSEIEVPREALEPSVPLMVSLEISLE AAEEKSRISLIPPEERWAWPEVEAPEAP ALPVVPEMPEVPMEMPLVLPPAELELLN WKTVHRAVALELQANREPDFSSLVSP LSPRRMAARVFYLLLVLSAQQILHVQK EKP\YGRLLIQGPFRFH |
| 3156 | 11207 | A | 4107 | 136 | 423 | SPEHPQLPGSLLRPPGAQIPSEWQVAEAT ALVHTLDGWSVVQTMVVSTKTPDRKLI FGKGNFEHLAKKELEAAWGVEVFDRFTV VLHILRCNARTK |
| 3157 | 11208 | A | 4108 | 1 | 212 | RPPRRVVRGRHQPHGEPVRS GAPVRVP GEDDAAQPSAAERVGPRAVPGAGFTVH QHHRGGLHRRRLRQ*RHQPHGEPVRS GAPVRVPGEDDAAQPSAAERVGPRAV PGAGFTVHQHHRGGLHRRRLRQ |

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| 3158 | 11209 | A | 4109 | 1 | 1746 | AGRRTPGAAALPRGPRPLGSAGSRAVLP RARASRCRPQEPRESGGAVGRREGPAGG RRTKTERKTTRRSRKMRTTRPRRSCCGE SLCCRRGPKRVCLVHPDVKGWPGKSQM TRAEWQVAEATALVHTLDGWSVVHTM VVSTKTPDRKLIFGKGNFEHLTEKIRGSP DITCVFLNVERMAAPTKELEAAWGVE GCLTAFTVVQLHPACNARTK/ERARLQ VALAGDARLHRSNLKRDVAHLYRGVG/ SRAYIMGSGESFH/MQLQORLLREKEAKI RKALDRLRKRHLLRRQRTTRREFPVISV VGYTNCGKTTLIKALTGDAANQPRDQL FATLDVTVAHAGTLP SRMTVLYVDITIGFL SQLPHGLIESFSATLEDVAHSDLILHVR DVASHPEAELQKCSVLSTLRGLRLPAPLL DSMVEVHNKVDLVPGYSPTENVPVPS ALRGHGUQELKVELDAAVLKATGRQIL TLRVRLAGAQLNWL YKEATVQEVDP EDGAADVRIISNFPYKGFRKLFPRMN GRPQKACGVGASPALGELRRYPLCWGQ LGVRCRSVLLVWFCTRLASQPFAGMYR ACR |
| 3159 | 11210 | A | 411 | 136 | 251 | IHQEKPPNIFSVKKRHYD*PGQHDPLASA SQSAGITGV |
| 3160 | 11211 | B | 4110 | 50 | 382 | XGEQLVRQDLDAGVSEHSGDWLDQDSV SDQFSVEFEVESLDSYSLSEEGQELSD EDDEVYQVTVYQAGESDTSFEEDPEIS LADYWKCTSCNEMNPPLPSHCNRCWAH X* |
| 3161 | 11212 | A | 4111 | 1665 | 1787 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 3162 | 11213 | A | 4112 | 1431 | 1553 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 3163 | 11214 | A | 4113 | 1740 | 1862 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 3164 | 11215 | A | 4114 | 1 | 752 | DLDAGVSEHSGDWLDQDSVSDQFSVEF EVESLDSYSPSEGGQELSDDEDEVYQ VTVYQAGESDTSFEEDPEISLADYWK TSCNEMNPPLPSHCNRCWALRENNWLPE DTGKDKGEISEKAKLENSTQAEFGDVP DCKKTIVNDSRESCVEENDDKITQASQS QESDYSPSTSSSIYSSQEDVKEFEREE TODKEESVESSLPLNAIEPCVICQ/GST*K WLHCPWQNRTSYGLLYMCKEAKEKE |
| 3165 | 11216 | A | 4115 | 426 | 813 | SSRRFVWRAKLLCERAQSGTVYEI*QCA HRHPRHRHPGCCRHRLGYAGTAGPLAG YRPFRRQHRQSLWRAASAICVDAISMRT SRSTVRPLWPPSPARFATWSHYRLRDH GDHTRPVDLPTSQFTILL |
| 3166 | 11217 | A | 4116 | 1174 | 1354 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPLRPAGLFKHSPGLYSQ PILT |
| 3167 | 11218 | A | 4117 | 2251 | 2373 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 3168 | 11219 | A | 4118 | 1027 | 1193 | FFFFFFFFGFLVETGFHRVSQDSL DLLTS *SSRLGLPKCWDYRHEPPRAEEGI |
| 3169 | 11220 | A | 4119 | 983 | 1386 | QEVRYRKVETLRCLLFSSCLVPVCAASP VSRPGCRFLRSSLHWPTGRLVFRQRGET FLVPEKTVLRGVASAPAKAAGRTPVPG RPRDARLRADARS*SC*RAARPRRGASG AVGARGCPRPGFPFLRSGGIFV |
| 3170 | 11221 | A | 412 | 118 | 337 | IHQEKPPNIFSVKKRHYD*PGQYKTL SLKIQILAGYSGTCLAKSLLRRVGREVIQ LALKIRAPIWKIECL |

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|------|-------|---|------|------|------|---|
| 3171 | 11222 | A | 4120 | 6133 | 7646 | YMLFLFLSTKGWTVIQNRQDGSVDGFR KWDYPYKQGFNVATNTDGKNYCGLPG NEQACKIKSFYKWDFF*LKNIHCWKPV LGS*EEFPDKNVEAKDKGRKAVFSFPKF YFW*EILFCFSFRVEYWLGNDKISQLTRM GPTELLIEMEDWKGDVKVKAHYGGFTVQ NEANKYQISVNKYRGTAAGNALMDGAS\ |
| | | | | | | HLMG\ENRDHDPFHNGHGSFQPPYD\RD\ NDGWYVWHSLLLL*KSH*YHYSESLTIF LIATTSWALTVSHCPKLFMHHSKAFQL* GRHSYSHFTDEI*RDYVICPM SHNYPEIK LEFEHSYFLNNEHLDKYLYLYILKCV*KL SFSFPGFSDTKGCKSYSSIK*QTQSLDG LPQRPSYLSFLL*GTGGLWCISVTLCIAP KGKTTVHTSVAVFYG*SAKRNLT TVVLF LITPNTFSFRLTSDPRKQCKEDGGGWW YNRCHAANPNGRYYWGGQYTWDMAK HGTDG VVWMNWKGSWYSMRKMSM KIRPFFPQQ |
| 3172 | 11223 | A | 4121 | 333 | 430 | GRGDKPYPSPGDSWVQD*ILVQL*ICPQ EPS |
| 3173 | 11224 | A | 4122 | 2 | 1679 | |
| 3174 | 11225 | A | 4123 | 42 | 1465 | GRWPPRGRENALSKTLVDMMDMADYS AALDPAYTTLEFENVQVLTMGNDTSPSE GTNLNAPNSLGVSALCAICGDRATGKHY GASSCDGCKGFFRFSVRKNHMYSCRFSR QCVVDKDKRNQCRYCRLKKCFRAGMK KEAVQNERDRISTRSSYEDSSLPSINAL LQAEVLSRQITSPVSGINGDIRAKKIASIA DVCESMKEQLLVLEWAKYIPAFCELP DDQVALLRAHAGEHLLLGATKRSMVFK DVLLLGNDYIVPRHCPELAEMSRVSIRIL DELVLFPQELQIDDNEYAYLKAIFFDPD AKGLSDPGKIKRLRSQVQVSLEDYINDR QYDSRGRFGELLLLPTLQSIWQMIEQI QFIKLFGMAKIDNLLQEMLLGGSPSDAP HAHHPLPHLMQEHMGTVVIVANTMPT HLSNGQMSTPETPQSPPGSGSES YKLL PGAVATIVKPLSAIPQPTITKQEVI |
| 3175 | 11226 | A | 4124 | 3 | 1840 | |
| 3176 | 11227 | A | 4125 | 6233 | 6874 | VLIGCIPQVPPSISYSPLFWFSALGNVAEI FFCLCLGNHNSCWRTLVEVPESLCPHC *RLLV*HKS GDIWVLT PQMLQLDPAALP CPPSSIVDAKGLSDPGKIKRLRSQVQVSL EDYINDRQYDSRGRFGELLLLPTLQSIW QMIEQIQFIKLFGMAKIDNLLQEMLLG GPCQAQEGRGWSGDSPGDRPHTVSSPLS SLASPLCRFGQVA |
| 3177 | 11228 | A | 4126 | 1 | 1481 | GFGVGAQGRAGRRVEAGRMRLSKTLV VDMMDADYSAALDPAYTTLEFENVQVL TMGNDTSPSEGTNLNAPNSLGVSALCAI CGDRATGKHYGASSCDGCKGFFRFSVR KNHMYSCRFSRQCVVDKDKRNQCRYC RLKKCFRAGMKKEAVQNERDRISTRSS YEDSSLPSINALLQAEVLSRQITSPVSGIN GDIRAKKIASIADVCEMKEQLLVLEW AKYIPAFCELPDDQVALLRAHAGEHLL LGATKRSMVFKDVLLLGNDYIVPRHCPE LAEMSRVSIRILDELVLFPQELQIDDNEY AYLKAIFFDPDAKGLSDPGKIKRLRSQV QVSLEDYINDRQYDSRGRFGELLLLPTL QSITWQMIEQIQFIKLFGMAKIDNLLQEM LLGGSPSDAPHAHHPLPHLMQEHMGTV VIVANTMPTHLSNGQMCEWPRPRGQA ATPETPQSPPGSGSES YKLLPGAVATI VKPLSAIPQPTITKQEVI |
| 3178 | 11229 | A | 4127 | 602 | 799 | ENPKQENLWSQYFTLISTI*KKKSWLCI VAHADCSSTLGD*GGHIA*AQEFETSVG NIVKPPSLY |

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| 3179 | 11230 | A | 4128 | 646 | 1905 | |
| 3180 | 11231 | A | 4129 | 6717 | 7569 | |
| 3181 | 11232 | A | 413 | 160 | 437 | KRDITTSLGQYGQNP*SLKIQILAGYSG TCLAKSQLRLRLRHQNRNLNLRGGRGVSE QRSCHLHSWGGHSETVSKKKKKRERQQ WRQIGTCMP |
| 3182 | 11233 | A | 4130 | 2 | 93 | DFTMSHHYHSAHGTLLVAPRALGNPLSL YPSNYTFPFQHSPPDCTQSYSLPPEYAT HGSSCFDITDGGNLASRALAGSCAPVSG SLPCCPTLGIPSPPLPHMKSLLPTYPPTI SMKPP*PCPGSQGPWQSAFTLPI |
| 3183 | 11234 | A | 4131 | 743 | 955 | ESDFTYFTHNSCLFCYNKIYINIKLSL NCNYGNYFLYIVAAHTQTYIYI*NIFCFF CHLLLTFCCLGF |
| 3184 | 11235 | A | 4132 | 49 | 313 | PLRIWPC*ALFLKLSLGFSLF*FYSSFLFL SPPLC*SLPRVQYIYMYILYICIN*YTYI QVCICNGYMYSCSWCSNVWYGYTENM RT |
| 3185 | 11236 | A | 4134 | 508 | 780 | VFSFSPFSPHLSLFFSLSFSFPSPFLPSS FFTFGNHLL*ISCNPNLMYQWGIFKYK YYQCIFWLLSDF*LKYNENDMSVAFGLR TSL |
| 3186 | 11237 | A | 4135 | 34 | 329 | DRLKRKNKQSLSYLWEYNKKSNICVTQ SLEREEDDRAEKVVE*IMASNFPYLSRD VNLKIQDS*RILNWKLKKSISKYIIDLLE TKDIIRNLESSQR |
| 3187 | 11238 | A | 4136 | 582 | 869 | MCQRVQTPKSPSNPYVHSNICTQLFIAPL SIAKRWKQPKCPSAEE*INEM*YIHSME YDSAIRKNEVLHVTTWKNFENIRLMKD ASHKGLYVA |
| 3188 | 11239 | A | 4137 | 285 | 346 | AVLFYVFHIPPYLLVMTLLLYFLP*LPNQC RFSSLSHKTATWPSSTTVTLF |
| 3189 | 11240 | A | 4138 | 97 | 298 | DNLTLLPRLECGGMIMAHCSLNTFSSD PAASAS*VAGTTGT*HHAWIFVFLCNWL RNRGVTVKKRS |
| 3190 | 11241 | A | 4139 | 147 | 502 | IFHSMPISEWKL*TLWQFFKELKIELP FDPAJPLLGI*PKLAVVAPQHS |
| 3191 | 11242 | A | 414 | 2 | 150 | WLPSLLEPLHPSNHVQGPVAGIDLGT YSCVPINRRTTPSYVALRPG |
| 3192 | 11243 | A | 4140 | 435 | 660 | NLNQHEKLSMLE*ILKSYPKILDNDNDHE VSHCSKGNFKNRSKEWWCGTQDSWR LGNLKVGEFEFNDLTRNTL |
| 3193 | 11244 | A | 4141 | 293 | 563 | NVWPSSSVRGRNE*GREGRRRTQQA GLGPAPSDLWWLWSWCLQKNMSQGG ENLPAGPGSCCGREAGAGTSLEDAPF FEAQLQLH |
| 3194 | 11245 | A | 4142 | 1329 | 1563 | WPRNQPTRRPWLKDKLPVPGGLTGP PCGQPPGPPPLRPSALWSSHGPPNG EPLPRGE*YLHPSPRRTSYL |
| 3195 | 11246 | A | 4143 | 304 | 589 | RTWWTAASYFRSVGGSASNRPFSGPY EFQLPRGHSRKGTTRSRAREPSTLWSTP AAP*RTWWTAASYFRSVGGSASNRPFSI PGPYEFQLPRGHSRKGTTEEQSGAIYT VEYACSAVKNLVDSSVYFRSVEGLLKQ AISIRDHMINASAQGHR |
| 3196 | 11247 | A | 4144 | 131 | 690 | VSPAVTTSSLSWARSDLAEGHARCPL CSGWAQHLSNEEADALSPHTRPIPTCI* SRTSSLRASWPTSHWPCTGCRSMCV RSLPELAQHKADNAALGRSRAREPSTLW STPAAP*RTWWTAASTSAAWRVCSNRP SASGILNASCPGPQVAPGDRPPPLPFP QGPLSCAGEPLLLAY |
| 3197 | 11248 | C | 4145 | 332 | 421 | MEEKIFSQPGMVAPTNCNPSTLGGQGRWI T* |
| 3198 | 11249 | A | 4146 | 685 | 929 | KVGGAKPSLGYLRLGLRPLVFLCHIS*A GDFPRGV*LLPRRGSGVVAHTCNPSTLG GQGRQIT*GQEFKTGPVNMVKPHLY |

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| 3199 | 11250 | C | 4147 | 710 | 892 | MCVCAHTCPQTSIYIHVFTHGYDCIQVT AQKCLHMCFFHIHMSTHACVDTYICIYIH VKLI* |
| 3200 | 11251 | A | 4148 | 98 | 317 | |
| 3201 | 11252 | A | 4149 | 656 | 1037 | FVQVQAHKLACKHVQGAYFVFKEQQPE GNVFRQCQGVSTS*EHGASSEPWHPAGA GVTTSFSSPFGGDRHKFEVSGRRLPTEG LPSNSSFESFPSSIPWPFLFPQVQLSTIWG LKFQFFGDLKILP |
| 3202 | 11253 | A | 415 | 1 | 1786 | MCLLVITYSSRHVYNNLTTEEQKGRVAFA SNFLAGDASLQIEPLKPSDEGRYTCKVK NSGRYVWSHVILKVLVRPSKPKCELEGE LTEGSDLTLQCESSSGTEPIVYVWQRIRE KEGEDERLPPKSRIDYNHPGRVLLQNL MSYSGLYQCTAGNEAGKESCVRVTVQ STMFGQTLQLGIDLGTYSICVGVFQQR KSPRLIANDQGNRITTPSYVAFTGH*TG WIGDAAKNQVAMNPNTNTVFNKRSD LDGRF*MNAVCPVLIMKHWALYWVGE MMLGRPQGP*KDYKGEDQKAFYPEEGC LLWVPDKD*KEICRSPNLGEELVTNAVW TVPAYFNDISQRQATKDACTIAGLNVLR IINEPTAAAIAYGLDKKVGAEARNVLIFDL GGGTFDVSILTIEDGIFEVKSTAGDTHLG GEDFDNRMVNHFAEFKRKHKKDISENK RAVRLRTACERAKRTLSSSTQASIEIDS LYEGIDFYTSITRARFEELNADLFRGTL PVEKALRDAKLKDSQIHDIVLVGGSTRIP KIQKLLQDFFNGKELNKSINPDEAVAYG AEMRQDKKELLDPDIAEDFLEEVAFDKK RMGFGGF |
| 3203 | 11254 | A | 4150 | 1365 | 1503 | LKTLQRAGCSAHACNPSTLGGQGRWII* AQEFNTSLGNVAKPCLY |
| 3204 | 11255 | A | 4151 | 397 | 682 | YSKSchkAYRMKCQLNVGLSCKCECT EWRDPCELEGQESLWGQVQLAHACNPN TLGGQGRGRIA*GQKFKNSLNNIARPHLF KKRKKISLMRWLK |
| 3205 | 11256 | A | 4152 | 477 | 684 | LYLCSALKKNQ*EPGMVTHAWNPNSTLG GKGRRTA*AQEFQTSLSNVGRACLKYIY IFKISQAWWHAFVI |
| 3206 | 11257 | A | 4153 | 108 | 419 | SHTLGGQHGRIMRSGVRDQPGQHGETPS LLKIQKKKKLPGRAGRHL*SQLLRRLRL ENRLNLGGGGGSETEIEPLPPQPG*TQ*R LPSQKQKNKLETVSKKKS |
| 3207 | 11258 | A | 4154 | 175 | 190 | DKVRVSQVRLTSRHLITLR*IRKGRGKK RGCRERNRENRGK*KYV |
| 3208 | 11259 | A | 4156 | 20 | 430 | RPQTYTMVHLTPEEKCAVTALWGKANV DEVGGEALGRLLVVYPWTHRVFETFGD VSTPDVAVMGIPNGNADGMNVLWASIDG LAHLDNLRGTATLTHEHD*D*LHVDPEIL MLLGNVLICVLAHHCVGESPSWQAA |
| 3209 | 11260 | A | 4157 | 31 | 492 | QRILQSRPFEGRVKQGVTWLLQLVGLVS ESHIGPELHLPCEECHLLVSFGVNSPE DSSPLLTEWLWTHLPFLHCLFGASGR GLQTVPPFVSTALQNVCFPQKGKAPFLL LSCATGGCSAGLRVYKLRSAPSCD*AGR TRGSSGESAPML |
| 3210 | 11261 | A | 4158 | 165 | 433 | GSGQADHPCVGVWRQNSVNPQVFLQAT G*LISASSGSINTNMAQGTAVVCFGPVYP PKAKGRARSQVTPCLTLPSKGRICKILC YLFLK |
| 3211 | 11262 | A | 4159 | 132 | 257 | |
| 3212 | 11263 | A | 416 | 1 | 154 | PQRRVARRKRAVLPSTKA*PENTPSTFTS ASMEWASRSVHLGHSKRFGNLP |

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|------|-------|---|------|------|------|---|
| 3213 | 11264 | A | 4160 | 2 | 111 | QLLKDSARSTLVLYPCWARVVSQKSGCCP LKVLSQRPQKGLGLLWVEAWECPGAVA RCLCHPGPLCPASGTFTVPGTEPHS*LLL RNELPSPLF*LLGQSEPEKWMLPPQGAIS ETR |
| 3214 | 11265 | A | 4161 | 3 | 116 | GWRAPTSQPGGPAQVPCSSF*KILPGQH WSSTPAGPE |
| 3215 | 11266 | A | 4162 | 273 | 793 | DSLILLIQVDTMPFTLHLRSRLPSAIRSLIL QKKPDIRNTFSMAGGAPTSQPGGPAQVP CSSF*KILPGQHWSSSTPAGPE*ARKVDAA PSRCYL RDQPKGPFKVPGTEPHS*LLRN ELPSPLF*LLGQSEPEKWMLPPQGAIS SLRDLSKCLAQNLTHDCCSGTSCPPHCS DSFPYHLAPVLAEIFEIMEKVQWRNPT GSAICPLHRPSQKPACTGLRRK |
| 3216 | 11267 | A | 4164 | 212 | 494 | FSEAQFLANVAIKAILSEEISEGKGDRRM LADHTLILTERGSEGPCC*PQEV RPTVLS EWGCKCAQANCECSP*PWP HKSRAGHF PPLSLGKLL |
| 3217 | 11268 | A | 4165 | 281 | 587 | EIFFNPKREYLSLHWMDEHQCPNFIHHV GQGGLGTIWQDVLQEQYNQKNFLYNISLK DKFLGWMW*LTPVIPALWEAEVGGSL PRSSKTSLGNMARSHPYKK |
| 3218 | 11269 | A | 4166 | 113 | 564 | IDRLDSAKIFGHLISIFDRCEKRRPDVSG TGTCSGSFRRVTFQPAVPGRTDSPIPRTH GPNFVP*TLVEKKPPAAW*TPACDLTSK PSIGPTILVPTPKVEPGSLPTPA*DPLEPIQ SPEKK*SIVPQTGSFQTASQLTEAVPELV LVAH |
| 3219 | 11270 | A | 4167 | 1173 | 1432 | PIPVDLNLTLMFCHYFIYVYHPCLEMFST CGLLSL*AQRPSDGYFFEAFIYIILFCTMF FLNVQILYSSEKNTVFVDNHSYYTVLR |
| 3220 | 11271 | A | 4168 | 75 | 270 | QYISVVDTYLLMPRLATAIILWITN*VFE KRVAHFGYHWSLMVRDRRISGVDRYYV SKGLENID |
| 3221 | 11272 | A | 4169 | 271 | 825 | SPPACLVDGQQALPSGGGLYPNSLRQGS VGQAGRGCLSWFCMVHFANPEDQFLGF QASGFLHLVLPKPPQGAATPSGSSQGGPA MFSGLPSEPPTPATPQNPHLSSTKLLCE AAPTRGKPCPTSSIFQPWHRTDGKGRA GFSASGTRGRPHLTPSPVHQGT*EASQK GPALMPPGFQPPKKGK |
| 3222 | 11273 | A | 417 | 1 | 893 | PTRPCMAGEKVEKPDTKKKPEAKKV DAGGKVKKGNLAKKPKKPKPHCSR PVLLRGIGRYSRSAMYSRKAMYKIRKYS AAKSKVEKKKKKVLATVTKPVGGDKN GGTRVVKLRKMPRYPTEDVPRKLLSH GKKPFSQHVRLRASIV/TPGTILILTGR HRGKR VVFLQLASGLLLVTGPLVLNR VPLRRTHQKFVIAFTTKIDISNVKIPKHL TDAYFKKKKLRKPRHQEGEIFDTEKEKY EITEQRKIDQKAVDSQILPKJKAIPQLQGY LRSVFALTNGIYPHKLVF |
| 3223 | 11274 | A | 4170 | 1 | 211 | THPPPAEAPGAEGPQ*G*AKHPSAP*APL L/PRRRARASSRPVTSVTPSSGGSFRPGTP AQQVITAVTSA |
| 3224 | 11275 | A | 4171 | 1 | 424 | NSRVDDFVRPGGSSAAGRQMRGGGQOV PNPRPGFRGQQP*RNHPPVSPWALAG DAGGMLWNMMRSWPVSGRPTLNPFNK QSGPRQHEQGPGEVPDVTPEALPELPP GEPEFCRPERVMDLGLSEDHFSRPVGLFP GL |
| 3225 | 11276 | A | 4172 | 1091 | 1421 | RGHTEINKHPDHIHSPTHTCRHTFTNMH AHTHTPTYMHTHTGMFW*K*N*GSLNS RSGFK |
| 3226 | 11277 | A | 4173 | 1407 | 1607 | LSDLNGNFHSKVMTKRVNIKGNYLKNM RPGAVAHACNCSTLGGQGGQTA*AQEL ETSLGNVVRLCLY |

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| 3227 | 11278 | A | 4174 | 1 | 294 | FSRPDLNNGHIKQVHTSERPHKCQVWV GSSSGLPPLPLEPLPSDLPSWDFAPALWR/ CVPFGS*HRLFPFSKKIHPSP*KPGPSTLQQ HSDLDPAFISG |
| 3228 | 11279 | A | 4175 | 560 | 824 | FWKVGCLPWELAHAPAYLLPPLGITSP*A LGFPRTGGPWPTFPPLPRVSRPSQRLG TIPT*SQPHACPLPLPHSGSRSCFHWLV K |
| 3229 | 11280 | A | 4176 | 3 | 325 | FFHVSRLNFYFFRYIKHCYFIFSLILVSGS RVNLLLLGLIVYCFVVFMMNF*TWISHF LSFFFFFCRDGVSHCVAQAALFTPGLKC WDSRREPPRAEMFLFLT |
| 3230 | 11281 | A | 4177 | 292 | 543 | SPGTYAPKRIGKGAGNWKPGVPFRSSM WKETQPLSSRVSKVLSVSPSPPIVPVP LLPALPK*GHSPLVSPPLHRSSQGESP |
| 3231 | 11282 | A | 4178 | 3 | 367 | IQMDCVLLFPAQAQISAPLIMKTTPITIS WGLEHICPSYPWNHSPSLYHRYAMGFG MFFQSGPCSSWAWKLSRTLPSLVVALSS AWPLTRG*RLDLGPPAPSSYVGFSSQASP SPSPAAQC |
| 3232 | 11283 | A | 4179 | 67 | 283 | MCAYIKIDKGNRMCTNMIYLVEGIGVT FSLTLMYKYTKLIIMLSYVKRLTLISCAF YVNLWINLYYAMFI*MCAYIKIDKGNRM YCTNMIYLVEGIGVTFSLTLMYKYTKLII MLS YVKRLTLISCAFYVNLWINLYYAMF IK |
| 3233 | 11284 | A | 418 | 934 | 1272 | WCILGLCTSLMSRTALFPSRHTFFA/RSH SAASKL/EKKKKKEKVLATVTKPVGGDKN GGTRVVKLKMPRYPTEDVPRKLLSH GKKPFSQHVRKLRSITPGVILILTGARH RG |
| 3234 | 11285 | A | 4180 | 268 | 467 | GNRRALLRLPALGPPRSSP/DGFTPGTTA RPSILKRCMPMTPLPPDPSAAAAGTSELW TSPDSSSSSR |
| 3235 | 11286 | A | 4181 | 880 | 1200 | GNPTWFLPSYQGNSGPAEIQS*GFTPGT TARPSILKRSPMTPLPPDPSAAAAGTSEL WTSPD*QQQQQDGKEAPQSGRHDSSSA LRPAAPEALPVSRRPPPLAA |
| 3236 | 11287 | A | 4182 | 343 | 720 | SCLLTVISFHQIKKYIYVHTQLTKAGQKE FICRLSLALTNLPPAAPPLAMAPCVSPAS RQDTVLGAGPQPPSGPAPTAPQQA*AR WQLGPPSPGPSILPPREGRPSAPSGAGWG GDLAGPSQVHF |
| 3237 | 11288 | A | 4183 | 789 | 1015 | MSLMVPLMPYGP*YLPSPPAYPIWEL PLPQRDSADVSRRLGGRGVAVERDSPTE KSNISKFLYQVACAVTHL |
| 3238 | 11289 | A | 4184 | 319 | 471 | IMWYIHIMEYI*PQKGRKILTHATI*MKL EDIMLSEISQSQKNKYCIISVI |
| 3239 | 11290 | A | 4185 | 68 | 422 | GSPSRCPAFLSSPVAARPPLTHFTGAGL LRASGEPAQLTGSVSQ*PPRAPSSGLPL KHSPHQCSAQHSGKEGLGGGTNTTREN* PSPRPLCMGAQAGRMLLLPAAVRNHVL ESGSV |
| 3240 | 11291 | A | 4186 | 135 | 500 | PPWVTWRWGWGWVIRDTGDRVRSQRQ QGLPPKLQSGWEVESWLGPRPRVFPGS VPGTPR/SPAAGGSQPRCPDARPAHKGPR APGARCGPPAPPGLPAY*PGRPR/PRP ARR*TPLTAA |

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| 3241 | 11292 | A | 4187 | 365 | 1452 | IGPEVPEGCHFRSGESRGDATLAYRVESE HHLGLEGCAGNATLVQGVGRKIPCLGLR GAILGPQIAVRLGSRIMARPAAPGLSQA RSLARRGCPAAGGSQPRCPDARPAHKGP RAPGARCGPPAPPPGLPAY*PGRPRRG LHGGRRHSRRPPRRGPAAPGSPA EVAG ASARGRAPGPPCPRPPPIPAAPRVEAG PSARPSVPAPAPAPSRSPRLQPPAAPWG GRASGPKDPGTAPPPTRTQSARNPSRSP PPAPSPASAGASADDPGTPWHRTGPPC QSQTRKHTGP*AARDQQRQSRKDDSPG LCHCLRPGAPKCLKGLWFAFSVHPPWSS TPWLQSGRVNLPLAQDIFLL |
| 3242 | 11293 | A | 4188 | 200 | 390 | GPHAKSAFFPP*LSEQLGQG*QPGQTPVG RLALSVAFPPQGVGFPAAGGGTGEAFGG LACPLP |
| 3243 | 11294 | A | 4189 | 805 | 1030 | LVLCPHLSQLTKGTSHTCLTLQGGL*KL TRLALFRLGAVAHACNPSTLGGPRGPIT* CQEFKTRLANMVKPLLY |
| 3244 | 11295 | A | 419 | 1 | 2607 | MAFAWWPCLILALLSSLAASGFPRSPFR LLGVANGIEVYSTKINSKVTSRFAHNVV TMRAVNRADTAKEVSFDVELPKTAFITN FTLTIDGVTYPGNVKEKEVAKKQYEKA VSQKGTAGLVKASGRKLEKFTVSVNVA AGSKVTFELTYEELLKRHKGYEMYLK VQPKQLVKHFEIEVDIFEPQGISMLDAEA SFTINDLLGSALTCSFSGKKGHVSFKPSL DQQRSCPTCTDSSLNGDFTITYDVNRESP GNVQIVNGYFVHFFAPQGLPVVPKNVAF VIDISGSMAGRKLEQTKEALLRIEDMQE EDYLNILFSGDVSTWKEHLVQATPENL QEARTFVKSMEDKGMTNINDGLLRGIS MLNKAREEHRIPERSTSIVIMLTDGDANV GESRPEKIQENVRNAIGGKFLYNLFGF NNLNYNFLENMALENHGFARRIYEDSD ADLQLQGFYEEVANPLLTGVEMEYPEN AILDLTQNTYQHFDGSEIVVAGRLVDE DMNSFKADVKGHGATNDLTFTEEVDK EMEKALQERDYIFGN YIERLWAYLTIEQ LLEKRKNAHGEEKENLTARALDSLKY HFVTPLTSMVVTKPEDNERAIADKPG EASYQPPQNPYYYVDGDPHFIIQIPEKDD ALCFNIDEAPGTVLRLLIQDAVTGLTVNG QITGDKRGSPDSKTRKTYFGKLGIANAQ MDFQVEVTTEKITCGTGRASTFSWLDT VTVTQDGLSMMINRKNMVVSFGDGVT VVVLHQVWKKHPVHRDFLGFYVVDSDH RMSAQTHGLLGQFFQPFDFKVS DIRPGS DPTKPDATLVVKNHQLIVTRGSQKDYRK DASIGTKVVCWFVHNNGEGLIDGVHTD YIVPNLF |
| 3245 | 11296 | A | 4190 | 90 | 417 | LAL EILSYFYLLYLPVWHFGNSVVALSL KILNIIVYLFSSFKSLRNFSALVSIFVFCF SSFSACFSLNSKDF*NPDIKKPHVKNS RIYKTQYSKDHPQRENQFR |
| 3246 | 11297 | A | 4191 | 2 | 672 | GRVGFTPGSWEAFMVKNIVPKLGMCLG ELVINPHQQHMDAFYWVIDWEGMISVSS LVGLLEKHFFPKWLQVLCWSLNSPNYE EITKWYLGWKSMSFSDQVLAHPSVKDKL NEALDV MNRAVGSYVGAYMQPGAREV NIAYLTHERRKDFQYDAMHERRAGPQI GLLRSLGKNLKICAKKEPLEIYLWANLK EYYLAKTGQGPPPFLLTRAPEGLITAWA LWG |

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| 3247 | 11298 | A | 4192 | 1642 | 2785 | RMTSSCPMADRTCPLPFSHRLIWEVWMP FVRNIVTQWQPRNCDPMVDFLDSWVHII PVWILDNILDQLIFFPKLQKEVENWNPLTD TVPIHSWIHPWLPLMQARLEPLYSPIRSK LSSALQKWHPDSSAKLILQPWKDVFTP GSWEAFMVKNIVPKLGMCLGELVINPH QQHMDAFYWVIDWEGMISVSSLVGLLE KHFFPKWLQVLCSWLSNSPNYEEI/TPK WYLGWKSMSFSDQVLAHSIWSRDKFNE ALDIMNRAVSSTVGAYKQPGARENIAYL THTERRKDFQYEAMQERRRPENMAQRG IGVAASSVPMNFKDLIETKAEHNIVFM PVIGKRHEGKQLYTFGRIVYIDRGVVFV QGEKTWVPTSLQSLIDMAK |
| 3248 | 11299 | A | 4193 | 264 | 638 | PSRTRIKTKQMATSEILPSFVATMDASNF SFWQVLCSWLSNSPNYEEITKWYLGWK SMFSDQVLAHPSVKDKFNEALDIMNRA VSSNVGK*GFPFWMSWPQVSDPTHVND TESEFSGSCRQPKP |
| 3249 | 11300 | A | 4194 | 2413 | 2707 | EMHVY/WTERSGSRL*SEHFGPRWVDH */RQEFETQPGQYGDTPSLLHPLSTSCPS FLSLFSFLVTFSSSSFLSLFLIYLLSRHDF LACDCFPLFLD |
| 3250 | 11301 | A | 4195 | 835 | 1050 | GSR*HNLQIIGRPRRADHLRSGV*DQPGQ HGETPVSTRNTRISQAWWTPVIPATQE AEAGESLEPGRWRLW |
| 3251 | 11302 | A | 4196 | 2 | 112 | |
| 3252 | 11303 | A | 4197 | 36 | 172 | |
| 3253 | 11304 | C | 4198 | 1 | 1482 | MVTHACNPTTIGKLEPSYVIRKFLDAQRI HNLTAYLQTLHRQSLANADHTLLNC YTKLKDSSKLEEFIKKSESEVHFDVETA IKVLRQAGYYSHALYLAENHAHHEWYL KIQLEDIKNYQEALRYIGKLPFEQAESNM KRYGKILMHHIPEQTTQLLKGLCTDYRP SLEGRSDREAPGCRANSEEFIPFANNPRE LKAFLEHMSEVQPDSPQGIYDTLLELRL QNWAHEKDPQVKEKLHAEAISLLKSGRF CDVFDKALVLCQMHDQDGVLYLYEQG KLFQQIMHYHMOHEQYRQVISVCERHG EQDPSLWEQALSYFARKEEDCKEYVAA VLKHENKNLMPPLLVVQTLAHNSTATL SVIRDYLVQKLQKQSQQAQDELVRVRY REETTRIRQEIQELKARVKAMPPPGKVPR KENLWLQCEWGSCSFVCSTMEKFFEHV TQHLQQLHSGSEEEEEEEEDDPLENSV NKDIRNKSAILPSRSNC* |
| 3254 | 11305 | A | 4199 | 913 | 1299 | ELGIVGKHAPTGGAGYHFLGMAAEVL SKFTAVLEGAGTAPFATQHHRVVLADCF VFTETDCVLPHADKTTQDCRRNSVPGAT HSAPTDNRKWSGISGMTFRLWKSRLMQG PRSAWLC*ACSPHCFSLVW |
| 3255 | 11306 | A | 42 | 1 | 818 | MAGAEGAAGRQSELEPVVSLVDVLEED EELENEACAVLGGSDSEKCSYSQDKAK VNSGNKYNDNFFGLYCICKRYPDPPEDE VRELEVKPGVTKISTEDDGLVRNIDGIGD QEVIKPENGEHQDSTLKEDVPEQKDDV REVKVEQNSEPCAGSSSESDLTQVFKNE SLNAESKSGCKLQELKAKQLIKDTATY WPLNWRSLKCTCQDCMKMYGDLVDLF LTDEYDTVLAYENKGKIAQATDRSDPL MDTLSSMNRVQQVELIC/GIQ*FED |
| 3256 | 11307 | A | 420 | 1 | 1842 | |
| 3257 | 11308 | A | 4200 | 1 | 587 | GAEETWEPTDGGSGSAAQDGVQWCDLGS LQPLPPGLKPSSHLNLPSSGTAG*RPCAL PGKVPRKENLWLQCEWGSCSFVCSTME KFFEHV TQHLQQLHSGSEEEEEEEEDD PLEEEFSLWAGMWLLFSGQFCLTSSAM SYFHCYHTKLKQWGLQALQSQADLGPC IRGISRAGTSSLSLITSCVWGTTCGLD |

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| | | | | | | IPGISRAGTSSLISLTTCVWGTGTEILR |
| 3258 | 11309 | A | 4201 | 262 | 409 | RSGGRNISSRKSITAHRSISAPGSISAQGSI PALKSILAHGSIPSQG*DTPLGWDAPMG* DALEGWDAPLG*DASRG*DTPMGRDAL SG*YVPSPTPSSWANALPCHFLPQMFLPT NVMPNTPISAEINLCGRGAGWQEWMCPCG LLQAPVPNHIHSCSPTASRGLRGLSSQL PETAKAAW |
| 3259 | 11310 | A | 4202 | 729 | 922 | WFETIEATQLYFNELPDTHFCVLCFLLCH FYINVKAFCSCSCC*NTCSLIFRPTV YYALML |
| 3260 | 11311 | B | 4203 | 306 | 392 | LTSGTYPKSGKAVEEAQPNSPAEDVRD R* |
| 3261 | 11312 | A | 4204 | 965 | 1298 | GNLVTAFLVLCIPDESLYRSICFLLHHQ KLHISVPQSPRWGWTSLGLAGTPRCSP PTPPRLLLPQSPRPGATGKIPRPDRRT VRPLGHKEPRGT*GKSWPAVAQPPG |
| 3262 | 11313 | A | 4205 | 1 | 324 | |
| 3263 | 11314 | A | 4206 | 310 | 513 | |
| 3264 | 11315 | A | 4207 | 65 | 191 | QEISIMVGFKATDVPPTATVKFLGAGTA ACIADLITFPLDTAKVRLQVRG*SLGVLM VSTLFPPQRHRPLKGQCLEHRDDWRWE GQHAYPCSYVLAALQIGESQGPVRATA SAQYRGVMGTILTMVRTEGPRSLYNGL VAGLQRQMSFASVRIGLYDSVKQFYTK GSEREYGARV*AGNQHHGWVQGHRC PYCHCEVSWGWHSCLHRRSHHLSGYS |
| 3265 | 11316 | A | 4208 | 12 | 237 | NFKYILFKILHLGEKIYNVYTCFNNLFH CTTYILYNSTINQPKKITS*HLNKNLPCK KHSMDHYKVVFJKIFFK |
| 3266 | 11317 | A | 4209 | 361 | 444 | QRLKNNCVITCS*QRPRVFSSSPQGLAA CHYRGLRSPQSRGRCLSHFSCQGVHPR SCQRGSAWSPRTTGQRGPTVGTGRTRK RLNTAYLLGAASADILRPISTSR |
| 3267 | 11318 | A | 421 | 3 | 377 | |
| 3268 | 11319 | A | 4210 | 89 | 198 | APP*THKWKIPHTSCDRSLSTCWHTTV DSTSLREK |
| 3269 | 11320 | A | 4211 | 119 | 698 | PTLMLHYIPWGRGRLGGWGQCGQSHSA RCAGTGTCLPMGTLMMHMEASRQVWG GCILPLFPYFLPPQLPS*LGPSNIWVAKD GWLRLDLDPP*YEWTLGVNWPSGILAY WTVSAPSLGFGSPITDAALPCPYNLGGSS PHPRRGRSFQKTGLSLTEGNLFPFPIPT PYLPHFLHIRVWPANVEQMRCK |
| 3270 | 11321 | A | 4212 | 728 | 916 | FFFPI*SV*KVSAQG*SLWPGVAHIYHF SILGGQGGRIT*QGEFKTSLGNIVRPHLY KSGG |
| 3271 | 11322 | A | 4216 | 162 | 528 | LLPYGLDRGPYGGVWCGLPYP/SGTVST GPPQRTASPLPKQSS/GPQPPEFAACTGT DAI*DARDAGDAGEGGSS/GAEPASSPAG AAGGGCGLAARSQVPSEIRSGWLKGLP QLASSGALVICP |
| 3272 | 11323 | A | 4217 | 160 | 835 | GGCGRRTVLVKDYQFFAEGRLIQFRWE NAAARFSALAPDMQRQNFPPPPYGP GGGGWGTGSNFRGTPGGGGPRTALPSR RVRGVTRTRRTGPRS*ARNGSKSLSAK RRQLSRGARFGSPSPGGYPGSYSRSPAGS QQQFGLLPRAAADPPPRVLQGHLLHLD QGVLEKKECLMSWKINFKAFLKCLKIPW GWPRTQICSGYKPNNTAILKHSQAKKE DTFC |

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| 3273 | 11324 | A | 4219 | 198 | 392 | |
| 3274 | 11325 | A | 422 | 1 | 621 | MTKRCLDHGEWLPAGGGGHTEGTRC LHHAPVTWVGIEVDIFEPQGISMILDAEAS FITNDLLGSALTKSFSGKKPVWLRGRHT PKGNLDSEVLAGLSPCPIPLAGLTVNGQI TGDKRGSPPDSKTRKTYFGKLGIANAQM DFQVEVTTEKITLGTGRASTFSWLDTVT VTQDG*APLQGLQGGGLQGEGDHSGPQP NPGALSEPELV |
| 3275 | 11326 | A | 4220 | 318 | 718 | YHHLQGRDIPGNLRVEGSPVHPAVRPRF SASCSQPPFPPLSPHLRARARPRWERQK FTPSLDGSFWGETPAGGCGSHHPWQGP RALFRRRSQ*PRR*AHMEGRVGRSPLL HPPWEKTPS*LSGLTDRKQA |
| 3276 | 11327 | A | 4221 | 1 | 563 | ETFSHFERYLQFKAEPPLTSRGFVEKS TALHRISAEHPESMMSEVHERALQQHPQ AQGGELLETRKMHADNNFTKTQDRLHA SSDAFSGLRFGSGTSRGYQRQMVPREI KSTSASSSVVSADTAPNFSRLLSNVTV MEGSPVLEVEVTGFPEPTLTWWVAYN DKP*METNSITEKNHSVSTN |
| 3277 | 11328 | A | 4222 | 366 | 622 | LSTMLHQHLLSVLLKLSQSLYVVVSFFLI QSTLQSGTRVTFLKRLQAGAVAQACN ASTLEG*GGWIARAQEFETNLGNRARPC L |
| 3278 | 11329 | A | 4223 | 43 | 245 | |
| 3279 | 11330 | A | 4224 | 634 | 1316 | GSGPHSPGKWMVDDSDREHSRDVRSGR LTLMVTECLSLQEFNSMDLWDFHKYMR SHKAESSELVRNSHTCLYQGEGAHHIM RAIRQRVLRRLTRLSPEIVELIEPLQVVRYG EGGHYHAHVDSGPVYP*TICSHTKLVAN ESVPFETSCRYMTVLFYLNNTGGGETV FPVADNITYDEMSLIQDDVDLRDTRHC DKGNLRVKPQQTSSLLVPTCLMGKV GWVT |
| 3280 | 11331 | A | 4225 | 506 | 708 | FLMRSEFL*KVFFHP*HS*GFPCVCSLMS CVG*LLGEGFSTFTFIRFFPWCSPDDSD GFEIFPLIS |
| 3281 | 11332 | A | 4226 | 1 | 1662 | MIISIDA EKAFDEIQQC FMLKTLNKL GID GTYLKIIRAIYDKPTANIILNGQKLEAFPL KISTRQGCPLSPLLNFIVLEVLARAIQEK EIKCIQLGKEEVKLSLFADDMIVYPENPI VAAQNLKLISNFSKVSGYKINVQKSQAF LYNNRQTESQIMSELPFTIASKRTKYLGI QLTRDVKDLFKENYKPLLSEIKQDTNKW KNIPCSWVGRINIMKMAILPKGIASFTGY CIPKPEVILKLETGKEPWILEEKFRSQSHL EEPSEYNNNGNSFWLNEDLIWHQKIKN WEQPFEYNECGKAFPENSLFLVHKRAYT GQKTCKYTEHGKTCYMSFFITHQQTHTPR ENHYECNECGESIFEESILFEHQNVYPFS QNLNPTLIQRTHSISNIEYNECGTFFS*D RVSLCLPG*STVARSQLSAASISQVKRSS H/CLCLLSTSDYRCMPCLANLCIFCRDN CAMLPRLVNS*AQNLKLISNFSKVSGY KINVQKSQAFLYNNRQTESQIMSELPFTI ASKRTKYLGIQLTRDVKDLFKENYKPLL SEIKQDTNKWKNIPCSWVGRINIMKMAI LPKGIASFTGYCIPKPEVILKLETGKEPWI LEEKFRSQSHLEEPSEYNNNGNSFWLNE DLIWHQKIKNWEQPFEYNECGKAFPENSL FLVHKRAYTGQKTCKYTEHGKTCYMS FFITHQQTHTPRENHYECNECGESIFEESIL FEHQNVYPFSQNLNPTLIQRTHSISNIEY NECGTFFSEKLALHLQQRTHPGEKPYEC HECGKTFTQNFTEHLRRHTGEKPGCNE CGKTFHQKLALIVHQRTHTIRQKPYGCNE CGKSFCVKSKLIAHHRTYTGEKPYECNS GGVRPALWDERSCGYVSAGTKRAEGEV |

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| | | | | | | WKQGGEEMGSIVERLVTLSK |
| 3282 | 11333 | C | 4227 | 472 | 681 | MNHKIYVYGHTQQFLYCSYVFKRYEFY SNPTLQGFLCSPHSYFYKYLLLTGRNLAI IILNIFAWYQSL* |
| 3283 | 11334 | A | 4228 | 2 | 277 | RAEIPTAGEVWDGAGPMGAELKPWARQ RKVEMDHVGPLLSPPGRS*SPGPGRGR SRWTMLGPFSPRPQAAVRGPRPGVLGSP REALEPPGARHPRAVTAAPRELQCGGST VRAVAR |
| 3284 | 11335 | A | 4229 | 1 | 240 | ALLGWVFNLYKEITTTTSPFRRRSYILGF VKLYVSEHFHFFFWVLYYFL*MHCEKFY FRRCNAGRRSQIMYIVFLKSLSS |
| 3285 | 11336 | A | 423 | 3 | 2722 | FSDGLCMVALSHLGSALQLGSLCFPRSPF RLLGKRLPEGVANGIEVYSTKINSKVTS RFAHNVVTMRVNRADTAKEVSFDVEL PKTAFITNFTLTIDGVTYPGNVKEKEVAK KQYEKAVSQGKTAGLVKASGRKLEKFT VSVNVAAGSKVTFELTYEELLKRHKGK YEMYLKVQPKQLVKHFEIEVDIFEPQGIS MLDAEASFITNDLLGSALTCSFGKKGH VSFKPSLDQQRSCPTCTDSLLNGDFTITY DVNRESPGNVQIVNGYFVHFFAPQGLPV VPKNVAFVIDISGSMAGRKLEQTKEALL RILEDMEEDYLNILFSGDVSTWKEHL VQATPENLQEARTFVKSMEDKGMTNIN DGLLRGISMLNKAREEHRIPERSTSVIM LTDGDANVGESRPEKIQENVRNAIGGKF PLYNLGFGNNLNYNLFLENMALENHGFA RRIYEDSDADLQLQGFYEEVANPLLTGV EMEYPENAILDLTQNTYQHFDGSEIVV AGRLVDEDMNSFKADVKGHGATNDLTF TEEVDMEKEMEKALQERDYIFGNIERL WAYLTIEQLLEKRKNAHGEEKENLTAR ALDLSLKYHFVTPLTSMVVTKPEDNEDE RAIADKPGEDAEATPVSPAMSYLTSYQP PQNPYYYVDGDPH/FSIIQIPEKDDALCFN IDEAPGTVLRLIQDAVTGLTVNGQITGD KRGSPDSKTRKTYFGKTGASPMQMGF PGWEVTTTEKITLLEQARCAFFSWLDTV TVTQDGHFLASSRRLSMMINRKNMVS FGDGVTFVVVLHQ/VCWKKHPVPTVDF LGFYVVDSHRMSAQTHGLLGQFFQPFDF |

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| | | | | | | KVSDIRPGSDPTKPDATLVVKNHQLIVT RGSQKDYRKDASIGTKVVCWFVHNNGE GLIDGVHTDYIVPNLF |
| 3286 | 11337 | A | 4230 | 1508 | 1686 | IFFQPKECLYKNL*GLGAVAHACNPSTL GG*GGWIS*VQEFETSLGNMAKPRLYKK YKN |
| 3287 | 11338 | A | 4231 | 596 | 729 | YFPNKHGILCRVQWLSL*YQPPLWESEV GVLELKSVRTAWATW |
| 3288 | 11339 | A | 4232 | 1212 | 1344 | ATCLSLEKIQKLLIQNPGR*ASCDSSLL GCSPDLSSHFTVL |
| 3289 | 11340 | A | 4233 | 2 | 114 | |
| 3290 | 11341 | A | 4234 | 1 | 326 | |
| 3291 | 11342 | A | 4235 | 37 | 199 | |
| 3292 | 11343 | A | 4236 | 3 | 263 | |
| 3293 | 11344 | A | 4237 | 164 | 298 | |
| 3294 | 11345 | A | 4238 | 60 | 152 | |
| 3295 | 11346 | C | 4239 | 512 | 805 | MSSLPLMITDTQQAVSSGLWIGIPNYRVF TPTGTWVRXPHATESLHKFNLNRTWEM GLQRRVXTXGTNVKALESAQQPWNQ AGRGDNFLLWRKGGD* |
| 3296 | 11347 | A | 424 | 1168 | 1627 | RAGRGGEHKLNSYGGRRARSQGHLLS SALSPFVSAASYQPPQNPYYYVDGDPHFI IQIPEKDDALCFNIDEAPGTGLRLIQDAV TGLTVNGQITGDKRGSPDSKTRKTYFG KLGIANAQMDQFQVEVTTEKITCGTGRA\ |
| 3297 | 11348 | A | 4240 | 1 | 361 | STFSWLDTVTVT EPRMLYTRYVSDPEFVISRVDDFVVLQL FRMSSLPLMITDTQQAVSSGLWIGIQIS LTQPGSTIS*YCSFFKSVIICHLMIT*YTTS SFFRPCGLASQIPESYPAGTWVRAPHAM EKLT |
| 3298 | 11349 | A | 4241 | 545 | 865 | PNNKHPYKSVTILSLCAVLFSLYIFNSGH FYFTSSIQFRHLNPKFNNLFYQTFVLRK FL*II*QIKAEPLIVEHK*KIYKPYLFNT QVLALKLKR*GFLYIIS |
| 3299 | 11350 | C | 4242 | 47 | 319 | MVFHKARTRMKERTDTAMQAESASETN KRAHPALPPVLPXGRWARRGQEAPRP HLLSPQSGQGGQAPPWRERGVTRLKLG EGCRGRLAP* |

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| 3300 | 11351 | A | 4243 | 211 | 472 | STLGGSLCAQSGCSFEPLPLRGHPAMPV KCAQPLFSSPCPPCLPRAAREGEQGEHA CWFQMHFLLALPYLCVPSSWSWLYGTP CF |
| 3301 | 11352 | B | 4244 | 1 | 1023 | MCWAPSTRGGSPALHPLLLLPHPLPAR CTGFRAPAVPSSPAGIFGHIAVIGSPFPTA GGNTSDSFSNGCSQDVGSRLCGCGLLG VGIWLSVSQGNFATFSPSPSLSAANLVI AIGTIVMVTGFLGCLGAIKENKCLLSFFI SPVAELILLILFFVYMDKVNENAKKDLK EGLLLYHTENNVLKNAWNIQAEMRC CGVTDYTDWLPSAGGEHGSRLHGHRT PRAAGATAPRLCGERAAMKRSWGMAFS MTLFQHIHRTGGNHVHLGPKIFASFGA TDISSGLGGDYIICDPKEKKYRKPKREPH LQ* |
| 3302 | 11353 | A | 4245 | 630 | 841 | DTGPCWRERGVTRLKLGEGRGLAP* HLLPPPKSSSQCAPLTPTAGWLPEEKAE VCSGCPPCSPSYKP |
| 3303 | 11354 | A | 4246 | 29 | 360 | HSLISQREKESERERARESERE**RASERE RERGRDKIPTRKGGEVQFLQTIHFFFLIF LTAFQEYFKERGSYYRYRGKAKKGG RGEEKNSRSRNPSSFTGRKKRV |
| 3304 | 11355 | A | 4247 | 253 | 451 | NWSAGAALLSAAPAHTPSPHQARPTPGS PPSAALWGSPSPSRSPPHFSPTDL*MRPE RHPSSAPP |
| 3305 | 11356 | A | 4248 | 355 | 500 | ARCGGMHLYSQIFGRRLWEHCLR*KVLS QVWWHAPVFADIWEVEVGALLEARSLR L*CAMLLPVNSHGPTWAMQ |
| 3306 | 11357 | C | 4249 | 175 | 387 | |
| 3307 | 11358 | A | 425 | 87 | 508 | MGCFIREGGEEGNLIKKRFVSEALADV RRKRRQEEWENVRKPEDPEECPEEVYDP RSLYERLQEQQDRKQQLRGTVSNCKN MVRGLDEDETNFLDEVSRQQELIEMHR IEEELIELNEYRIALWNVGISYENYEGRG |
| 3308 | 11359 | A | 4250 | 342 | 608 | AGSGTIGMLRPADERGGQSRGRSAHPI SQAAPCPAFLNRPFTGPS/CGPSVTSLRNT AGFCPEIGPGCPPSLAEASCLPSCRAGS HWA |
| 3309 | 11360 | A | 4251 | 56 | 277 | TVSVQRHQAVQSPVVVFTEHIPQDAWCS PSCAPGPN*PPLCPTNKPCALQQGMKPL ALKKSLGGTVCCGSKRD |
| 3310 | 11361 | A | 4252 | 235 | 721 | DLADCSLQLQSRSSWKKCSTMLQKVLV PPEAATSLSHPTPRPLPHPPALGSPLQPPS NTFGP*CCLSQDAPVFPSPVKLHLVTVPA SSLANESRKGPSRVFSRTPAPSSSITSIS DSGIQNATVWSGVRLSVSASSFGLTSPF SASGVSLSVSPLASTL |
| 3311 | 11362 | A | 4253 | 1866 | 2283 | IRILYRSPHLQLPCLTRFLVKKSYSVTGN WMVSLKD*SLRLDCWHGPLNLVKLDEV WQNLGTSTKSL*NNFKNILGKINTFKTL FGGGMKLPCKVSFSIYLMVNLESHDST WHLQANQTPHFDVSPVLVLEFPKF |
| 3312 | 11363 | A | 4254 | 2 | 767 | ELLFDKSTMRRPFGQKASSLPPIVGSRS KSGNDRHSKSTVGSSDNSSPQLKRRKG KKEDVNSEKLTCLKQNVKLKNSQETIPN SDEGIFKAGAERSETRGAAEVQEDEDTQ VEVPVDQRP AEIVDEEEDGEKANKDAEQ KEDFSGMNGDL*EEGGREATDAPEQVEE ILDHSEQQARPARVNGGTDEENGEELQQ VNNELQLVLDKERKSQAGSGQDEADV DPQRPPRPEVKITSPEENENNQQNKDYA AVA |

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| 3313 | 11364 | A | 4255 | 79 | 928 | TWQRCNLNCLHIPVLCSLSSSTMWDVLL PLDRGDLHLSCIDSSNWALFRCQSKVVL YHCVEADSKGLRSVLDLTLNKTNLELK MESQTEKLNLYLRNNHEEAGTTQNEFKV SVCQYLSRYGGGGYHYKRQSFHKTQSK ELMGRHRLLLTIANRHEIAELRWTLQTL ELELQAQWPLVRMLQQ*EP*ERLTC*R* RENQEPVQVVEEQPRANTKETRKKSSF SQPMSASTKEESQDGRRK*GK*LGKGRARE GKMLHQKSLGFKYFEGRGAGPTPSGPT VTQLK |
| 3314 | 11365 | A | 4256 | 235 | 674 | SGKQNNPQATAKAEACTETRSQMGATE TSSTFDYLGATSLKSPPHRKVVFFCFTIET SLHSNSL*ILLPLHSISNIQKQTQTSNLNIN LQPATAGPPSQAPPTALSELPGGRSAPEP SHAAFPARVPPSSGSPRPNARWAARA A |
| 3315 | 11366 | A | 4257 | 60 | 471 | CLGSLQPPPTRVKQFSYLCPLISFFFFLFF FGLFLRFSLCHRF*AV*L*CSLVLFSSCFL CLGFAMVFGSVGL*FSSSLECFQALFLQT FLLSFPLFFMNSN*PCIRLTEVVPRLSDAL FIFKNSFSCCADAWADAW |
| 3316 | 11367 | A | 4258 | 392 | 517 | MTLKDVVAHACNPNTSGGRGGWIT*GQ FKISLANMAKPRLY |
| 3317 | 11368 | A | 4259 | 446 | 767 | IWYKSTHSSVIFKCEFFLOFLSQSLALSPR HECSGAIMAHCSPLLGSSDLPASFLNFS WR*CLHYVAQPGLELLGLK*SIPPWASE SAGITGLSHHAWPKYELLLF |
| 3318 | 11369 | A | 426 | 90 | 549 | QGASQTRSETSCGLIAR*TFLGLFVRIE RIDGNLKMMLHIVEPYVTWGFNPKSVRE LILKRGQAKVKNKTIPLTDNTVIEEHLGK FGICLEDLIHEIAFPKGKHFQEISWFLRPF HLSVAHHATKNRVGFLKEMGTPGYRGE RINQLIRQLN |
| 3319 | 11370 | A | 4260 | 119 | 342 | ISICIKININIIYACYVYIILCIRIYLSKYILL ENCI*CTILFYVIFYVYIYLHIIYILLRLCPF FIYSWSPV |
| 3320 | 11371 | A | 4261 | 374 | 471 | GKK*KCPTHLSHLYINPGEKSYLFETSGL NF |
| 3321 | 11372 | A | 4262 | 255 | 496 | LYKFQTSVPLT*FIKALYITFYNSR*RG YYSKFKT*S*RPGMVAHACNPSTLGGRG GRIT*SQEFETSLANVAKPHVY |
| 3322 | 11373 | A | 4263 | 231 | 417 | CELPVTRHGAGCVCSSDTVLP*PCPFSPV SQSPSVCLSPLFSDPCEPPYPVLESPLDC SF |
| 3323 | 11374 | A | 4264 | 1204 | 1398 | ASFLAISMVVRVGVPFYHLFFLRQSLIL SPRLVGVR*CDRG*LQPLPGYK*FSCLG LPSSWDF |
| 3324 | 11375 | A | 4265 | 581 | 705 | LLAECGAHACIPSTLGDQGRQIT*GQEFE TSLANVVKPLY |
| 3325 | 11376 | A | 4266 | 3840 | 4074 | AQEYRGQLRQYSETMSLQKKFKNRSAG CGATCL*SQLLRRLGWEDHLSPPGGRGCS EP*SHHCSPA WVTQDLSPCHP |
| 3326 | 11377 | A | 4267 | 173 | 421 | |
| 3327 | 11378 | A | 4268 | 423 | 595 | SCLSNFHLGQAQWLMVPVIALWEAKVG RSP*VRMVSIS*FRDLPASASQSAFNISH |

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| 3328 | 11379 | B | 4269 | 1 | 1224 | MPTVGKAQARRRTRDTLLDITQVLIDQ SPRKDTGLAQQTGIVVPSKGIVKYWRAQ LKGDMMKYASPAFELFYFSVRAQSTDGIV TLLDPTTREDCDISSAPNPEVRTQRAEV AGVGLLAVKVRDEEGLGGAPGPQKR SRVCGEPTLQRRSGPLPVARPGSRCPPT SVSSPVEDEYGRTVVMIRLDNPGISGRT IENNPPELEKQLPGEPSENSPYLGPPQVLF LLRDPREDVMLLNQPTTTAEKQAVLQ AAEIFRNEQQISYNTSKGKKGDRECEEIA ETPFQIGSEAVPLDNPDWNSSSSAGEWK RRHFLICILEGLERTKAKFLNCSKLSMVD QKPDENPAAFMERLREALIEQTSLSPDV EKQLILKDKFVTQSASNIRRLKQKAIGP ISTLKNLLK* |
| 3329 | 11380 | A | 427 | 215 | 870 | RAPPNGLTQQKKGKGLRFRKLESFLHD SWRQKRDKVRLRRLEVKPHALELPDKH SLAFVVRIERIDGVSLVQRTIARLRLKKI FSGVFVKVTPHNLKMLRIVEPYVTWGF NLKSVRELILKRGQAKVKNKTIPLTRH/S Q*WRSTWGKFGVICLEDLIEIAFPKHF QEISWFLCPFHRLSGPSCYQK*SGLPQGD GHTWAIGVNASQLIRQLN |
| 3330 | 11381 | A | 4270 | 1016 | 1393 | IFQLGEYIFLFLSVFEMESHVSTQAGVQ WCNLSLQPLPRFK*FSCSLPSSWDYR QMPPLANFCIFSRDGVSPCWPGWSQTP DLKRSAGLGLPKCWDYRRETTAPSMFL QNLLALVPMQQR |
| 3331 | 11382 | A | 4271 | 825 | 1246 | RAEGFCPNWCCQSNILIPCHDPGSRSAQS DWACHLGWQSGSGQNHGVPAPFGDAL QLPGNTSRVGAPOGGSGRGRKDGPGNS H*AHGTGWRECYGDRSRKRNQFWHL APPRSEIFLILACTLRNNGSASCPRSCFDS SFLRVPRTRGRFWGSTWGVTPGI |
| 3332 | 11383 | C | 4272 | 442 | 522 | MRCASPSTSKEFSCALLQCWLDLQ* |
| 3333 | 11384 | A | 4273 | 322 | 1025 | PLLCVLLAPPEGAVGDICKEDAGNMPS TSEGSYLEMAHFLRNKLAGSSVRKPDS GFLWEGALRAWNMAAPSGGVNCEEFA EFQELLKVMRPIDDRIVHELNTTVPFSP AGKIDASQTKQLYESLMAAHASRDRV QKNCIAQTSVAVKNLREEREKNLDDTL LKPT*EKSQRS*KWVQSELNVVEVVNDR SWKVFNERCPNSLQASKE*IKRDSFFFF FLRTGSSHKS |
| 3334 | 11385 | A | 4274 | 22 | 54 | |
| 3335 | 11386 | A | 4275 | 506 | 622 | TRDSAHAYNPSTLGG*GGRIA*VQEFKT TRAHSYTLIPT |
| 3336 | 11387 | A | 4276 | 296 | 495 | KHVRPYITHSLGGKKDFLILEKIWLGIVA HACNPSTFRGQGGRTA*A*EFKTS LGNIV RPLYLKT |
| 3337 | 11388 | A | 4277 | 270 | 558 | FWIFLRSFYVIRKHLIGHFHPWPRVLKC* KHGGWKVHGGPGQ*ROKGTGKEGRKG LRGRRELTEGARPLFSSGPVESTQIVPLP QPPYVGAAAS |
| 3338 | 11389 | A | 4278 | 51 | 113 | |
| 3339 | 11390 | A | 4279 | 179 | 387 | ILVGFCCLFPPPSNK**THHTHTHTHPH THPVVTNRISLQICRKKGKQKTSQGPTA TSLSPLSDSAV |
| 3340 | 11391 | A | 428 | 476 | 821 | TFTWPLFVRIDERIDGVSTWCREPLQDFA LRKIFSGVFCKGTPQDSKMLRIVEPYVT WGFPNLKSVRELILKRGQAKVKNKTIPL TDNTVIEHLGECYSLGVSWGRKPGSLK L |
| 3341 | 11392 | A | 4280 | 464 | 596 | EFSPGMGAYTRSPSTLEGHSGQIT*AQEL ETSLANRVRPCSYMW |
| 3342 | 11393 | A | 4281 | 468 | 564 | YAFYRTQVPGGIRLV*CRLRVLWSNLIK KQS |
| 3343 | 11394 | A | 4282 | 780 | 837 | |

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| 3344 | 11395 | A | 4283 | 993 | 1050 | |
| 3345 | 11396 | A | 4284 | 175 | 387 | HFGEAEAGWITRSGDRDHPG*NDETPSL LKIQNISRAWWQAPVVSATPEAEAGEW HEPQEARACSEAEFEP |
| 3346 | 11397 | A | 4285 | 161 | 409 | PPGVIIYFLVKVRLIWGNVMTV*VYMTL LSFPYPQICIYTYIKYVYILPI*NIYIYTHIC IYIPLFLCLLILAIKEGAAFNV |
| 3347 | 11398 | A | 4286 | 1910 | 2120 | SVSGFWLEAMLPSLSEGGPCRLQPFIGN KSLTGWVAHACNPSTLGG*GKWIT*AHE FQTS LANMMKPCLY |
| 3348 | 11399 | A | 4287 | 1156 | 1320 | KNSS*FFYFLSYLKNKNRPGAVAHTFNP NTLGGGWIT*YQEFETSLANIGKPCLY |
| 3349 | 11400 | A | 4288 | 1497 | 1767 | PSASPPQVPIPALPQWTGPGRQNPL*CLH IGLCSPQPSDGPWRKACSLFQVPSHQCG RIRKKINKVHICVFTASRVRWKPKPAAA NDQL |
| 3350 | 11401 | C | 4289 | 1434 | 1655 | MKKFSHILKKKFFCTLVPIIMKLMLNKL SQCKTKEGKYCTLAENLFHHKIHCFPS DHRSHFSLELAVVKKL* |
| 3351 | 11402 | A | 429 | 33 | 370 | ATRSRLGKHTRRSKSSAIQAVRIISQVLR CKQRCMHCPRTIPATLQEHKSVNNPSAQ QRTKTWSIHTPAPHPHPAPHPSTHQ/HPH PST/PAPHPSTHQHLIHPHTSISSIRTRG |
| 3352 | 11403 | A | 4290 | 275 | 485 | TNWKLSLCEKLYSTHFCTDHKAVLFP*C LSCFVLLCVLFICVLFVGFRLSFCFVFTT SVISTSFFLAVS |
| 3353 | 11404 | A | 4291 | 889 | 1199 | KKCVCVCVCVKVC*LLKMLVGNFRA LWGSEWFLHHHLSSTNRKMLSLQGHV |
| 3354 | 11405 | A | 4292 | 502 | 768 | SPCDQTPVEEGMLPKFRKSLQGFSLNFH DILILPSQK*FCIRGSKTMYIWPGTVSHTC NPSTLGGQGGWIT*DQEFETSLANKVKP RLY |
| 3355 | 11406 | A | 4293 | 3 | 309 | IFGRDGFHHVGQAGLD*TPDLK*STHLG LPKCWDYRHEPPCLARRYFKNNKKDN LLSHHTKTTVNILPIFSSCTDVFLHNHD VECNVFSLDLVNIFQSC |
| 3356 | 11407 | A | 4294 | 204 | 317 | |
| 3357 | 11408 | A | 4295 | 1905 | 2032 | VKHLDTGTQK*GCNAFNVGQSGPGPDAA PRWASRTPGGVNAGI |
| 3358 | 11409 | A | 4296 | 2 | 225 | KWQVTWLSFCSTFMSPPSSWSSCS/PPCSA QPYAPVSCDGPFRFPPELLD*GRLKTY FPPPCVNWGCWGQCVISQ |
| 3359 | 11410 | A | 4297 | 299 | 663 | IAHITEIRNLILHSLNNPLWLEPTRIEKFSP RGKVTSLHPRVKMSPSSPKNSHPPEEV GSASSFLREPSPGGSQHSPPAPSIDAM VPPYRV*TPFGIKEDLTKPLFWGITFLL PCV |
| 3360 | 11411 | A | 4298 | 1 | 406 | MDWEGSLPLVFNYCRDASLIHPRFKGV RPRRDACLGPSPLAASPAFLGKGQTITDA ELRVTLTVEDSARLHPGEINSHVAHTKP VWWSLHTDARETTHLQRTHFQQSWLV/ CIRP/MNPAKSTVSSVRTQT*APLP |
| 3361 | 11412 | A | 4299 | 236 | 768 | VPCRESPRALALPRKEMMRA*NQNKTK HDSRHCRISPVGNMDIAENNYNSFKAEL GPNSSASTPPYNLFASPPHTCSGLQFH STITDAELRVTLVEGNRMSVVRSSFLGL NQLKLAKSMMAAYSIFEELASLYSNFH TK |
| 3362 | 11413 | A | 43 | 46 | 511 | QLRMAGAEGAAGRQSELEPVVSLVDVL EEDEELENEACAVLGGSE/SEKCSYSQGS VKRQALYACSTCTPEGEPAICLACSY ECHGSHKLFELYTKRIFRCDCGNSKF*N FGMQLLP*QSK/DVNSGNKYNDNFFGLY CICKRPYPDPEDIPDE |
| 3363 | 11414 | A | 430 | 42 | 334 | |

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| 3364 | 11415 | A | 4300 | 302 | 897 | SVAKEGVEVEVSHTCGLKWGDIRGGCE GGFGLGEKAAMRCGCSPGIVREADNLV KVSPPSVLIKKGTDLPTVTRRSASV MVLTMPLAPATFLRGNCWAGGGGLVTE *NCKPDQV*GGEMIKGL*GGG/VRGCGRI ET*LGLARRSLGRRGEVRLVWRS GTLLP KYCAFPPTVFTTARPGDPLCLAQWVPCP WSLAHC |
| 3365 | 11416 | A | 4301 | 111 | 275 | SRNETESRTRCEEGR**KDYRVEEQRLR KNWDLARPGKEQLPAFQSGNLSRQLH |
| 3366 | 11417 | A | 4302 | 3 | 220 | SLQPLSREDLGRSQSESLGPEFQGLWEW LPGELNSPICSGVPHRWDA*EESWAAG SPWPGGQISGTCSKLL |
| 3367 | 11418 | A | 4303 | 2 | 347 | LTMPLAPATFLRGNCWAGGGGLVTE*N CKPDQV*GGEMIKGL*GGG/VRGCGRIET *LGLARRSLGRRGEVRLVWRS GTLLPKY CAFPPTVFTTARPGDPLCLAQWVPCPWS LAHC |
| 3368 | 11419 | A | 4304 | 2 | 265 | |
| 3369 | 11420 | A | 4305 | 3 | 865 | |
| 3370 | 11421 | A | 4306 | 288 | 597 | TDFSVRCKGCRTPGFLRLIFQDRIVGVEL IAV/C*RHGPRFSSCRLSCRRPFDKTCRL MCHQRLSGFPQEQTQDRSRCIQLLRQR FAAASCPTHQVLLQTQYF |
| 3371 | 11422 | A | 4307 | 3 | 188 | KPRRSRSSESLGPEFQGLWECLPGELNSPI SSGVPQRWDTA*EESWAAGIPWPGGQID FWHL |
| 3372 | 11423 | A | 4308 | 498 | 803 | HLGPEFQGLWEWLPGELNSPISSGVRHR WDVA*EESWAAGIPWPGGQISGTCSKLL EEVLEEGLA AAVQAFGSSCVLEMWLG FVSQWRQGIATFFYYCTP |
| 3373 | 11424 | A | 4309 | 3 | 338 | KPRRSKGESESLGPEFQGLWEWLPGELD SPISSGVPHRWDA*EESWAAGIPWPGG QISGTCSKLLGEEVLEEHLAAAVQAFGSS CVLEMWLG FVSQWRQGTATFFYYCTP |
| 3374 | 11425 | A | 431 | 55 | 1078 | SERRRGPLCLPSDSVLDCSGPPMYCGIAE PSLRRWDPQRSFLESASCRLGCLAIPRH PNFPRPIASSILQIKMATAAAAAVMA PPGCPGSCPNFAVVCFLERYGPLLDLPE LPFPELERV LQAPPDVGNGEVPKELVEL HLKLMRKIGKSVTADRWEKYLIKICQEF NSTWAWEMEKKGYLEMSVECKLALLK YLACECQFDDNLKFKNIINEEDATMRLQ PIGRDKDGLMYWYQLDQDHNVRMYIEE QDDQDGSSWK CIVRNRNELAETLALLK AQIDPVLLKNSSQD NSSRESPLEDEET KKEETPKQEEQKESEKMKSEEQPM DLE NRS |
| 3375 | 11426 | C | 4310 | 321 | 734 | MIKHQGKAAPVDRRQSFVSTDKTCLL CLSQKMKGIEIKRRERLKSGKEKVWLRD RERLEKRTILRASVFKGEKPAAGERGKV WSCDSIHVLQEKGSRPQISVLCILNRKY SPRFSVWSLKPPSMKLEVRKQCR* |
| 3376 | 11427 | A | 4311 | 867 | 1111 | RHCRYGTR/ARCRSANAGAMILTMKQL AIVMRVYQHQRVRRSMRPNRGARSGMS AVGAYYSSCIRVMTALQSCTGDDEAVL L |
| 3377 | 11428 | A | 4312 | 1 | 560 | |
| 3378 | 11429 | A | 4313 | 2 | 268 | |
| 3379 | 11430 | A | 4314 | 11 | 783 | NLFLRPQKDQTYWYHRIQLGQTKHLLKEL KVYTYLLYATISF*DV*RHC/RSAILAEAK ETKETHFIRGPKTAPVTDWEGSLPLVFN QCRDASLIHPRFKGFRPRRDACLGPSPL AASPAFLGKGQRLKTD TARLPWKPPDH HRRRASGNHSGRVQPPSRLPWAHVEC LRLFQEHGASCQWIYRSGIWRVVFMC VRVKRPPNRLCVSNMAVYFTWVQVHYP LYENNKTLRALRMHVESLACGVRESS |

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| | | | | | | TNDNYY |
| 3380 | 11431 | A | 4315 | 177 | 434 | LCLWLQPPF*E*IAGQVGEG*SRNETVSR TQCEEGR**KDYRVEEQRLRKNWDLAR PGEEQLVPSSEKRDPLRVKDQGRCPV V |
| 3381 | 11432 | A | 4316 | 1332 | 1602 | |
| 3382 | 11433 | A | 4317 | 797 | 954 | |
| 3383 | 11434 | A | 4318 | 1 | 817 | |
| 3384 | 11435 | A | 4319 | 3 | 93 | LSPS*AIISVPCTYTPRWPEATEDPQKK |
| 3385 | 11436 | A | 432 | 1 | 568 | |
| 3386 | 11437 | A | 4320 | 874 | 1114 | ESLGAQAEDYCRSGALTESLY*SSSKRK CGVGVPKQSLLYSTV*WSCGRGSLSRFP QNDRASSFQPQYEKSTEAKLPKGL |
| 3387 | 11438 | A | 4321 | 264 | 1259 | GDRWEGKKEDLGRVALGTETRKGLMC KRMPGH/AGTSDHLSILGQELFRSCRM KLK/RAI/CPAIWNYCRVCIGVKRHCRRK *DA*ILQDLNNSCPKIDKWSEVPDVQAFF YTSVPS |
| 3388 | 11439 | A | 4322 | 607 | 769 | SQVLRPTQPKEHLANFKSEDRSVRPLSPS *AIKSPVTCTCTSR*PEATEDPQKK |
| 3389 | 11440 | A | 4323 | 495 | 658 | GLTGTTWAHAFTHWLVVLSHSTELSGC ERLCGPAELGTFTLWLF*RKPFADHWP |
| 3390 | 11441 | C | 4324 | 218 | 352 | |
| 3391 | 11442 | A | 4325 | 444 | 994 | PMTHPFFFFPAEVHEPNQRQAFLVPVSQ ARWTASSLFSSWVSASTSPQLEELQGST QTWHFSATCSQQPSRCVETVDPSSLLTQ QGLAFSAPTGRQAQRCSARMAWNPDP LPPPSVHPCTPHCP*GPPQPPSASTPWG SCCSRWGHQAILGCRDRERCRCGTSSRP WLPLCLLPRFPDKWS |
| 3392 | 11443 | C | 4326 | 296 | 625 | MVSEGHTSPLAKSSASELHRTSWSTDNG MDFWRECQFRAKEIQGENEALNKSSKR AQKLVSIDLNMERQVRRKYTVNAGSLH FILSLLSSIHLLKTAFCVLLQGNLYTL* |
| 3393 | 11444 | A | 4327 | 221 | 344 | KVLSSDFCSVPFCVCVCVCVCVCVCVCV LTLL*NSSIIYGH |
| 3394 | 11445 | A | 4328 | 441 | 656 | AHNYIYFQRYIHIQTYTDTGRGMRIGMR DQKKRPGTVAHTCNPSTMGG*CRKTSQ GQEFKTRLSNTVRPNL |
| 3395 | 11446 | A | 4329 | 409 | 749 | RRGRERKRHTHIHTHTANLFVSVFLY FLSLLHLCALCLS*WM*RCSANPILPTGP YASQTFMILPSCCTTVISLPCHWLLFPQYS QTLYSLFTELNGQITVTSAKITYTSKI |
| 3396 | 11447 | A | 433 | 1 | 572 | ANNSPALTGNSQPQHAAAAAAQQQQQ CGGGGATKPAVSGKQGNVLPWLGNEKT MNLNPMILTNILSSPYFKVQLYELKTYHE VVDEIYFKVTHVEPWKGRKTAGQTG MCGGVRGVGTGGIVSTAFCLLYKLFTLK LTRKQVMGLITHDTPYIRALGFMYIRYT QPPKDLWDWFESFLDDEEVCQQG |
| 3397 | 11448 | A | 4330 | 1682 | 2410 | LNKGGQTDIASSQTCLVGHVESDGALHT TMIGPNPAFLSPENNNCPWQRRWTH QKKKMNGMHTHRNEAETIAGILTVQE LFPRTNSTLVIDVSHSVLFCTTIQVLISQ VNHLYLPLPAFKFPVIFIIITSTGLLFTYV RVVMYNFVISYNGKKNQNI*KVICTELY FSSFLKMICMVRKRRGQPGEGRASRELC TFYTFVLCTALLILHPIMILLEPICKLLR |

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| | | | | | KFICVYVNNIT |
| 3398 | 11449 | A | 4331 | 2 | 57 |
| 3399 | 11450 | A | 4332 | 19 | 192 |
| 3400 | 11451 | C | 4333 | 218 | 364 |
| 3401 | 11452 | A | 4334 | 172 | 304 |
| 3402 | 11453 | A | 4335 | 258 | 509 |
| 3403 | 11454 | A | 4336 | 1 | 2411 |
| 3404 | 11455 | A | 4337 | 17 | 300 |
| 3405 | 11456 | A | 4338 | 257 | 476 |
| 3406 | 11457 | A | 4339 | 283 | 494 |
| 3407 | 11458 | A | 434 | 6 | 223 |
| 3408 | 11459 | A | 4340 | 766 | 1083 |
| 3409 | 11460 | A | 4341 | 2 | 163 |
| 3410 | 11461 | A | 4342 | 192 | 440 |

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| | | | | | | YD*T |
| 3411 | 11462 | A | 4343 | 1875 | 2210 | PLSQVITGKHQKRKRHLEEGKERPEKEQ SKHKRKKSYEDTDLDKDKSIRQKREED RVKVSSGKCLKHRKKKKSP*VYPPRKKN VSTGKRKRNLKKKGQKRKCFGMSLFLG F |
| 3412 | 11463 | C | 4344 | 217 | 396 | MSEETAKEVMRAYLQQLRQETGLRLCE KVFDPOQNDKPSKWWTCFVKRQFMNKS SXPGQ* |
| 3413 | 11464 | A | 4345 | 1 | 546 | |
| 3414 | 11465 | A | 4346 | 216 | 324 | VFFFSL*NEADRTLIIYITLYISECLKKLQK VIKLG |
| 3415 | 11466 | A | 4347 | 71 | 650 | NPGAAKMPAYHSVSLMDPDTKLIGNMAL LPIRSQFKGPAPRETKDITDIVDEAIYFK ANVFFQNYEIKNEADRTLIIYITLYISEC LKETAQSGNSKKPKVEERKCFITLGIH*FF PFPGEPPGFPL*RQFFAKPANKQDEVM RAYLQQLRQETGLRLCEKVFDPOQNDKPS KWWTCFVKRQFMNKSLSGPGQ |
| 3416 | 11467 | A | 4348 | 552 | 872 | SGPNCEEADAQLAEESGNASHTSFTV* VRPRRACHACNPSTLGG*GGRIA*SQEFE TNLGNTVRPCRNSEVLNRKTVSIRRAL RVFSPHTARLHPAAAAARA |
| 3417 | 11468 | A | 4349 | 199 | 375 | FSLGGIPPFHRRGNWVSREWPGTVAHTF NPSTLEGRGRWIT*GQEFETSLTNMVK CLY |
| 3418 | 11469 | A | 435 | 3 | 685 | RTQSGNVYFASTSVPPRGAAPGHILVLS RLQPLRAEVSRSRLLRVEYSYVKTTLV FKGTKAKSKKKSKDKK*QREDEETQL DIVGIWWTVTNFGEISGTIAIEMDKGT HALDNGLFTLGAPHKEVDEGPSPEQFT AVKLSDSRIALSGYGYLGINSDGLVV GRSDAIGPREQWEPVFKMGKMASTSN SCFIRJHEAEDIEAKSKTAGEEEMIKIRS |
| 3419 | 11470 | A | 4350 | 368 | 546 | |
| 3420 | 11471 | A | 4351 | 2 | 211 | VYIYKIGIESRVSRACITPSMAALVDKR WKKPKCPLMYEWINKM*YTHTMEYYTE *KRKYCSTLSHATI |
| 3421 | 11472 | A | 4352 | 1 | 676 | PK*WGFLPLIYKKGKDGGGTWGGDVLP SPSLGQGGGKKGWPKREGGRDLGAERK AGKCREKWKQSKMKGRSRKTGGERVK KPEKHQDTGLFPFIQGGGLRLSRVCVP QPQVGRGSVSLAQFLSCTSSD |
| 3422 | 11473 | A | 4353 | 1029 | 1252 | CKFVYSSLLFIYSSFFICLFIPLFPAPVLIYP LAH*LCKPCSSYMSWVNIQYSIYFRHCK FRNIVQKILYSIKM |
| 3423 | 11474 | A | 4354 | 299 | 561 | FPSWORDAQASLTSPAPLIYPKATPFRKR PFRRQLWNKGLIQSKLTQRLYTVAHTCN PSTLGG*GRQMTWGQKFKTSLANMVKP RLY |
| 3424 | 11475 | A | 4355 | 17 | 195 | FMDAQVTFKLYIYIYTYVCTYMYIYTY V*MCEYLFYIYARIYMYI*MHYYTYISL TP |
| 3425 | 11476 | A | 4356 | 3 | 565 | |
| 3426 | 11477 | A | 4357 | 1 | 597 | |
| 3427 | 11478 | A | 4358 | 1 | 567 | |
| 3428 | 11479 | A | 4359 | 1596 | 12368 | |
| 3429 | 11480 | A | 436 | 115 | 662 | AGFSLSAQKSPGAMA*YSYVKSSKLVK GTSKKKKSKEKKRKRREEDEETQFD/IVGI W*TVTNFDEISGTIAIEMDEGTIHALDN GLFTLGAPHK/ERIALKSGYGYLGINSD ELVV/GRSDAIGPREQWEPVFNQACAA VFTVIGSEKQSECSLLRESRAKYHGCTH GOISSSLKQHPRWMY |

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| 3430 | 11481 | A | 4360 | 48 | 436 | RTGSSSGLSISATCLISQRRYSEDWNVY SLVRSG*ERGS*LLSTYYYVLGSLPDVFTY INSFQKTYLK*MGPGMVVHAWNPNSTLG G*GRRTA*GRELETSLSNIVRPLNNNN NNNSNNEVNGIRKEG |
| 3431 | 11482 | A | 4361 | 2 | 2551 | |
| 3432 | 11483 | A | 4362 | 322 | 1288 | RKNWGLRKIPWSSLKQEQNLPEFSGSKK AFFGSTWRKKDGEPEFQGS LGCP LLKAR PLLSQLPLLRAISTRKPGQTWKNKEHHL SDREFVFKEPQQVVRRAPEPRVIDREGV YEISLSPTGVS RVCLYPGFVDVKEADWIL EQLCQDVPWKQRTGIREDITYHQPRLT WYGELPYTYSRITMEPNPHWHPVLGTL* NRIEENTGHTFNSLLCNLYRNEKDSVDW HSDDEPSLGRCPHIALSFGATRTFEMRK KPPPEENG DYTYVERVKIPLDHGTLIME GATQADWQHRS AQKNTTLREPRVNLTF RTVYPDPRGAPW |
| 3433 | 11484 | A | 4363 | 249 | 906 | RIHFPRVSGPSQSNPKFAVASRGFFSLSL SAQDPLPPLGEALALSLHPVRRSTET VAGDSSELQLGLRSPQQPLAGLAFLARL FLLFPPP*RCKSKPN*NDRRRSSVDSQIHL VGRESAHLPLAGLRVCVSLPLARCFGQV LQGVPLWIPSPGGS/AGVSGRRREERH MGVVVMRVRVEARVSS*ESK/SRALR*S THLGLPKCWDYRREPPCPAH |
| 3434 | 11485 | A | 4364 | 843 | 1186 | QHSTKNSGGWAQTPYGSSQISVCVYIHT YIHIYIFFFFLVETESH SVTQAGVQWHN LSSL*PPPPGFKRFFCFSLPSSWDYRRTTP HPANFCIFSRDGVSPYWP GWSRTD LRL |
| 3435 | 11486 | A | 4365 | 127 | 601 | NLILNVTWPTQLAKQERLHLRLKTSVV WVVRKEKPTRFPRLGAVSHCPQLLILQL VLSPTSTK TLP*EPPDSESP*PKRK GKPSW GRTGAPNLHSPPLSPEGPPWAAWNPLKL PPPHSSGAVPSSACSPWAGSVPAAPPSV CYLIYWNLHSQLAHR |
| 3436 | 11487 | A | 4366 | 30 | 436 | RRRCGGCFPALPGSPHKPHEQLPPLCPRV PVA*PSSSAEHPDPRAGKGGGRGL*AGS SPGAVPHPPSIPGRKNRMGSLEG/RGAP APRRGSGAGAAE/ASLTWPGSTGPAPG SHGCSAGVGPSRWAWSLPQRCGRG |
| 3437 | 11488 | A | 4367 | 497 | 924 | KRGSRGWFFSTFHHLWGRLQAHLLGPT PALQPCDPGAGARTARPGQTASAAPAPL PPRRGAGAPPLRLARVPAPPCAQRAP PSSSQPGRNQ**AASGPWRPPRQAEKEA SAGKRRDRPVGARKTAAERDRRGQASG GQTR |
| 3438 | 11489 | C | 4368 | 226 | 405 | MCEKQPQNTTSFQGSYPKYTRGSLPELR QLLKVELFKKGNWEHLQPRSM LVRSG LSQE* |
| 3439 | 11490 | A | 4369 | 3 | 275 | TSMYVGPVAKDLLHPSAEEENRKHTMK RLAQSPNSYFMEAKSP*CYKITTAFTHA QTVGWVWGCVTLQCPTGGEARLTERC AFTRNQRF |
| 3440 | 11491 | A | 437 | 1 | 380 | GPPASVRTDSGHPRRAEGAVSTRTQAD PLAPCGPPRPAGGQGAYARLLLLQCLLA AARPSSANDGSAPDSPFTSPPLREEIMSN FSLESHNISL TEHSSMPVENNITLERPSNV NLTCQFTTSGD |
| 3441 | 11492 | A | 4370 | 266 | 455 | AQWHTSIVLAAWEAAAAAGLLEPRS*SRL KCTMIIPINSHCTPAWQHMRPCLLKNF SNSFISK |
| 3442 | 11493 | C | 4371 | 409 | 507 | MNTRFLT CVPGWVKNDNYSIVCIDFLV VIAI* |
| 3443 | 11494 | A | 4372 | 870 | 1027 | HLCMCVRVCVCACMCTLLHLFSNGFII* CFCTST*AIHVMG*VAIKMYINDP |

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| 3444 | 11495 | A | 4373 | 1 | 690 | FHHLEDSIIEIFDAFLTLRKKRKKKHNG NMPIFSKLFHVMVNP MKISTSLFF*HKYMI VPISPOSHQYSSNGLSVLFLPVYRHS LFF MILSTLSFRCLANILSHSLFILLGLLINRSL SM*SVLLIY*Y*SYILLQYLLTVLEFFSFHI *VFSLLRILFFFKIFTFSIWMPLSQSYLLR HSVFTDVPYLI SYILICVDLFLNTLFC SIG LFILGLTQHCLNSSSFIIIVI*QSISSHLVQ* DCLCLHLCIFCALSCATKTKNKDVEIFIG LTM |
| 3445 | 11496 | A | 4374 | 393 | 491 | GLYLHRPIFPHDKLLVQLSCPFRH*THRG TES |
| 3446 | 11497 | A | 4375 | 435 | 524 | |
| 3447 | 11498 | A | 4376 | 293 | 1228 | NADNSLENFCRKSASCDLEQRRFIIRFIKL RRGSFSEKQQHSVTRKY SFIQNWVLEK DNKALNTRVIYNRFLFMMYKIKQNTDD GDCRLLCSYHVLDRHCCKGSTCIDPFFL MTNYWCNYHAHFIDEHTEAQRARNGK QGDECEVGGIESRRRSGNSGARYVHDSS PPTSGIHSNARPSVRLFLATLSKIAFLLT SLLYEMTVHIYGEPLPRRQRTQLLEGVG TLNGSVASVDPVFRNQQLHLATGSLMA SSSFCFSVLREIIGQSLIMKTL*ITHTHTH THSHTHHTERERERERETEREERVKF |
| 3448 | 11499 | A | 4377 | 953 | 1317 | VLTGVSPLYVSKGFWFFLLFS*TMFSH SPTWAILESWSSLARFSGMSGEPQMTPIG LQYLA*G*RPRNPTLVTFTEIS*VYFFILP LMSQ*MCLMHLFPLPQTFCQILQLYFFM AHIST |
| 3449 | 11500 | A | 4378 | 9 | 359 | PRKAELRIFEKVSVDAMAEDMEKLRPR LKKVHIRELVL AISIMPKTHKPM LTLRVT WREMLRVRDLK*EVEGGCRRCSSPR/V DPPGGRREFRGGVRVRGRG/SAPPGGPG LSAML |
| 3450 | 11501 | A | 4379 | 223 | 458 | CLRRINPCSPRCRRPAWRRRRPGPRTRR RTDS*IRPKSGAASHPPGGAEGIPRGQCS TRSRTRRRPEAPASRPCCLRI |
| 3451 | 11502 | A | 438 | 3 | 217 | RVMSHRKVASAPRRGSLGFLPRKRSSRH RGKVNSLPKEDLVHPLHLTCYLEDSPAF ADIVRNVYKTGGSAMN |
| 3452 | 11503 | A | 4380 | 887 | 1172 | FFPESELAQPEKRF*VPGKGRGLSPRRL PPRCRRPAWRRRRPGPRTRRTDS*IRPK SGAASHPPGGAEGIPRGCGQTRSRTRRR PEAPASRPC |
| 3453 | 11504 | C | 4381 | 22 | 255 | MPSSSAQLLLPHEVSPVLSCQLCFLK ITR VCSYLWATVILGLDYCNLSLIPCLVSYFLL SLSLPCISVVVRTQILLHY* |
| 3454 | 11505 | A | 4382 | 23 | 361 | LTTLVFA GTPGKKRRGGNQWR*SPHYSC SGGTGGRPRPAFSLPGAPGQSGQISQSD WRRGPCS*SSGWCNSC/HPGWPGLVRRG MTS*WSYS*ATGP/GPGYKAIPGAS*RST SL |
| 3455 | 11506 | A | 4383 | 2 | 310 | PLLPAHPPPWSLPVTS*PRCGSPQRTSSW NRHSHRPA*SLPCLGFA GTPGKKRRGGN QWR*SPHYSCSGGTGGRPAFSLPGAP GQSGQISQSDWRRGPCS |
| 3456 | 11507 | A | 4384 | 1021 | 1565 | PHLSPAGTPLPAHPPPWSLPVTS*PRCG SPQRTSSWNRHSHRPA*SLPCLGFA GTPG KKRRGGNQWR*SPHYSCSGGTGGRPA AFSLPGAPGQSGQISVPPCRVPPLLQ SRA AGPSPSSFSKWELYC SHHILPPLLYAHCQ ESLSNTQQRLEASLSSLNASEPTTAKCPH GTAACLLGD |
| 3457 | 11508 | C | 4385 | 361 | 612 | |
| 3458 | 11509 | A | 4386 | 448 | 683 | VNMERKKDLTESSLPVPTKVPGMRMK LS*TLKTSLATRCQTL SRLCSPTNQRLS QQEGVGVEKGELRIYLA MWIK |

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| 3459 | 11510 | A | 4387 | 1977 | 2160 | VNMERKKDLTESSLPVPTKVPGMRMK LS*TLKTSLATRCQTL SRLCSPTNQRLS QOEGV |
| 3460 | 11511 | A | 4388 | 145 | 370 | GRVLLVLCFFETESRSVA*AGVQWRHR GSLQP*ASVSYELEAAVGYGGTTALQPG RQSRALYLKTKTKNFLNLS |
| 3461 | 11512 | A | 4389 | 248 | 452 | GWVFTMLARMVLQ*NHLNPGGGGSEL RSHHCTPAWATE*DSVSKKKEKEKKMR NETKTKWTCSPFIT |
| 3462 | 11513 | A | 439 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGTG AQLSELHCDKLHVDPENFKLLGNVLVT LAIHFGKEFTPEVQASWQKMTGVASA LSSRYH |
| 3463 | 11514 | A | 4390 | 141 | 354 | ARWADWLPLGIANCPRAHLAYLETWEL EAHWKRTIVNFCVCVCLCM*VCLVALR LFCSSGMHHSFNALQ |
| 3464 | 11515 | A | 4391 | 354 | 592 | IRCTQAFALTSVSGPGTVAHASNPSTLG G*GGQIT*PREFKTSLGKMAKPLYKNL GRHGDLCQARLLQLAEVEGFT |
| 3465 | 11516 | A | 4392 | 63 | 353 | ATEPVWPPCLWPQPLCAKDCRGVARP* CVRPPKASLVLPSSAGNASSIFMDYKCL SPCPFQFLSSPPQSTEPSPACELGLINVN LSSRPSLPSR |
| 3466 | 11517 | A | 4393 | 357 | 559 | LILETGSVCVFQAGVK*LCTSVIIAHYSL DLLGSSNPPTSDSRVPGCGDVHLYSQVD AAANLVVVA |
| 3467 | 11518 | A | 4394 | 1048 | 1599 | CRSKWGLASILWKSFLGHHLGGDGFK A*FKFHSKFTVLASSKCLLVGF*SHNYG *VRIHLFIY*IFIHF*KDFKSMFPRLVLSSW PQAILPPWPKVLGLQVLANCIPMFHF NWLKSSKWLR |
| 3468 | 11519 | A | 4395 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGTG AQLSELHCDKLHVDPENFKLLGNVLVT LAIHFGKEFTPEVQASWQKMTGVASA LSSRYH |
| 3469 | 11520 | A | 4396 | 38 | 553 | APSPDAMGHFTEEDKATITSLWGKVN VEDAGGETLGRLLVVYPWTQRFDSFGNL SSASAIMGNPKVKAHGKKVLTILGEMP* KHLDDLKGTFAQA*SELALVDKLAHV S*RTFKLPGEMLLVTRFWQSHFRQKNFT PEGARLSWAERWVTWSWPVALVPLPLP LKLNCP |
| 3470 | 11521 | A | 4397 | 74 | 432 | TTGTLESLSNNACFGALLPHPPAPGE*R PWS*HFTRYLGPLNRCAWEGGRG*TGPG LPSLGKALVEGIPSESPGPTVSHPCSPRP DPDQSAASLHQVPPPTVHCSHLTPMG WPGPQ |
| 3471 | 11522 | A | 4398 | 1 | 176 | |
| 3472 | 11523 | A | 4399 | 1 | 188 | |
| 3473 | 11524 | A | 44 | 275 | 403 | FSHFWPPEFLRD*MWLGWVAHACNPST LGGRGRWIT*GQES |
| 3474 | 11525 | A | 440 | 37 | 527 | APSPDAMGHFTEEDKATITSLWGKVN VEDAGGETLGRLLVVYPWTQRFDSFGNL SSASAIMGNPKVKAHGKKVLTSLGDAIK HLG*SQGAPFAQA*SELHCDKPAWDP ENFKAPGEMLLVTRFGQSHFRKNFTPE GCKASWAERWVTGVAASALVPSRYH |
| 3475 | 11526 | A | 4400 | 1 | 118 | |
| 3476 | 11527 | A | 4401 | 1 | 227 | |
| 3477 | 11528 | A | 4402 | 1 | 157 | |
| 3478 | 11529 | A | 4403 | 1 | 133 | |
| 3479 | 11530 | A | 4404 | 1 | 169 | |

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| 3480 | 11531 | A | 4405 | 1 | 143 | |
| 3481 | 11532 | A | 4406 | 1 | 89 | |
| 3482 | 11533 | A | 4407 | 1 | 166 | |
| 3483 | 11534 | A | 4408 | 1 | 190 | |
| 3484 | 11535 | C | 4409 | 21 | 218 | |
| 3485 | 11536 | A | 441 | 68 | 398 | GPASNRLGFVVLLLETRMVSAVSDPPTS TTGSTMCECISIHVGQAGVQMGNACWE LYCLEHDIQPSGTMPSHKALWSSDNSFN TFFRETQPGRHVPGLSVDLEPAVIAQ |
| 3486 | 11537 | A | 4410 | 1 | 206 | |
| 3487 | 11538 | A | 4411 | 2 | 185 | |
| 3488 | 11539 | C | 4412 | 247 | 393 | |
| 3489 | 11540 | A | 4413 | 1229 | 1784 | RCRREMGSLSHSMVDSGFLWPCWRG PGSRTSNTVENRNPPPPRHPLGQLFILFQ SLSLHLSLS/CLSLSTFFQSLFLNLSVSLC QSLPSPSL/CFSIPLSNTHHTHTHTHTHT HTHTHTHTESGRC*SVLFFPPCPYLHYR *G*GVGSAALSLTPHYEMTVFKGNLLY LPAVSIVSRVNL |
| 3490 | 11541 | A | 4414 | 76 | 297 | EIRTLRSRSQLWRRDVRWISGSCLKGH ASDHQLCQH*CTHTHTHTHTHTHTHT HTHTHTHTHTHTHTHTPKMA |
| 3491 | 11542 | A | 4415 | 48 | 327 | EELALRR QRLAELQAKHGDGDAVAQ QEAHREAEMRNSILAQVLDQSARARV SEQGLIEILKKVSQTEKTTTVKFNRRKV MDSDEDDDY |
| 3492 | 11543 | A | 4416 | 786 | 905 | VSEQGLIEILKK*COLTEKTSTVKFNRRK VMDSEDDDDY |
| 3493 | 11544 | C | 4417 | 58 | 237 | MAAELEALRRPEAGRAAGPNTGDPGD AAPTGSQSTGQAEMRNSILAQVSGSSPA PGPG* |
| 3494 | 11545 | A | 4418 | 115 | 432 | LSK*CNKYTIHTHTHTHTHTLLNQPL K |
| 3495 | 11546 | A | 4419 | 10 | 398 | ENTVFIGLLKQQTRNIIPLKIFCLRLKIPP LTMPSPPPSPFRKSPDLVPAHTPKEGRLW PWPGPPGGPSKAAHARRPLSTCQD*PPQ REILPGPQPTSPTHCRMSREGRSGGTGAR ACQLPLLRPLAS |
| 3496 | 11547 | A | 442 | 3 | 398 | |
| 3497 | 11548 | A | 4420 | 551 | 792 | INFFFF*IIDRFSLCHPGWTAVAQSRLTAT LLPSRFKRFLCLSLPSSWEYRPLPPYPAN FCSKLLICLSTFYKDCGNSA |
| 3498 | 11549 | A | 4421 | 56 | 193 | |
| 3499 | 11550 | A | 4422 | 1 | 3552 | |
| 3500 | 11551 | A | 4423 | 373 | 593 | KKSLESINSRLQLVMKSGKYVLGYKQTL KMIRQGKAKLVILANNWPALR*SKRLNV LRLPRIHRERIYRSVNL |
| 3501 | 11552 | A | 4424 | 118 | 206 | VGGRPRSLRQGRWVARKEDEKSRWESI NSRLAQLVMKSGKYCPWGTSETLKMIR QIGKAKLVILANNCPALRKSEIEYYAMLE KTVGVHHYSGNNIELGTAICGKYRVC LVAIDSGGL*PFI*KACPEQTW*KEDEKS RWESINS |
| 3502 | 11553 | A | 4425 | 1134 | 1287 | HGQINQMEVNLPMDRKV*THHTHTHT HTHTHTHSSTSCPYTLKRNVKS |
| 3503 | 11554 | A | 4426 | 102 | 443 | SPIIPLPITTINILVYVLLAFLCIYIHT*IYLY IIFFTNIVSYTYCFITCVFHLIYIVNIIVY SLKNFTDITCSLWKIRSYRYAKRKYNC KSHLPEINAFILWQVSFQTL |
| 3504 | 11555 | A | 4427 | 263 | 615 | LVNSEGNIWVKLCHLQHGFLNSSFLLIL LSHSEKINRASIMLKRKYKLINNYILSAF NPPPGKIHTHTHTHTHTHTHTHTESQKVK ST*EIT*JFPQYTNLCQREEHCYFLSHSE |
| 3505 | 11556 | A | 4428 | 839 | 963 | CVNGLVLGQAQLLRPVIPAL*EAEAGRL LEPRSSRSWANM |

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| 3506 | 11557 | A | 4429 | 526 | 710 | MGVWLNILTPTFGDQSAKLGTLQFKPAR HEFSQSGRTSFPIMPSPRLPDVA*ENPNG SLDP |
| 3507 | 11558 | A | 443 | 1 | 255 | |
| 3508 | 11559 | A | 4430 | 2 | 539 | |
| 3509 | 11560 | A | 4431 | 920 | 1110 | TAVVFLNKLQLHF*KFLSEAFDNEYGIA YNSLSSEILERLQKIDAPPSASVEWCRKC FGAPLI |
| 3510 | 11561 | A | 4432 | 38 | 571 | GSHRRCSEFITNYVHLYIFTLYIYIYIYIY IYIYTQMHSPPAHSVT*LYGNTSLSATLE RPVTPAVVAVGFRVRSEKQLIVYEGARP RG |
| 3511 | 11562 | A | 4433 | 145 | 675 | NVAVASLSGAHTWKKQSQVCFVSAGLE TSMEAAIGDLSVFPGLTQLEGIQGLVEP VQA*ASSWSSR*AAHSQGGHPSPYHRSH LPKPTQRNPERSQMEAPSPKPLDQPVPE KRHRGASAMRRRKPIISFGFLAEMLVLA VREIELTNCPHPEPNLATGKMTWLRSSS GFCESNRVT |
| 3512 | 11563 | A | 4434 | 328 | 333 | AFEFKRIDILTFKSSFAGSL*E*LHTHTHT HTHTHTNTCFLTMKELSNHPGNK |
| 3513 | 11564 | A | 4435 | 1461 | 1710 | SGVLGRAALLKPPSRARSSGGSSLSILR LSSPGPLSSPLPCPTSQDRGIPFQTHLN VALT*AAHEMDWREPCVKTRTGS |
| 3514 | 11565 | A | 4439 | 3 | 451 | |
| 3515 | 11566 | A | 444 | 2 | 732 | YLVSCFRDMAFNFGAPSGTSGTAAATA APGVGFGGFTTSTTAGSAFSPAPTNTG TTGLFGGTQNKGFGTGFGTTGTSTG LGTGLGTGLFGGFNTQQQQQTAVGYS CMPNKKDEGLVVLVFNKKETEIRSQQQ QLVESLHKVLGGNQTTLVNVEGKTLP DDQTEVVIYVVERSPNGTSRRVPATTL YAHFEQANIKTQLQQLGVTLMSRTELSP AQIKQLLQNPAGMFLESQSS |
| 3516 | 11567 | A | 4440 | 26 | 529 | NSTDSETHPWLLSPADKVTNVKAWG KVGAGAGEYGAEALERMFLSFPTTKVY FPHFDLSHGFAQVKGHGKIVADALT KAVAHVDDMPKRRCP*SDLHAHKLAR VGPSTFKLLSHLPCLGEPWAAHLPRPS FNPWRLQRLPWGQSLGFLKHRCLNLP NTR |
| 3517 | 11568 | A | 4441 | 294 | 600 | ISCFCLSETLSNFALFLKESNGPVKVWGS IK/AMTENLHGFHVHEFGDNTAGRVLCF FLECIWEL*FII*LFLLLINR/CTSAGPHFN PLSRKHGGPKDEER |
| 3518 | 11569 | A | 4442 | 517 | 758 | |
| 3519 | 11570 | A | 4443 | 80 | 725 | SPAASGGFPLQSLPRTLGRGLSDFGDRS PVCVLKGRPKCRGIINFQKCRESNGP VKVWGS/IKGLT*KALHGFHVHEFGD NTARLYQVQGGPHFNPLSQKTTVGPKDE ESHC*DLGQCDCLTKNGVADVSNEFV NLTLQGDHCHNGRTLVPVWKKPDDLGP KVGNEESSKTGNAGKSVWPCGVIGIA RINIPLGCSLRPPKLCVSC |
| 3520 | 11571 | A | 4444 | 415 | 635 | |
| 3521 | 11572 | A | 4445 | 2 | 478 | MAGKQAVSASGKWLMGIRKWYYNAAE FNKLGLMRDDTIYEDEDVKEAIRRLPEN LYNDRMFRIKRALDNLKHQILPKEQWT KYE/EGLCSSSALCFLLR*KDQPIECPSR SQEELL*SKLSPL*TAFET*AKENFYLEPY LKVEVIRERKEREWAKK |
| 3522 | 11573 | A | 4446 | 323 | 400 | |
| 3523 | 11574 | A | 4447 | 2 | 396 | RPPTTTKFAAARQMAGKQAV*STQAKG LNG/IFKKWYYNAARIQNLGLMRDDT IYAEDEDVKRSP*EDFPENLYNDRMFRH* EGHWTNLKQHILPKEQWTNFEENFY LEPYLKE/VLFRERKEREWAKK |

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| 3524 | 11575 | A | 4448 | 3 | 314 | |
| 3525 | 11576 | A | 4449 | 5 | 340 | GGTSAKAFRSIWGPLPPVHRHGSRRSSV QR/DGPGLGTGEPRVYIRNKVANTGVPG APGPSIGGVTA PATDYCHRIAPILAARRR RRRRRRRRRRRRRRGGGGGVAGGGGGG G |
| 3526 | 11577 | A | 445 | 2 | 681 | AREGSALRVAGVTYLVS CFRDMAFNFG APSGTCGTAAATAAPA/GNTFLLFGGGF GGFGTTSTTAGSAFSFSAPTNTGTTGLFG GTQNKGF GFGTGF GTTTGTSTGLTGLG TGLGFGGFNTQQQQQTTLGGLFSQPT QAPTQSNQLINTASALSAPTLLGDERDAI LAKWNQLQAFWGTGKG YFNNIPPVEF TQENPFCRFKAVGYSCMPSNKDEDGLV VLVFK |
| 3527 | 11578 | A | 4450 | 1 | 117 | |
| 3528 | 11579 | A | 4451 | 1 | 1973 | DGGARARGRAAARRRRRRRRRRRRRRR RRRRRRRRRRRRRRRLGLERPQTSRGR APGASRAEEKMEELVVEVRGSNGAFYK AFVKDVHEDSITVAFENNWPDRQIPFH DVRFPFPVGYNKDINESDEVEVYSRANE KEPCCWWLAKVRMIKGEFYVIEYAACD ATYNEIVTIERLRSVNPKNPATKDTFHKI KLDVPEDLRQMCakeAAHKDFKKAVG AFSVTYDPENYQLVILSINEVTSKRAHM LIDMHFRSLRTKLSLIMRNEEASKQLESS RQLASRFHEQFIVREDLMGLAIGTHGANI QQARKVPGVTAIDLDEDTCTFHIYGEDQ DAVKKARSFLEFAEDVIQVPRNLVVIGK NGKLIQEI VDKSGVVRVRIEAENEKNVP QEEEIMPPNSLPSNNSRVGPNAPEEKKHL DIKENSTHFSQPNSTKVQRGMVPFVVG TKDSIANATVLLDYHLNLYLKEVDQLRLE RLQIDEQLRQIGASSRPPNRTDKEKSYV TDDGQGMGRGSRPYRNRGHGRGPGYT SGTNSEASNASETESDHRDELSDWSLAP TEERESFLRRGDGRRRGGGGKGQGGGR GRGGGFGND DHSRTDNRPRNPREAKG RTTDGSLQNTSSEGSRLRTGKDRNQKKE KPDSDVGQQPLVNGVP |
| 3529 | 11580 | A | 4452 | 1 | 2115 | |
| 3530 | 11581 | A | 4453 | 2 | 424 | |
| 3531 | 11582 | A | 4454 | 1 | 456 | RPRRPQREPTMVLSPADKTNVKA AWGK VGAHAGEYGAEALERCFLSHHQDLLS HFDLSHGSSQVKGHGKKVADALTNVAG HVDDMPNALSALSDLHAHKL RVPVNF KLLSHCLLVTLAAHLPAEFTPAVHAFLD KFLASVSTVLTSKYR |
| 3532 | 11583 | A | 4455 | 25 | 640 | EFHRLRENPPWCLSPA DTKAQRPPRLK LGAHA/GEYGGEPLERMFLSFPTTKDLLP ALRP*ATVSAQG*RAHGK/VADALTN AVA/HVD/DMPQTALSAPERTCNGAQAF GWDPVQLSSS*SHLPCLGEPWAAHLPRP SSTPGGCKASLGTKFPGLFVEAPLLEPSK LPLKLGSLRVGHCFAPLGLPPSPSPSCT RTPVVFE |
| 3533 | 11584 | A | 4456 | 906 | 1046 | PDHHNWSQ*TTTGAQRQT*KRTVKEV*S AHNEAMCFGTCASDCLYR |
| 3534 | 11585 | A | 4457 | 1 | 383 | MVLMPPVVS AIPAEAKSSLIENDVCLSA KENHKS KRAITRTAERFPTE/SPHD/YPRK TARTGLRHAQQASLPNWSTPLAARIAP VPPAANPQGVLLKSAGPHLLLARTTTC NR*VPIASPQTTHRME |
| 3535 | 11586 | A | 4458 | 1 | 1509 | |
| 3536 | 11587 | A | 4459 | 579 | 919 | PGSM/IPLSVSHSTGDDGRSLPKRRSTAPS MTSVYCFNCERCLVSCSLLLLSSLGPPCL AVLLAPFFAPFF*VFLLCVVVAGLPALLL LLVSSLLFLVLLSFC AASACFGFLSV |

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| 3537 | 11588 | A | 446 | 1 | 459 | HRRPLYPAGIARMTRGDRTRTGCTRPKG SRTGGAVGAAMQEIIIGSVVDHIKFDLEIAV EQQLGAQPLPFPMD/KTPDSQAPISTVW GLLLPSLGLRSSLPRIFGPLRLFESGA CEFFLKAACGKGGMCPFRHISGEKTVVC KHCLRGLCMN |
| 3538 | 11589 | A | 4460 | 1477 | 1691 | YCNVSFGANLERA*TSFSALFIDLQPPGY RTTTSKHKVSSSLIKGHVLLDHSFHDNT QLWISTNAFRFGN |
| 3539 | 11590 | A | 4461 | 1076 | 1354 | QQKCAVNLHSFLPITKLCRLFASCRAAR CCSHLTSQPVT*LAGKVNPLPLGNLWE CDTKAGSQAMRTHLSITWRAVMQLPVI NTTYQRGKR |
| 3540 | 11591 | A | 4462 | 880 | 1242 | |
| 3541 | 11592 | A | 4463 | 832 | 1386 | |
| 3542 | 11593 | A | 4464 | 46 | 492 | HPVTLGDNTYRTHIKQLIKGEVLFLHFTP DAVDVFRIT/MTLPL*RLQLSSQRADDQ RTLRCVSRGRDAVHAHVWQFVCIRLD/E VTEAVIFQPPQLSDSETVSQRCVDVGTL FCRQYTFIFRRIFYFAQMSNTLRLFDDYA EEIIDHRQ |
| 3543 | 11594 | A | 4465 | 7259 | 7441 | IASPGWS*RQECSSRSCAQCCQSTTTTCR HAKQRLALAHKPLAKLAGNGITPRLRQ ICR |
| 3544 | 11595 | A | 4466 | 538 | 1056 | |
| 3545 | 11596 | A | 4467 | 1 | 1134 | |
| 3546 | 11597 | A | 4468 | 745 | 1263 | |
| 3547 | 11598 | A | 4469 | 3506 | 3826 | EVWRPARRSRDVSCSRSHAYVVPGTA DWLWPS*RPSTTGVC*PVTWRWLEGQ WPHLGRVLQEDSDSPFPALGIQETRP EPLKSPREVPTSGRTGVFHYPA |
| 3548 | 11599 | A | 447 | 1 | 811 | DGTMEDSEAVQMATALIEQRLAQEEEN EKLRGDARQKLPMDLLVLEDEKHHGAQ SAALQKVKGQERVKRTSLDLRREIDVG GIQNLIELARKKRKQKKRDLAASHEPPP EPEEITGPVDEETFLKAAVEGKMKVIEKF LADGGSADTCDFRRTALHRASLEGHM EILEKLLDNGATVDFQDRLDCTAMHWA CRGGHLEVVKLLQSHGADTNVRDKLLS TPLHGAVRTGQVEIGEHLGLLENNAR NREGDTALHDAGRNVNRYPILO |
| 3549 | 11600 | A | 4470 | 1 | 751 | |
| 3550 | 11601 | A | 4471 | 482 | 1200 | VFSGPFSGVGFPPFSGLCPCELSATVLEV APPLLPGNRMSSRITMLSESCQRMVIVG YGRCFADRQNLMLVCLRSMPNVFTGSCA RMRCCLSEN/LPVPPSKRAHTGRVAVKE SNQRWCSDGFECCDNGERLVRTFALD CCDREALHWA VTTGGFNSETVQDVMLG AVERRFNGNDLPSSPVEWREGVFNIDE EFGNESAQTMGLHHQLDPSVEGELHQN TGSTACCRADSTHISHWRFM |
| 3551 | 11602 | A | 4472 | 1271 | 1681 | TVITTGIGRPFSMESVFALNALQNSMMF TPC*PRAGPTGGLGCTSFSDPILDGWPP QSSQLMIRMCFSVYTMLESCQGMVIVG YGRCFADRQNLMLVCLRSMPNVFTGSCA RMRCCLSENLLYRHRNGHIQAEWP |
| 3552 | 11603 | A | 4473 | 739 | 1257 | |
| 3553 | 11604 | A | 4474 | 1 | 2661 | |
| 3554 | 11605 | A | 4475 | 1 | 2370 | |
| 3555 | 11606 | A | 4476 | 421 | 972 | |
| 3556 | 11607 | A | 4477 | 766 | 1073 | HRQLVIVFQQPLVSGFHEAELSLDDAKW VLHPGPDAGFHVFDVDGRFVLA*CCFK VLTLPGRSAISQSTPPRPAPRAVAPLGS HRLRQIAPLHAADYPAD |

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| 3557 | 11608 | A | 4478 | 1662 | 2045 | PTALAAFSRRIVRITFLPVGDPGFHQSGS LRLS/NPDALQIQPACRIFSSALITSVFACS VHEGE*LPVDPGHIRALLHR*R*KAESAC AVPCI*AWTDREYGCHNRRKSGVILRRT DDWMDGRRSRHT |
| 3558 | 11609 | A | 4479 | 1 | 1803 | |
| 3559 | 11610 | A | 448 | 100 | 1532 | EARRNWGAMGKARRSPGHRHCEGCF NRHCHIPVEPNTSCLVISCHLLCGATFHM CKEAEHQLLCPLEQVPCLNSEYGCPISM YRHLAKHLQACPASVVCSSMEWNRW PNVDSETTLHENIMKETPSEECDDTALAL QDQKVLFRSLKMVELFPETREATEEEPT MNGETSVEEMGGA VGGVDIGLVPHGLS ATNGEMAELSQEEREVLAKTKEGMDLV KFGQWENIFSKEHAASALTNSSASCESK NKNDSEKEQISSGHN MVEGEGAPKKKEP QENQKQDVRTAMETTGLAPWQDGV ERLKTAVDAKDYNMYLVHNGRMLIHF GQMPACTPKERDFVYGKLEAEQVKTV YTFKVPVSYCGKRARLGDA MLSCKPSE HKAVDTSDLGITVEDLPKSDLIKTTLQCA LERELKGHVISESRSIDGLFMDFATQTYN FEPEQISSGTELADLTAATPGGLHVELHS ECVTKRHN |
| 3560 | 11611 | A | 4484 | 875 | 1075 | |
| 3561 | 11612 | A | 4485 | 2097 | 2179 | |
| 3562 | 11613 | A | 4486 | 4274 | 5255 | HTLFGDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNP NLPRLVRPEVD VMCTAFHDNGETFLKK*VIRCL*FKIKK HGVTP*ANTL*KLP*QKYFQH*DLEVLL* *FFKEVVFDTTKFYTAKNMIKDILKFIE GYNLSQKFKIDKFFNVFRRYVYMVVID FVLVSNIILPKFNHLCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LAESLEFGGS GENVDYNYFCNIVCYRK/ADCFSFLKFR YLYEIARRHPYFYAPELLFAKRYKAAF TECCQAADKAACLLPKVLC TRIEKSLL SNLILSILWLDLGTLSV |
| 3563 | 11614 | C | 4487 | 102 | 230 | MFLSCRSVXXXXXXXXXXXXXXXXXSPLF LSPLLFLLFHTYMRA* |
| 3564 | 11615 | A | 4488 | 2 | 567 | |
| 3565 | 11616 | A | 4489 | 125 | 522 | |
| 3566 | 11617 | A | 449 | 124 | 602 | WATTPFQPKSNSKMAELFMECEEELEP WQKKVKEVEDDDDDDEPIFVGEISSKPAI SNILNRVNPSSYSRGLKNGALSRGITA KPTSQHYTNPTSNPVPASPIKFHPESRSS DSSVIVQPFSPVSVSKTIRPAQGSIGCCL SISTVPSYNSGLS |
| 3567 | 11618 | A | 4490 | 195 | 473 | |
| 3568 | 11619 | A | 4491 | 1 | 966 | |
| 3569 | 11620 | A | 4492 | 1 | 960 | |
| 3570 | 11621 | A | 4493 | 1743 | 1935 | |

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| 3571 | 11622 | A | 4494 | 1 | 1540 | NSGGSGGGTSGSGSSSGQGMGQSQSG GHGPGGGKKDDEDKKKKYEPVPTRVG KKKKKTKGPDAAASKLPLVTPHTQCRLK LLKLERIKDYLLMEEEFIRNQEOMKPLEE KQEEERSKVDDLRTGTPMSVGTLEEIHDD NHAIVSTSVGSEHYVSILSFVDKDLLEPG CSVLLNHKVHAVIGVLMDDTDPLVTVM KVEKAPQETYADIGGLDNQIQEIKESVEL PLTHPEYYEEMGIKPPKGVILLVPPGNTG KTFLPKAVANQTSATFLRVVGSSELIQKY LGDGPKT/LSRELFRVSEELAPSLRFIDRI LPPLGHKRYD\SNS\GVRRELQRTMLELE LLNPVGMGDFS*GRL*KLSWATNR\ETL\A DPALIRPRPAFDSKIEFPLHDEKTKKRIF QIHTSRMTLADDVPLDDLIHGLKIDLS\A GA*HSRAICTEAGLMGL*GERRMKVTN EDFKKSKENVLYKKQEGTPEGVVSLMN HGLSSGKWLGDIPSIPERDEVGGSCPEESL FPLIFY |
| 3572 | 11623 | A | 4495 | 125 | 320 | |
| 3573 | 11624 | A | 4496 | 1376 | 1509 | |
| 3574 | 11625 | A | 4497 | 2120 | 2313 | |
| 3575 | 11626 | A | 4498 | 2 | 266 | |
| 3576 | 11627 | A | 4499 | 918 | 1475 | |
| 3577 | 11628 | A | 45 | 2 | 343 | NLCQVFIPFLFHSLLYVFKTLKGLFQASF LGHLPLSGTPGRPGGGGAGGSGRGD PPAAGASRTIPWPLLLQLSSSSSHFKA/P SKLSSHG*PRALGPPGPYHRPPSPGTT |
| 3578 | 11629 | A | 450 | 1 | 368 | ICRFNPYVFLAAKADQLQVRTTQLT/CKS CWLYHCINHSTLQTCNISTL/M/LGHIPG LWILINLSEPWDATPVWHFVKLLLTCLT HHACRASGNIFAIVSLVTLITSAVMSSVA LHSSVQMAQ |
| 3579 | 11630 | A | 4500 | 1 | 822 | |
| 3580 | 11631 | A | 4501 | 158 | 668 | |
| 3581 | 11632 | B | 4502 | 151 | 336 | ANSDSMVGYVLGPFFLITLVGVVAVG GPAHHLLPMYSYDPAEELHEAEQELLS DMGDPKV* |
| 3582 | 11633 | A | 4503 | 748 | 949 | |
| 3583 | 11634 | A | 4504 | 1139 | 1241 | |
| 3584 | 11635 | A | 4507 | 41 | 488 | |
| 3585 | 11636 | C | 4508 | 187 | 342 | MICKNKNKVILLXXXXXXXXXXXXXGG AXXXXXTTPRRRGKKQFLLPPKQ* |
| 3586 | 11637 | A | 4509 | 1304 | 1434 | |
| 3587 | 11638 | A | 451 | 126 | 373 | GRGTSKILMALQRTHSLLLLLLTLLGLG LAYPSYGHVLYVHRVVADNGHLEETLV MDRCLSVMILLRIISRDDCERLIGLA |
| 3588 | 11639 | A | 4510 | 1 | 1383 | |
| 3589 | 11640 | A | 4511 | 1 | 674 | |
| 3590 | 11641 | A | 4512 | 19 | 249 | |
| 3591 | 11642 | A | 4513 | 1000 | 1174 | |
| 3592 | 11643 | B | 4514 | 60 | 378 | NAVLEADFAKRGYKLPKVRKTGTIAG VVYKDGIVLGADTRATEGMVVADKNCS KIHFI PNICYCGAGTAADTDMTTQLISS LAAMAVFEDKFRPDMEEEAKNLX* |
| 3593 | 11644 | A | 4515 | 1 | 437 | DPRATEGMVVADKTCQKSTGRPELV AIRMLKQMLFRYQGYIGAALVLGGVDV TGP/HLYSIYPHGSTDIAAGIFNDLGS IDLCVSKNKLDLFRPYTVPNKKGTRLGR YRCEKGTAVLTEKITPLEIEVLEETVQT MDTS |
| 3594 | 11645 | A | 4516 | 1 | 1059 | |
| 3595 | 11646 | A | 4517 | 1115 | 1307 | |

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| 3596 | 11647 | A | 4518 | 3 | 866 | FLGKMAAVSVYAPPVGGFSFDCNCRRA VLEADFAKRGYKLPKPRKTGTITAGVV YKDGIVLGADTRATEGMVVADKNCISKI HFISPNIYCCGAGTAADTAMTITQLISSN LKLHSLASTGRNLPVVTANRMLKQMLF RYQGYIGAALVLGGVDVTGPHLYSIYP HGSTEKVPYVYTHGFLAPLAAMALFER* V*APDMEEEEAKNLVSEDSPPQFPSPSW RIFNDLGSRKPNIDPLSSARNKLGFSPP HTQLPNKKGTRLGWP/RYRCEKG/TTAV LTEKIPLLWST |
| 3597 | 11648 | A | 4519 | 4 | 181 | |
| 3598 | 11649 | B | 452 | 1 | 1812 | MPSPLFFVATIHDCELETTETGPS LQDVPLEKADATVFTDGGSSFLEQGVKA GAAVTTETDVLWAHALPANTSQAQKEL IALTQALRWGKDINVDTSRYAFATVHV HGAICQERRLLTSAEKAIKNKNPPSSKPN RSSSLGNLRPDGSMYMHRSKGVPAV SVNVNLTPESELNLESSCVTKLSPEKEI YEMESLQWENMGKRINHHLQYNGLD NMECKGNLEGQEAQEGLYMCVKITCE EKATESHSTSTFHRIPTKEKLYKSPNPS QDTGYSQHHTRTTFSKRQPKNCERFPVE GRPLTLPAQTSXGYSKPDVITLLEQK EPCVVARDVTRRQCPAPMVDLIARV GVMARGNAITLPCGRDVKFTLEVLRG DSVEKTSRVWSGNERDQELLTEDALDD LIPSFLLTGQTPAFGRRVSGVIEADGSR RRKAAALTESDYRVLVGELDDEQMAAL SRLGNDYRPTSAYERGQRYASRLQNEFA GNISALADADNISRKNTRCINTAKLPKS VVALFSPHGDYLPVPQAKGNVVTISY MTNRGFFEDKKATFAPSLMNIKGNKTS VVKNSILEQQQLTVN* |
| 3599 | 11650 | A | 453 | 305 | 1088 | NHWPMHLVTFRDVAIDFSQKEWECLDT TQRKLSRDVMLENNYNNLGLTG/SDILGS KPVVITLLEQKKEPCVVARVDVTGRQCPG LLSRHKTKKLSSEKDIHEISLSKESIEKSK TLRLKGSIFRNEWQNKSEFEGQQLKER SISQKKNSLKMSADRKRPSFTLNQRIHN SEKSCDSHLVQHGKIDSDVKHDCKECGS TFNNVYQLTLHQIHTGEKSCKCEKCGK VFHSYQLTLHQRFTGEKPYECQECGK TFTLYP |
| 3600 | 11651 | A | 4538 | 1511 | 1687 | |
| 3601 | 11652 | A | 4539 | 425 | 619 | |
| 3602 | 11653 | A | 454 | 1 | 2088 | |
| 3603 | 11654 | A | 4540 | 122 | 621 | |
| 3604 | 11655 | A | 4541 | 2315 | 2790 | AATTPALRPLRRSSFLMATTITKASTGT WSSSPSLPTPPPTSLRKAPTTLIQKWRP GAQQPSCPKPRS*PSSSTPRTGPIGTSTS EPMITTQWP*STPSMR*LPPALTHPRSCVP SRTAAWVLGWYATHIERWLSAYSROPD SGLGWQTCFAQNLPK |
| 3605 | 11656 | A | 4542 | 645 | 766 | |
| 3606 | 11657 | A | 4543 | 294 | 502 | |
| 3607 | 11658 | A | 4544 | 969 | 1158 | |
| 3608 | 11659 | A | 4545 | 147 | 402 | GRGIQLFHEIQLQLSKTLCEPAVPVQRLR GRTAARWPGSRESPLRPVFDVEYCGVLI FIILFI*WRHFHSLCWSGDDIILACLL |
| 3609 | 11660 | A | 4546 | 240 | 433 | |
| 3610 | 11661 | A | 4547 | 3 | 310 | GGQPPHPPAARPGGRWGCQPPARQPLRP GGSVSTGTGFPGRWQPETSWVSCRHC GPHLSAVWGLPR/LSPLPAGPNRPQQLS EFPRPKEFLTPTQTKPN |
| 3611 | 11662 | A | 4548 | 3 | 195 | WPPGLOPRGTEHRPPTDTPPRAARSTR SHSPSEPRTRTPWQQR*LPRPSKPSHGPD VIEAA |

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| 3612 | 11663 | A | 4549 | 1 | 1439 | |
| 3613 | 11664 | A | 455 | 140 | 511 | PTQSTRRIATVSIAAAVAPLTLFLYRGDG GLSSRRRADAAGG/APFSLCGEVAVKPPI NPFTELMENAVNDGSHSEELFCHLKTIS QKEDLTRCTSESHLSWYSHQYQGKSKF PILGFPVLSII |
| 3614 | 11665 | A | 4550 | 292 | 573 | |
| 3615 | 11666 | A | 4551 | 376 | 456 | GEEPTSVF*RNQWNLRPKHFGNASPW |
| 3616 | 11667 | A | 4552 | 1663 | 1984 | |
| 3617 | 11668 | A | 4553 | 1735 | 1868 | |
| 3618 | 11669 | A | 4554 | 138 | 279 | |
| 3619 | 11670 | A | 4555 | 72 | 192 | |
| 3620 | 11671 | A | 4556 | 571 | 690 | CQQGFSFLQAYGPAQHAISMRKFKAKY PDYEVTWANDGY |
| 3621 | 11672 | A | 4557 | 130 | 943 | |
| 3622 | 11673 | A | 4558 | 45 | 405 | GIPGRRNMAVADLDLIPDVVIDSDGVFK YVLIPSPLGIPAPGIRPAESKEIVRGYKWA IGHHADIYDKSVGATCRKQGLRTVSILG GGRIS/HTKSPGQERFTVYGYSMGLWSC PRTPIST |
| 3623 | 11674 | A | 4559 | 613 | 866 | |
| 3624 | 11675 | A | 456 | 1 | 1014 | |
| 3625 | 11676 | A | 4560 | 69 | 430 | |
| 3626 | 11677 | A | 4561 | 144 | 294 | |
| 3627 | 11678 | A | 4562 | 13 | 759 | |
| 3628 | 11679 | A | 4563 | 177 | 328 | INAHLKFKVYFLSQAPLKCTWKTSAARE NHV*LTFLMFYGTGTVGCFL |
| 3629 | 11680 | A | 4564 | 218 | 343 | |
| 3630 | 11681 | A | 4565 | 708 | 916 | |
| 3631 | 11682 | A | 4566 | 829 | 1002 | |
| 3632 | 11683 | A | 4567 | 51 | 209 | |
| 3633 | 11684 | A | 4568 | 8 | 218 | |
| 3634 | 11685 | A | 4569 | 3 | 357 | |
| 3635 | 11686 | A | 457 | 577 | 2195 | IMGCVQCKDKEATKLTEERDGSLNQSSG YRYGTDPTPQHYPVSFGVTSIPNYNFHA AGGQGLTVFGGVNSSHTGTLRTRGGT GVTLFVALYDYEARTEDDLSFHKGEKFQ ILNSSEGDWWEARSLTGETGYIPSNYV APVDSIQAEWYFGKLGKDAERQLLSF GNPRGTFLIRESETTKGAYSLIRDWDD MKGDHVKHYKIRKLDNGGYITTRAQF ETLQQLVQHYSERAAGLCCRLVVPCHK GMPRLTDLVSKTKDVWEIPRESLQIKR LGNGQFGEVWNGTWNNGNTKVAIKTLK PGTMSPEFLEEAQIMKKLKHDKLVQLY AVVSEAPIYIVTEYMNKGSLLDFLKDGE GRALKLPNLVDMAAQVAAGMAYIERM NYIHRDLRSANILVNGGLICKIADFGLAR LIEDNEYTARQGAKFPIKWTAPERALYG RFTIKSDVWSFGILLTELVTGRVPYPG MNNREVLEQVERGYRMPQPCQDCPISLHE LMIHCWKKDPEERPTFEYLQSFLEDYFT ATEPQYQGENL |
| 3636 | 11687 | A | 4570 | 2 | 217 | ECGDVCDTGDRAVSDEEGYIWLGRSH HTINAS/GVVKALIVLTPQFLSHDKDQLI KELQQHVKSVTAPCIGC |
| 3637 | 11688 | A | 4571 | 1 | 846 | |
| 3638 | 11689 | A | 4572 | 361 | 916 | |
| 3639 | 11690 | A | 4573 | 128 | 416 | RQVLLFWGRGKYHNPFSPLYPFSAFLG EGQVPLNPFSFTLSGKSRFSRGOEP/LNPL FPHPDLLSVCPNPLFPHDPFPFAPLEGKN PRTPRTRGST |
| 3640 | 11691 | A | 4574 | 127 | 135 | NKIVLKCWGGENFWGVVWRENGRCFS GLLQAGLGAAWEPRVG/IVRRNICCIE*L VMAWIRFCMN*KTK |

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| 3641 | 11692 | A | 4575 | 35 | 386 | QLKTDTAQSPRSPLDHHGHRASGNSHSG SIHPDGLK*LKNHNRSEKPCPTLTDDIPP QKKCKWPVLALSADITL*KSFSWLILAQ KAPPLSTL*PPLLPAREQMSFDCNFPLPT QIL |
| 3642 | 11693 | A | 4576 | 148 | 336 | IRTPKIGLFNSPGSHSQSPWNSGPRLSD/ WTPSQIFSA*QLKTDAAAGSPRKPSPRT PSFR |
| 3643 | 11694 | A | 4577 | 4418 | 5130 | DTISYQLEWRSLSQSETTDQAPMSSL*NF LRSNPWLS*RLGA*/WNADEQGVPLIQE MLESWASICKVPKYPNAEAVRPEEQTPH LHPGEINSHVAHTKLWWSLHTDTHET WCRDSDRGTSLSGRSIPCPALCSVRKIHL RPQVLRPTSPRNISPISNPHTRT/SQTPEPQ RPGVPEPPSPGACYKCKQSDHQAKECL QPRIPKPCPICAGPHWKLDCAHLAATL RAPGTLAQGSL |
| 3644 | 11695 | A | 4578 | 522 | 923 | PSAAGLLEFAGGPLQTLFAWVSAEAAE QRVLLNSQ/WLLPDRSSGSFVS/GSIWPCE VSVCPSSRCWRPRRPLEAHLVQPQPT LLAPVLVLLAVCYGWSRPLAHTLFAAS RLAHHGVDRQNNLVDKAQILN |
| 3645 | 11696 | A | 4579 | 1 | 569 | MGKKQNRKTGNSKKQSTSPPPKERSSSP ATEKSWMENDELREEGFRSNYSER EDIQTKGKEVENFERNLEECITRITNTEK CLKELMELKTKARELCEECRLRS/LMRS TGRLLIKKTPFSSG*SRI*FNN*ASNSLY* NINSNKSPL*PLKGPILSKPSASNIPCISLQ WVQAFQKSESLPAPR |
| 3646 | 11697 | A | 458 | 561 | 966 | GALCAASVPRCVWSSAGVVALFEEHCA PLVWVYTYECCHYMCSALLSLSCPCPAP SERAAGLCCRLVVPCHK/GMPRLTDLSV KTKDVWEIPRESLQIKRLGNGQFGEVW MGMLRLNYSLSFPVWKIPNTKDG |
| 3647 | 11698 | A | 4580 | 23 | 660 | FIDSMPSPSRYQ*LSSQNWKLL*SSYGT KEEPASPSQS*AKRTKLEASHYLTSNYTT RLQ*LFQKHTMLSPRENLTQPACTQVK* TAMLLTQ/RPVWWSLHTDAHEIWCCDS DRGTSLSGRSIPRPPALCSVRKIHLRPQVL RPTSPMNISPILNQLSSLRLTLPDRLRSPL DHHGRRASARLHPGEINSHVAHTKPVW CSLHTDTHENDKNKQ |
| 3648 | 11699 | A | 4581 | 1 | 764 | MIQEHADKQVQRLQGVLLGSIPTAASRA RLHPGEINNHVAHTEPVWWSLHMDAYE IWCRGSDRRTSLGRSIPLPPALCSLRRIHL RPQVLRSTSPRNISPISNPGHLSDYTPTFQ GCQTMQGRLPWSFTLSGKSRFSGEGATQ RQYPIPPQALKGLMPAITRL/STAWPFA YKLSLPPHFTCPKTRQALQVSSGSAPYQ PNCFAYPHGAAPYSSILNTCLYNPLFCS RSQTSFLYYSFAPFIPASLRIHLD |
| 3649 | 11700 | A | 4582 | 1 | 400 | MWNAVTLWQQRESCIEESEIGTLETKE THFIRGPKTLAPVTDWEG/SPSLGV*SMQ GRLSDYTPTFQGFQTTQGRLPWSFTLSS KSCFS/AGRGKLLARPS*VPILPQPLLLH PTILLSPPLTPGQAYSFIP |
| 3650 | 11701 | B | 4583 | 1 | 933 | MEEKEERKRRRKRKRREERGDRGERKR MEKQKENQDPKDPPTSGPQTDQPKKH LTNFKSETKETRFIRGPKTPAPVTDWEGS LPLVFNHSRDTSLIHPGFRGVPRRDAC LGPSPLAASPTFLGKGPAAPRQTELGPNS SSASAPPYPNFFIASPPHTWSGLQFPMT SPPPPAQQFTLKKVAGAKGIVKDLNLT KVYNNRKKLQFLASTVRQTPATSPAHK NFQTPELQPPGVPEPPPRGACYKFKKS GHRAKECLQPRIPKPHPCVGPVHKSD CPHHLAATPRAPGTLAQGSLTPSQIFLA* |
| 3651 | 11702 | A | 4584 | 1 | 582 | |

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|------|-------|---|------|-----|------|--|
| 3652 | 11703 | A | 4585 | 1 | 622 | MAKSFSGSGKSVCKSPKGKNNWETRM IGDGGLOEGSLTMKFEDGKYLFGFNIEG DFCEDSNFQTGESVSDVYFENVSAQRE STGSGIAQERNDEGLESGRAVLCEIECLS ASLASTSQSSIEQPLTSSVPTKTKQNMT DIAEYPQWAIWTSKTTTTIVLRPS*VLILP QPPLLHPIIFLSPLLTPAPAYSFIPTSPS FG |
| 3653 | 11704 | B | 4586 | 102 | 1151 | MEEHFMLMGSKNQYRENGHTAQEKLL YAFHNISLKQSSLSLQNFNNENNDGS KDDDDGGDDDDDCQASEAKPNSACLHP GEINSHVAHTKPVWWSLHTDTHENDNG DVGDDNVDDDDVDDGGDDGKDDGDD DDGDTVMVMMMMMLVMVMIVVV VVVVVVVASRKAFLFLINGEESELESLT GFANIPNHHLTVQHIYTPPLPSGETKETR FICGPKTPALVTDWEGSLPLVFNPCRDAS LHQPRFKAASPAILGEGQVPLNPFSTLS GKSRSFSGEGARAYYKCRKSDHQAKECP QPRIPKLCPCAGPHWKSDCSTHLAAAP RTPGTLAQGSLTDSFLA* |
| 3654 | 11705 | A | 4587 | 258 | 479 | TAAARRSSRTSSHRSLHVPEIWPLGQG MPAARDSS*AASHLCRTTPPKIGLFNLP HSQSPWKSGLPRLSD*LLPRSSRLSS*RAL GQISRGSGSGCQVS |
| 3655 | 11706 | C | 4588 | 259 | 531 | MSPAHKNFQTPEPQRPPIPPEPPPGACY KCQKSGHQAKECLQPRIPKPRPICAGPH WKLDCPHTLASTPRAPGTLAQGSLTASQ IFLA* |
| 3656 | 11707 | A | 4589 | 1 | 446 | MNLNRNALVLTFLSDSARLHPGEINSHV AHTKPVWWSLHMDTHEIWCRRSDRGTS LGRSIPCTPVL/VLSRFKKIKACYHSPATS WPFKYKLSLQLPHFTCPKTRQALQVSS GAVPYQPNCFAYPPCGAQPVPSFVLNTF LHNSLCRA |
| 3657 | 11708 | A | 459 | 46 | 949 | ARRPRPWLSSARTPRRPFWRPSPCCSPM LTTSETLMMKNIDPSGLETQPF/YEVLQ SNIQHVLVYENPALQEALACIPVQELK RKSQEKLSRARKLDKGINISDEDFLLEL LHWFKEEFFHWNNVLCCKGGQTRSR DRSLLPSDELKWGAKEVEDHYCDACQ FSNRFPYNNPEKLETRCGPWCE |
| 3658 | 11709 | C | 4590 | 228 | 260 | MFLGLVGLRT* |
| 3659 | 11710 | A | 4591 | 268 | 390 | |
| 3660 | 11711 | A | 4592 | 1 | 499 | MAPTNCKGSRKCGRPHEQMHPYPLPLL TLFSDSARLHPGEINSRVPHTKPVWWSL HTDAYEYIWHSDWGDLPWETIPCPPA LCSMRKIHLRPQVLRPTSPRNISPISNPEK *NGLKVF*KHTSPSSATNLKRPQGYFYH FPFSEFRPVLGMLQVTSFAQKFLL |
| 3661 | 11712 | A | 4593 | 1 | 355 | MEVYTQKAYWRVPLGSTVGDDGGHGR FIHPFAIKIEQGSTNRCPSGSPATKYVLLC LHGEKVDLLPADQQSIFSPGRSTQGHLSI TGVLMNRHSTYMDKEKVKMVTALWTD EELSKLTWTRMKFDAMTQLGDLPWEN PLSSCSLLREKDPPTSGPQTDQPKHELT NFKSTTNHAPLTIPLKPNHSYPAECQYPV POHALKGLKSIITRLLQHGLLKPINCPYN SPILPVLKPKAYRLLQDLRLINQIVLSIH PVLKPNILLSSIPPSTTHYSVLDLKHAF TIPLHLSSQPLFAFTWDPDTHQAQITW AVLPQGFTDSPHYFNQAQISSSVTYLGII LMKTHVLSLLIVSG*ESIWWQHGVDRQ NNLVDKAQILK |
| 3662 | 11713 | A | 4594 | 260 | 487 | AQACMYTSRWPEATEEPQKK*KWLVPA LTDDITL*HSFSGTVSLRSSPLSTL*PPPLP AREQPPLTVIFHHLPKS |

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|------|-------|---|------|------|------|---|
| 3663 | 11714 | A | 4595 | 1 | 508 | MNMNIKKIVKQATVLTFTTALLAGGAT QAFKENNQKAYKETYGVSHITRHDML QIPKQQQNEKYQVPQFDQSTIKNIESAKG LDVWDSWPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKTA/PSPGQ A/TVPILQPPLLHPHLLSPPLTPSPAYSF VP |
| 3664 | 11715 | A | 4596 | 1 | 1246 | MGKGRRSLWLLPADGGSSGNGNELQGT SPHDYFSIAIKSTHIGLEYPTSRQSNRVSP QSKRIRQPLGLPSGSITERGPPNNRQKGY TRQQFCHESTPNKGDRVIYNLTCLLYCC VRFLAGTGPHILYLSRLASNLELFKRD GRGEQRKEEVTCFHKLLAEKENNPPFSFI YPNPIKRPHPYLPSLTLFSDSAHLHPGEIN SFMAHTKPVWWSLHTDAHEIWCRRSDR GTSLSRSLRPPALCSMRKIHLRPQVLR SPRNISPISNPHALKGLKPVITRLLQHGLL KPINSYPNSPILPVLPKDPKYKLVQDLCLI NQIVLPIHPMMPNPYTLSSIPP/CHNPLF CSGSQTCFLYYSFVPVIPASLRFHLD*P*H SS/WFSKLPGLYCRKASQTAPITSVKPKF HPHLLPISA |
| 3665 | 11716 | A | 4597 | 182 | 750 | KWPYCPSSAGQQTQLCSSSTNSNNCLPY RGTSLSGRSIPCPPALCSMRK/MPPTSGP QTDQPKKHLTISNPVAEAKGIVKVNAPF SLSD\PPKIS*RLGSFSSNHPYLGQRQYPI QQALKGLKPVITCLLQHVLKPVNSPYN SPILPVQKLDMPYRLVQDLCLINQIVLPI HAMVNPETFIPLTVLNP |
| 3666 | 11717 | A | 4598 | 3 | 504 | KRPHPYLPLLTLFSDSAHLHPGEINNHA HTRPVWWSLHTDVHEIWCRRSDQGTFF WEINPPSSCSLLREKDPPTTSGPQTDQTK KHLTNFKSGKRPLFTPSPTSLTIPQPLSPF NLGATLQSLPSLNFSHFVLVFTKETCFI HEPKTPAPVTDWEGSLPLVFNHC |
| 3667 | 11718 | A | 4599 | 1 | 1032 | |
| 3668 | 11719 | A | 46 | 105 | 328 | RDLHMKTITSKVY*LTWH*SGSVGRDYE LHENPLVGPNIKLGDVFDISHPNDEYSPL LLQVKSLKEDLQKETIS |
| 3669 | 11720 | A | 460 | 3 | 284 | |
| 3670 | 11721 | A | 4600 | 72 | 724 | FQIAGKWHFQFFHPTRSK*FLS*N*QMV* GA*CPGILLHISPLVSVSATRPKSSFFPS HLSPQYQPVSLSLNLPFLQTHVTS AFL PRLLARPS*VPS/RSSASA/LSTLQSLYHL PSSHLVRLTVSFRDYPSTCPAIIYS*KGG WSQRHSQG*CSF/SLYPKSDSV*ALFHQI* KSSPVHGSFGSNPKTLSPSP*KVKRPSY SQYTFYYPICSRH |
| 3671 | 11722 | A | 4601 | 2009 | 3197 | |
| 3672 | 11723 | A | 4602 | 3948 | 5007 | VLQTFAVSVTAHKGGTTPRVVCSQWVR GLADFRNEAADPHDQGMENPTDFLER LRGALVKHMSLSPDLVEGQILKDKFIT QAAPDIERKLQKQNGPSLRDIFFSPQNGY NWRMASFYLPVANKWKILKSLYQILHL GPDWEGPYTVFLSTPMAVEVTGIDSWIH YTQVKA WKADGATSVNPEEHPKYQGEI NSHVAHRKPVWWSLHTDVNEIWCRRSD RGTSLGKS/HPRSSCVLCVRKIHLRPQV LRPTSPRNISPILNQELATRA/VKSGH*AK ECLQPGIPIKPHLICVGP*KSDCS/TPSGS HSQSPWNSGPRLSD/WTPSQIFSA*RLKT DTARSPQKPPRPSRMPFSR |
| 3673 | 11724 | A | 4603 | 567 | 678 | |
| 3674 | 11725 | A | 4604 | 1 | 305 | |
| 3675 | 11726 | A | 4605 | 3474 | 3657 | |
| 3676 | 11727 | A | 4606 | 796 | 937 | |
| 3677 | 11728 | A | 4609 | 664 | 1059 | |
| 3678 | 11729 | A | 461 | 420 | 690 | |

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| 3679 | 11730 | A | 4610 | 775 | 944 | |
| 3680 | 11731 | A | 4611 | 279 | 416 | |
| 3681 | 11732 | A | 4612 | 36 | 4704 | |
| 3682 | 11733 | A | 4613 | 124 | 672 | |
| 3683 | 11734 | A | 4614 | 688 | 940 | |
| 3684 | 11735 | A | 4615 | 561 | 663 | |
| 3685 | 11736 | A | 4616 | 217 | 378 | |
| 3686 | 11737 | A | 4618 | 198 | 347 | |
| 3687 | 11738 | A | 4619 | 201 | 424 | |
| 3688 | 11739 | A | 462 | 557 | 753 | IIEIGIMEQRKPWKKICYFICCASHAKGSL /CRRMKRAPVYYGRTVPSPDGSIHGEY HVLLELNT |
| 3689 | 11740 | A | 4621 | 305 | 440 | |
| 3690 | 11741 | A | 4622 | 936 | 1380 | |
| 3691 | 11742 | A | 4623 | 9 | 1230 | |
| 3692 | 11743 | A | 4625 | 942 | 1293 | |
| 3693 | 11744 | A | 4626 | 40 | 154 | RCWLCPHALFLWLASHLCHFYTFCVQ AEC*VMPPHPL |
| 3694 | 11745 | A | 4627 | 4 | 436 | |
| 3695 | 11746 | A | 4628 | 465 | 748 | |
| 3696 | 11747 | A | 4629 | 92 | 393 | WPRSGPLRLLRTVCCCVLPLLSHSKLHKI SVSAPGP**QIPPPFQNRSFCDTERG*GG ETPLVPGKFSSPHQTL*GTSSGRTGSAG QLPLLYLSYKTR |
| 3697 | 11748 | C | 463 | 137 | 274 | MRKQLLLPQKKRRVYLLRITKKVEMIPQ DNENPGNTNCHDVVLVQ* |
| 3698 | 11749 | A | 4630 | 1 | 1614 | |
| 3699 | 11750 | A | 4631 | 1 | 410 | KGKVKEAAQRYQYALKKFPREGFGEDL KTFRELKVSLLLNLRCRRKMNNSSSC VHILSSRQFAAALEDLNEAIKLCPPNNREI QRLLLRVEEECRQMPPPPPPPPPPQ QLPEEAPEP*RT*TRPSSCVPTTVRSRDF C*EWKKSVD/TMQPPQPPPPPPPPQQL PEEAPEPQHEDIYSVDIFEE |
| 3700 | 11751 | A | 4632 | 1 | 972 | |
| 3701 | 11752 | A | 4633 | 196 | 390 | |
| 3702 | 11753 | A | 4634 | 2 | 4417 | |
| 3703 | 11754 | A | 4635 | 158 | 358 | |
| 3704 | 11755 | A | 4636 | 4 | 152 | |
| 3705 | 11756 | A | 4637 | 382 | 458 | |
| 3706 | 11757 | A | 4638 | 46 | 314 | |
| 3707 | 11758 | A | 4639 | 46 | 271 | |
| 3708 | 11759 | A | 464 | 1 | 2155 | MKKKKMKEEEEKEKKEEEEEEEERR KEEDDFCNRTSPAGGSEGPQGESEQPAQ PPEQAGGRPGASPAPDEDAEAAGAEQG GDSTEATAKPKRSFYAARDLYKYRHQY PWKLSQFHSSVSHRRKEIDCKAFKWQDL AFFGELTRGKRSQHNYLRITRILKSLGEL GYESFKSPLVKFILHEALVENTIPNIKQSA LEYFVYTIRDRERRRKLRFQKHYP ENFIWGPPRKEQSEGSKAQKMSSPLASS HNSQTSMHKKAKDSKNSSSAVHLNSKT AEDKKVAPKEPVEETDRPSPEPSNEAAK PRNTEKDSNAENMNSQPEKTVTTPTIEKK ESVSPENNEEGGNDNQDNENPGNTNCH DVVLPRSPAPAAASSMGNLLGGVSFREP TTVEDCDSTWQTDSEPEPEEPGPGGSE GPGQGESEQPAQPPEQAGGRPGASPAPDE DAEAAGAEQGGDSTEATAKPKRSFYAA RDLYKYRHQYPQNFDIRYQNDLSNLR YKNKIPFKPDGVYIEEVLKWKGDYEKL EHNHTYILWLPLTEQGLNIFYAKELTTY EIDESSKTKEAIRFPWAYKNDARIFWN KT/GLIKLGMFARGVYWQESFQHLNESQ HNYLRITRILKSLGELGNEFSKPLVKFIL |

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| | | | | | HEALVGGILFPILRQSALAEYFVYTIRRTG RRKGRKA/LCGFAP/WKHYTAFQGNFIW GDPPSEKEQFGGGGQRPREM |
| 3709 | 11760 | A | 4640 | 1 | 1815 |
| 3710 | 11761 | A | 4641 | 1 | 1284 |
| 3711 | 11762 | A | 4642 | 1 | 1650 |
| 3712 | 11763 | A | 4643 | 1 | 1605 |
| 3713 | 11764 | A | 4644 | 303 | 410 |
| 3714 | 11765 | A | 4645 | 92 | 395 HHHSKLTVTLSPPFPCKPLPPMKAKLV EERKRNARG*SAKRRKMRQRSQVNPSPF VAPVEATQEHETWNAQTLGMLGTSCGT ACYCLELVSMGSRTSSAL |
| 3715 | 11766 | A | 4646 | 362 | 497 |
| 3716 | 11767 | A | 4647 | 609 | 701 |
| 3717 | 11768 | A | 4648 | 1 | 104 TYV*PSVFKVN*HPT*SSS*HRKDQTDIL NAINQ |
| 3718 | 11769 | A | 4649 | 1 | 1398 |
| 3719 | 11770 | A | 465 | 226 | 486 NWKTKIITSMLCWGNASFGQLGLGGIDE EIVLEPRKSDFINKRVRDVGCLRHTVF VLDDGTVYTCGCNDLGQLGHEKSRRKP EF |
| 3720 | 11771 | A | 4650 | 1 | 1149 |
| 3721 | 11772 | A | 4651 | 3 | 242 |
| 3722 | 11773 | A | 4652 | 213 | 658 EGPARHRLSPVRASKMTKKRRNNGRA/ KKGRAPRQGTAPLKIFPSGPLPPNCARCV P/RRDKAIKKFRHSET*WEAAAVRDLSE ASVFDAYLALPKLYVKLHYCVSCAIHK QK*SGNRSS*SPAKTRTPPPRFRPAGCW PHGPPTKSP |
| 3723 | 11774 | A | 4653 | 161 | 295 |
| 3724 | 11775 | A | 4655 | 355 | 476 |
| 3725 | 11776 | A | 4656 | 662 | 979 |
| 3726 | 11777 | A | 4657 | 960 | 1387 |
| 3727 | 11778 | A | 4658 | 696 | 996 |
| 3728 | 11779 | A | 4659 | 240 | 461 |
| 3729 | 11780 | A | 466 | 674 | 1026 LWAEGTLVWGSIREWLQHTPPNGIRDW AKQRMWRTGQPQAPTRVNISRPSPTPF PRFTTKLMWALGTDPTHTHTSHSFAH IHSCTHA/HVQEHTYTYSLPHTSRPFLKG SKSTPKP |
| 3730 | 11781 | A | 4660 | 2939 | 3295 |
| 3731 | 11782 | A | 4661 | 44 | 319 |
| 3732 | 11783 | A | 4662 | 2 | 896 |
| 3733 | 11784 | A | 4663 | 68 | 438 |
| 3734 | 11785 | C | 4664 | 208 | 345 MSPDRNIECKATGFTETTYDLLFCKSVD SFYQLLISSSGKSJIT* |

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|------|-------|---|------|------|------|---|
| 3735 | 11786 | A | 4665 | 1 | 320 | |
| 3736 | 11787 | B | 4668 | 1 | 651 | MQKEDCVIVLVKLAVEGMAPTQQIHLF VAITFSGWPRQCTGSSFKAIDFLDPDSV MQQIYSFHFHGMCFDNHAFQNLMAVID NIKQDRDMDEAGSHHSQQTNTGTGNQT PHVLTHKWELSNENTWTQGGEHHTPGP WVLGLADFKNEVVDPHGVKPKQFTFVS TALKDDVSGIHSFLLVGSWSANFRNEAA EPSALFTIAKIWINLSIHQQMNG* |
| 3737 | 11788 | A | 4669 | 1 | 112 | |
| 3738 | 11789 | A | 467 | 153 | 380 | PRSWGQDTPSRGERSPNSSGTPGLPPPG GHPFSPQVPRPQLLPPTDLGPGGGQAG IQGVPSPGPTQDGANSRL |
| 3739 | 11790 | A | 4670 | 474 | 616 | |
| 3740 | 11791 | A | 4671 | 197 | 334 | |
| 3741 | 11792 | B | 4672 | 82 | 402 | MGLEKLHPFDAGKWGKVINFLKEEKL DSMLVEAREASEEDLLVVHTRRYLNELK RKVLRPLRTQTGGTIMAGKLAVERGWAI NVEAIXRKVELEWGTEDDEYLDK* |
| 3742 | 11793 | A | 4673 | 1 | 1524 | |
| 3743 | 11794 | A | 4674 | 39 | 786 | |
| 3744 | 11795 | A | 4675 | 434 | 1333 | |
| 3745 | 11796 | A | 4676 | 772 | 1107 | |
| 3746 | 11797 | A | 4677 | 282 | 377 | |
| 3747 | 11798 | A | 4678 | 233 | 459 | |
| 3748 | 11799 | A | 4679 | 761 | 962 | |
| 3749 | 11800 | A | 468 | 140 | 754 | TAMSSEEGKLFVGGNLNFTDEQALEDH HFSSFGPISEVVVVKDRGTSSGPGGFGFI TFTNPEACFKLPMKKPMNRRSLEWSVR SRCWIMQAKSASGEPEGGLLAGHWGL GSQLTFFKKVVGPGGLIGELSFAMRAMN GESLDGRQIRVDHAGKSARGTRGGGFG AHGRGRSYRGGGDQGYGSGRYYDSR PRGYRYRY\GRSRD |
| 3750 | 11801 | A | 4680 | 3 | 190 | |
| 3751 | 11802 | A | 4681 | 150 | 338 | |
| 3752 | 11803 | A | 4682 | 168 | 375 | |
| 3753 | 11804 | C | 4683 | 55 | 444 | |
| 3754 | 11805 | A | 4684 | 64 | 322 | |
| 3755 | 11806 | A | 4685 | 2 | 38 | |
| 3756 | 11807 | A | 4686 | 185 | 451 | SQHFRPRQVDHLRLGVGDQLDQHGET PSLLKIQNWPGVVAHACNPSSYSGG*GRR I/RLTLGGGGCGELRSCHCTPALATRAKL RLKKKK |
| 3757 | 11808 | A | 4687 | 344 | 468 | |
| 3758 | 11809 | A | 4688 | 204 | 286 | |
| 3759 | 11810 | A | 4689 | 206 | 395 | TFCLVFFQFSYNFQLVPVFNTALVC*RH* LIAFLNLRH*F*YKYISYIFVKL*QNQISK WF |
| 3760 | 11811 | A | 469 | 2 | 259 | GGNDLAFPH/HENEIAQCEVFHQCEQWG NYFLHSGHLHAKGKEEKMSKSLKNYITI KPSTTVTAPCSKLSSCSWGWALSWRTH VPT |
| 3761 | 11812 | A | 4690 | 2112 | 2221 | |
| 3762 | 11813 | A | 4691 | 116 | 382 | |
| 3763 | 11814 | A | 4692 | 11 | 666 | |
| 3764 | 11815 | A | 4693 | 47 | 241 | |
| 3765 | 11816 | A | 4694 | 246 | 485 | |
| 3766 | 11817 | A | 4697 | 3 | 728 | |
| 3767 | 11818 | A | 4698 | 825 | 941 | |
| 3768 | 11819 | A | 47 | 1478 | 1732 | GGQGRWITRSVQDPHGQDGEKPSLLKI QKLARHGGRRL*SQLLGRL/RQENCLNL GGGGCSEPRSHPTPAWVTEQDSVSKK KKK |

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|------|-------|---|------|------|------|---|
| 3769 | 11820 | A | 470 | 198 | 353 | |
| 3770 | 11821 | A | 4700 | 1 | 299 | MALRKNEVFEGWDGRKGVSHGEGCFSK GSNIGAYLGKSQEQQFEGNIRGNRQIIVNN ESKLKISEEDLTPRMRQRSNTLPKSFGSQ LEKEDEKKQELVDKAIKPSVEATLESIQR KLQEKRAESSRPEDIKDMTKDQIANEKV ALQKALLYYESIHGRPVTKNERQVMKPL YDRYRLVKQILSRANTIPIIVSRIPSRGWY NTFP*CPQGGCFPLASPGASSE |
| 3771 | 11822 | A | 4701 | 1 | 238 | |
| 3772 | 11823 | A | 4702 | 1082 | 1436 | |
| 3773 | 11824 | A | 4703 | 126 | 417 | |
| 3774 | 11825 | A | 4704 | 867 | 961 | |
| 3775 | 11826 | A | 4705 | 3 | 242 | |
| 3776 | 11827 | A | 471 | 103 | 483 | NTAVSTTVAGSCLASESAGAPLPSALSV GLGVPAPWNKGRSCLPGRPSTGEDLGA DFIPNPTLGLYIGWVQVPIRFLGSHVSLR PESLLTQLRLNAFVFSVSHLHAKGKEEK MSKSLKNYITIKKK |
| 3777 | 11828 | A | 4710 | 244 | 318 | |
| 3778 | 11829 | A | 4711 | 1 | 1605 | |
| 3779 | 11830 | A | 4712 | 1 | 816 | |
| 3780 | 11831 | A | 4713 | 395 | 1374 | KVTLMRWLYKG*NSGPMSV/TEEMDLAI EASEMIVLQSLHKYQPRHIVEVNDGEP EAACNASNTHIFTFOETQFIAGTAYLNAE ITQLKIDNNPFAKGFRENFESMYTSVDTS IPSPGPNCQFLGGDHYSPLPNQYPVPS RFYDPLPGQAKDVGGSSRVNREVS KDF ADFGTTIKQDFRLLGQTSVDRLLQLSQG QAVKGNQLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQLSQGQAV KGNQLLPVSLVKRKTTLAPNTQTASPR LADSLMQLARQVSRLESGQ |
| 3781 | 11832 | A | 4714 | 1 | 2109 | |
| 3782 | 11833 | A | 4715 | 251 | 623 | |
| 3783 | 11834 | A | 4716 | 36 | 69 | |
| 3784 | 11835 | A | 4717 | 328 | 441 | |
| 3785 | 11836 | A | 4719 | 560 | 688 | |
| 3786 | 11837 | A | 472 | 98 | 1339 | GLRAAQAWAPRCRPRWALGGLGGTGL RSLASAGGRGRAWLQPTGRETVQVYN SLTGRKEPLIVAHAEAAASWYSCGPTVYD HAHLGHACSYVRFDIIRILT KVFGCSIV MVMGITDVDDKIIKRANEMNISPASLAS LYEEDFKQDMAALKVLPPTVYLRVTENI PHISFIERIARGNAYSTAKGNVYFDLKS TGDKYGKLVGEVPGVPGEADSDKRHA SDFALWKAAPQEVFWASPWGPGRPG WHIECSCLASNGIWKVNLDIHSGGIDLA FPHHENEIAQCEVFHQCEQWGNFYFLHSG HLHAKGKEEKMSKSLKNYITIKDFLKT SPDVFRFFCLRSSYSAIDYSDSAMLQV SSCSWGLGSFLEDARALHGRGAAGRL RQGSDAVGEALQHQEGREGGLGR |
| 3787 | 11838 | A | 4720 | 245 | 382 | |
| 3788 | 11839 | A | 4721 | 235 | 425 | |
| 3789 | 11840 | A | 4722 | 253 | 363 | |
| 3790 | 11841 | A | 4723 | 235 | 320 | |
| 3791 | 11842 | A | 4724 | 1 | 1326 | |
| 3792 | 11843 | A | 4725 | 2 | 1502 | |

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|------|-------|---|------|------|-------|---|
| 3793 | 11844 | B | 4726 | 144 | 2704 | XHGSVVVWDLREDSRLHYSVTLSDGFW TFRTATFSTDGILTSVNHRSPLQAVEPIST SVHKKQSFVLSPFSTQEEMSGLSFHIALS DESGVLNVVVVVELPKADIAGSISDLGL MPGGRVKLWDSSTDSHAVTGLQWSPTR PAVFLVQDDTSNIYIWDLLQSDLGPAK QQVSPNRLVAMAAVGEPEKAGGSFLAL VLARASGSIDIQHLKRRWAAPEVHSCVE RKWSGHTASRVHTHSPSLLFCNPLDD WSRSFETEAPKHVVFFEPYRNVKFVKK ETSKKANDLPLSLTPREELARCLWAPPSP SVEGPMATAEVPWNESSHSSKGRREGPE PHRRRSSAEQEVQAARLQGKERKARGE HGRSIKGRENGAKQDKPRQAPPTVSFR QPSPPSRESAHSSGTRFQLGCSHTELTGG HLASLCDYLLQTPRPGVPEHRASPGSKC TRHSHSHTLGRGEGVVCTCPSATDTPQV VERESNPLDEVRRGHAGEHRLLSQSLST VGAESISSKSTGWAPLNAPVRTFLGESLG SAFSSASIALRTSVKRRHKWARPHTNGA RQPPGGKGTPPGGKEHPYEIKAPPCVSR WLSSPPPGTPSCTTVRRSWLPSALKHCC VLRREMAVCHRLSKCPANAIVKHPCEG KSPPYRALWHRSGVWTVAGTQRSFNIR AHRDQTLRNNYTILPNGNWRHGAYAG VSSFSRX* |
| 3794 | 11845 | A | 4727 | 8 | 3281 | |
| 3795 | 11846 | A | 4728 | 162 | 347 | |
| 3796 | 11847 | A | 4729 | 201 | 522 | |
| 3797 | 11848 | A | 473 | 414 | 833 | NVLVICQRNSNSFKKLFKVRDDGEQTQQ DFSALQ/AS/SQGRPELVHSRGVQGPWG HQPPWVCQNPLAKAAFTALLVLESREE ERTVTAEGAPLSFGGPHTSPSPGRDAGG SNLGTFSRSYSQRLEFLSSRKLCNINCKL S |
| 3798 | 11849 | A | 4730 | 205 | 424 | |
| 3799 | 11850 | A | 4731 | 343 | 500 | |
| 3800 | 11851 | A | 4732 | 103 | 361 | |
| 3801 | 11852 | A | 4733 | 1097 | 1298 | |
| 3802 | 11853 | A | 4734 | 874 | 1184 | |
| 3803 | 11854 | A | 4735 | 451 | 641 | |
| 3804 | 11855 | A | 4736 | 1 | 1215 | |
| 3805 | 11856 | A | 4737 | 1 | 417 | |
| 3806 | 11857 | A | 4738 | 19 | 345 | AATLGHCPSIQCWRSAGSCPRASSSGPQ ASPMWV*STDLR*MSWATSLQGWCPQ WPPTPSCSQSSWAA\HHRCGWVCHCH LTGEDLRPEARLPGGQQPGAGGPGPQ |
| 3807 | 11858 | A | 4739 | 40 | 209 | DGRCSQWSRRLQGPRVHTEGPGPAS ARLPQHPGPGCPLLCGHCVQPEPEEYFP *LPQHPGPGCPLLCGHCVQPEPEEYFP |
| 3808 | 11859 | A | 474 | 635 | 901 | PHPEPKGPKLRA\PLSPDFPPGSRLAGSP GAPPPPPHPEDRLHQGSSHPHPIRLLER SLAQGGAAPLGPPRMPHGAAPQGCSPT PT |
| 3809 | 11860 | A | 4740 | 2 | 4097 | PCPPHADCRDLWQTFSTCQPGYYGPGC VDACLLNPCQNQGSCRHLPGAPHGYTC DCVGGYFGHHCEHRMDQQCPRGWWGS PTCGPCNCDVHKGFDPNCKNTNGQCHC KEFHYPGRGSDSCLPCDCYPVGSTSRSC APHSGQCPCPRGALGRQCNSCDSFPAEV TASGCRVLYDACPKSLRSGVWWPQTKF GVLATVPCPRGALGLRGAGAAVRLCDE AQGWLEPDLFNCTSPAFRELSLLLDGLE LNKTALDTM |
| 3810 | 11861 | A | 4741 | 2 | 10321 | |
| 3811 | 11862 | A | 4742 | 157 | 273 | |

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|------|-------|---|------|------|------|--|
| 3812 | 11863 | A | 4743 | 469 | 676 | |
| 3813 | 11864 | A | 4744 | 237 | 497 | |
| 3814 | 11865 | A | 475 | 816 | 1099 | HFGEPPFFLRQSL/NSVAQAGVKWRDPS SLQPLPPGFKRFSCPSLPSSWDYRRVPPH LANFCIF/MSRRGFIMLARLAQPPQ/CDPPI SASQSARITGV |
| 3815 | 11866 | A | 4750 | 303 | 1978 | |
| 3816 | 11867 | A | 4751 | 142 | 408 | |
| 3817 | 11868 | A | 4753 | 49 | 163 | |
| 3818 | 11869 | A | 4754 | 665 | 733 | AQEP/LTWCLLPTLVPGKCEWRQV |
| 3819 | 11870 | A | 4755 | 334 | 520 | |
| 3820 | 11871 | A | 4756 | 3 | 222 | |
| 3821 | 11872 | A | 4757 | 133 | 205 | DLPQAQSNLQWPRKTS*LKPHERL |
| 3822 | 11873 | A | 4758 | 250 | 532 | |
| 3823 | 11874 | A | 4759 | 524 | 677 | |
| 3824 | 11875 | A | 476 | 3 | 232 | |
| 3825 | 11876 | A | 4760 | 110 | 1520 | |
| 3826 | 11877 | A | 4761 | 1 | 635 | |
| 3827 | 11878 | A | 4762 | 2 | 4398 | |
| 3828 | 11879 | A | 4763 | 2016 | 2227 | |
| 3829 | 11880 | A | 4764 | 1388 | 1520 | |
| 3830 | 11881 | A | 477 | 2 | 732 | FVPGAEMAASGRCLCKAVAASPPFAWR RDNTEARGGLKPEYDAGVIGAGHNLV AAAYLQRLGVNTAVFERRHVIGGA AVT EEIIPGFKFSRASYLLSLRPQIYTDLELK KHGLRLHLRNHYSFTPMRKRVQAAKVP RCLLLGTDMAIENQKQIAQFSQKDAQVF PKYEEFMHRLALAJDPLLDAAAPVDMAAF QHGSLLQKRRLSTLKPILLKAGRILGAQ LPRYYEVLTAITKVLDDQWFES |
| 3831 | 11882 | A | 4770 | 620 | 903 | |
| 3832 | 11883 | C | 4771 | 230 | 487 | MLNLASPLDKLTQNTTQNGDSSTHSS NSIHKHTSSSSSVLFPDGTLEALFVSSPKV EASPLEAXVPCSASHSCNTSSKLNRRRL* |
| 3833 | 11884 | A | 4772 | 1 | 350 | |
| 3834 | 11885 | A | 4775 | 97 | 185 | |
| 3835 | 11886 | A | 4776 | 845 | 942 | |
| 3836 | 11887 | A | 4777 | 510 | 636 | |
| 3837 | 11888 | A | 4778 | 22 | 333 | |
| 3838 | 11889 | A | 4779 | 310 | 422 | |
| 3839 | 11890 | A | 478 | 161 | 610 | GRRPSPQETPRPTSLSGAPPTPRHSRCPPN HTVSSASLSLPSRHRLFLTYRHCRNFSILL EPSCGSKDTFLLLAIKSQPGHVERRAAIR STWGRVGGWAMGRHLKTD/GSSYGWH DA/RTPTQLMAYESREFDDILQWDFTED FNLTLLKEL |
| 3840 | 11891 | A | 4780 | 1 | 140 | KIRCEGLSRDLKGE/RR/RGKGHDG/LYQ GLSTATKDTYDAFHMQUALPPR |
| 3841 | 11892 | A | 4781 | 17 | 283 | |
| 3842 | 11893 | A | 4782 | 2 | 673 | |
| 3843 | 11894 | A | 4784 | 131 | 523 | |
| 3844 | 11895 | A | 4785 | 197 | 582 | |
| 3845 | 11896 | A | 4786 | 235 | 416 | |
| 3846 | 11897 | A | 4787 | 280 | 569 | |
| 3847 | 11898 | A | 4788 | 208 | 486 | VQRHCLAGLIHHPFQKWNPKDQILDPIW RQGRSTSPRAPGRRGPGARGPAPSPAP RGVRRWRAGFRQRTPHTGPPAPTAKKT LLAGREPPR |
| 3848 | 11899 | A | 4789 | 190 | 594 | |
| 3849 | 11900 | A | 479 | 15 | 405 | GGTGAMAPW/AGGEHSRMNPLRAV\WL TLTAAFLTLQLLPPGLPGCAIFQDLI RYGKTKCGEPSRPVACRAFDVPKRYFSH LYTISFLWNDISAFW/LFLFLFLTPLFSY LRFLFHSHLASCFFHLV |

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| 3850 | 11901 | A | 4790 | 523 | 722 | |
| 3851 | 11902 | A | 4791 | 171 | 320 | QDLFSSSRQLEAFSNTCKRTQRTCTNR MYR*RYSCGGTE*GSYPTNLE |
| 3852 | 11903 | A | 4792 | 243 | 445 | |
| 3853 | 11904 | B | 4793 | 320 | 434 | XQCPLNRMAGHISSPYRSEAVVSSPGAP VRTGPSWEFGK* |
| 3854 | 11905 | A | 4794 | 146 | 609 | |
| 3855 | 11906 | A | 4795 | 874 | 1126 | |
| 3856 | 11907 | A | 4796 | 1 | 957 | |
| 3857 | 11908 | C | 4797 | 209 | 406 | MTRCGSLGPSPLQGVYMATVRRGDSVW WGTECGRDSPAVRVSLFLLCSCWGWS RGLTPWRPCGP* |
| 3858 | 11909 | C | 4798 | 133 | 237 | MFMDXXXXXXGGRFKGSLGGPKFTRAC KVKFFSL* |
| 3859 | 11910 | A | 4799 | 250 | 422 | ASAMVTSTSTPGSILMEVICTISEGLCKS MSRL*ILIWKRSVLEPSQGVFLVI |
| 3860 | 11911 | A | 48 | 1662 | 1858 | PSFLETEPCSIQARVGHDLGSLQPLPP VGSSNSPASASQVAGITGA*HHARLIFLFF VEMGCAE |
| 3861 | 11912 | C | 480 | 80 | 370 | MWAPREQLLGWAAEALPAKDSAWPWE EKPRYLGPVTFEDGAVLFTEAEWKRLSL EQRNLYQEAMLENLRNLGSLXXXXXXX XXXXLALDLNLGFWL* |
| 3862 | 11913 | C | 4800 | 33 | 158 | MRMQQPSVKPGFKDLQKCKTMPLLLM KYIVLENIGLKIFLR* |
| 3863 | 11914 | A | 4801 | 3 | 344 | AQDRLHWGQTQNNQQRGGHALVPAEV* WDHPSWQINSRFYPKEQ*KVFSTSSSSSS GGAVLKNPWGGQSLRGLARKNLFYRG PNKNLPGNFGKETLLWGGDKLGQPPSR NLRL |
| 3864 | 11915 | A | 4802 | 7 | 1268 | |
| 3865 | 11916 | A | 4803 | 65 | 376 | |
| 3866 | 11917 | A | 4805 | 64 | 1355 | |
| 3867 | 11918 | A | 4806 | 2 | 451 | AQKESRSVQRSWKLKPLIVLSPLQTGL TVQSTWSTCPVSRLVTLSQLLGVHSRSL SSRCRDEGFSDDPEATEPQGNPNPSC* GAGTAWGRMEPPAPQHFGDFPTPL*MS WC*DCVNPKTTHGPVLWPPFEAKTKQP DTLCSGAGLY |
| 3868 | 11919 | A | 4807 | 239 | 580 | ASTREVSLSGRTWPMIMVVPPTSAAWG MSLLSCTPLCFLPCRLSDR*PCSKASFSSD PRSSRRQVEVHLVKALPSPSEDAPPPPA RNSPAEASVMPQNFLISAKPNPLASL |
| 3869 | 11920 | A | 4808 | 1 | 180 | FPGLGPHPCSNCHLP*APSPPLPG*PPL SSQPLSEERGSEGRSEGVDAAHTARLAP NG |
| 3870 | 11921 | A | 4809 | 1018 | 1284 | |
| 3871 | 11922 | A | 481 | 1 | 1083 | |
| 3872 | 11923 | A | 4810 | 704 | 978 | |
| 3873 | 11924 | A | 4812 | 63 | 131 | |
| 3874 | 11925 | A | 4813 | 204 | 448 | |
| 3875 | 11926 | A | 4814 | 397 | 553 | |
| 3876 | 11927 | A | 4815 | 361 | 764 | RSKYAASKPALAIWDHHPGNLVRISAVH *RHTWFKLLFNVIITVFSSHFFNLFLLF CLFFIHHFFDQPGHCHLCVTPATCVRHL GIMRKSC |
| 3877 | 11928 | A | 4816 | 137 | 262 | |
| 3878 | 11929 | A | 4817 | 265 | 394 | |
| 3879 | 11930 | A | 4818 | 1817 | 2233 | RITFQERLQARSRREVGSRPKTARQVC RLPAAAAKSPLARSACFRCLQKVTEE RECGRITGSP*TSSFTKTLRTITPFTSHKR RVGHQSNQPPEPDSNDRTLPEPECGCW SESWAPPHFASSNRGLPGSESME |
| 3880 | 11931 | A | 4819 | 569 | 950 | |

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|------|-------|---|------|------|------|---|
| 3881 | 11932 | A | 482 | 3 | 503 | TGTPVSTISWCCYLVCLLLACVRAQMW APREQLLGWTAELPAKDSA WPWEEKP IYLGPUTFEDVAVLFTAEWKRLSLEQR NLYKEVMLENLRNLVSLAESKPEVHTW PFCPLGFGSQQLSODELHNHPGFGHA GNQLHPGNPCPEDQPQSQHPSDKNHRG AE |
| 3882 | 11933 | A | 4820 | 1868 | 1912 | TFVKN*DRSKHITY |
| 3883 | 11934 | A | 4821 | 1003 | 1094 | |
| 3884 | 11935 | A | 4822 | 810 | 970 | |
| 3885 | 11936 | A | 4823 | 133 | 261 | |
| 3886 | 11937 | A | 4824 | 76 | 475 | |
| 3887 | 11938 | A | 4825 | 1 | 1647 | |
| 3888 | 11939 | A | 4826 | 1 | 1459 | |
| 3889 | 11940 | A | 4827 | 456 | 705 | |
| 3890 | 11941 | A | 4828 | 417 | 791 | |
| 3891 | 11942 | A | 4829 | 553 | 734 | |
| 3892 | 11943 | A | 483 | 138 | 2125 | |
| 3893 | 11944 | A | 4830 | 246 | 346 | AFEENLLRVCKKLYSVFTQMPKMNAN VFIGAN |
| 3894 | 11945 | A | 4831 | 3 | 241 | SCERARFWAAAVAGVAATRVRRLAIT GLTMERKVLALHARKKRTKAKDKAQ RK*/RLVPQHPIILWIFLRHLLCSGFTS |
| 3895 | 11946 | A | 4832 | 195 | 266 | GVWRPLSGCNASSA*SQEPCTT |
| 3896 | 11947 | A | 4833 | 1 | 1278 | |
| 3897 | 11948 | A | 4834 | 2854 | 3176 | PVISSSVCRASPKSRIFSSQSSFTARLLGF RSL*IMSAECIYFRPRRIW*IRN*TWSSVS F*HFHNVVQICPHEMGHQIHIEFLQRPC RCKNVQQTNIHFMFHMFK |
| 3898 | 11949 | A | 4835 | 1 | 2991 | |
| 3899 | 11950 | A | 4836 | 472 | 575 | |
| 3900 | 11951 | A | 4837 | 1 | 248 | |
| 3901 | 11952 | A | 4838 | 676 | 788 | |
| 3902 | 11953 | A | 4839 | 212 | 677 | |
| 3903 | 11954 | A | 484 | 1 | 2580 | |
| 3904 | 11955 | A | 4841 | 92 | 316 | |
| 3905 | 11956 | A | 4842 | 1 | 578 | |
| 3906 | 11957 | A | 4845 | 788 | 1173 | |
| 3907 | 11958 | A | 4846 | 35 | 406 | SGTPASPCLEMDPNCSCSPVGCACAGS CKCKECKCTSCCKSECAFPANLGDGPS *SREPRALQAGAGQ*PASPNSFNT*FRIR PQIALKMGCCSCCPVGL/CAKCAQGCIC KGTSDKCSCCA |
| 3908 | 11959 | A | 4847 | 299 | 981 | |
| 3909 | 11960 | A | 4848 | 152 | 797 | |
| 3910 | 11961 | A | 4849 | 1 | 124 | |
| 3911 | 11962 | A | 485 | 1 | 687 | |
| 3912 | 11963 | A | 4850 | 2 | 719 | |
| 3913 | 11964 | A | 4851 | 98 | 263 | |
| 3914 | 11965 | A | 4852 | 741 | 965 | AHLPEFLLSPCPSLGGPRPRSHCRW*HCP RLRAAPPPA*SALCLGGCCECVAAPGRW YCWWPGDRACSPHTCAR |
| 3915 | 11966 | A | 4853 | 105 | 284 | |

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|------|-------|---|------|------|------|--|
| 3916 | 11967 | A | 4854 | 407 | 1815 | TRATRWKRTKRYTLRKTERWSPRVIMD SASR/HAPGNGLYVNYGLKALNIHGGQK LTLAEHGGAYGATADMSAKIGGEGDLAI NTVRQVSLSNQNDYQGATYVQMGTLR TDADGALGNTRELNISNAIIVDLNGSTQ TVETFTGQMGSTVLFKEGALTVNKGGIS QGELTGGGNLNVTTGGTLAIEGLNARYN ALTSISPNAEVSLENTQGEFSSKRRQTRK EIFLSRMEQILPWQNMVEVIEPFYPKAGN GRRPYPLETMLRIHCMQHWYNLSDGAM EDALYEIASMRLFARLSLDSALPDRTTIM NFRHLLAQHQLARQLFKTINRWLAEGV MMTQGTLDVATIIEAPSSTKNKEQQRDP EMHQTKKGHWPLWHEGPHCLVTTAA NEHDLNQLGNLLHGEEQFVSADAGYQG APQREELAEVDVDWLIAERP GKVPARHR LSAHGCVLYTALSRRIVALPLPV SAPP |
| 3917 | 11968 | A | 4855 | 1020 | 1352 | |
| 3918 | 11969 | A | 4856 | 491 | 628 | KTITNWRCSRWPTCFGR TK*YDWHRQ MTPPRQRAVLWTKSPKTV |
| 3919 | 11970 | A | 4857 | 1 | 1872 | MVIVPIGYAAQELFDVSQVRGGTPYGAT TIAGGDGSRQPSQEELSIARYQGEYVAG VRYRSTFYPGIS/ALSVLSHILVLYCTAGL HIGA/AIVPTRYAYCNSEFSSKRRQIRKEI FLSRMEQILPWQNMVEVIEPFYPKAGNG RRPYPLETMLRIHCMQHWYNLSDGAME DALYEIASMRLFARLSLDSALPDRTTIMN FRHLLAQHQLARQLFKTINRWLAEGV MMTQGTLMHQTKKGQWHFGMKAHIG VDAKSGLTSLVTTAANEHDLNQLGNL LHGEEQFVSADAGYQGAPQREELAEVD VDWLIAERP GKRSASCIQKLNTTMIYVT HDQTEAMTMATRIVIMKDGIVQQAER NDWHFTIGAMYEIENVEGYGEDLDGLA DPSVYFNAANGPCRIALGYHHEGPENIT RAPEEMRSFLLDAGAEYNGYAADLTRT WSAKMTNDYAQLVKDVNDEQLALIA MKAGVSYVDYHIQFHQRIAKLLRKHQII TDMSEAMVENDLTGPFMPHGIGHPLGL QVHDVAGFMQDDSGTHLAAPAKYPYLR CTRILQPGMVLTIIEPGIYFIESLLAPWREG QFSKHFNWQKIEALKPFGGIRIEDNVVIH ENNVENMTRDLKLA |
| 3920 | 11971 | A | 4858 | 1231 | 1407 | |
| 3921 | 11972 | A | 4859 | 491 | 553 | |
| 3922 | 11973 | A | 486 | 444 | 843 | EKSVYSLIFPCVFFLPSTWEKEDAVNIIQ FWLAADNFQSQLAAKKGQYDQGEAQN DAMILYDKYFSLQATHPLGFDRCCTIKKI ESNICREGGPLPNCFTTTLRQAWTMEK VTQNFKRIKLQEVLLVELNKI |
| 3923 | 11974 | A | 4860 | 3 | 278 | |
| 3924 | 11975 | A | 4861 | 2455 | 2871 | |
| 3925 | 11976 | A | 4862 | 656 | 949 | LLHRFCRWPALAPGAILRQIPKKQQRVG LHYSMSYVSWRYRVCHWTITVFCLSK TLATSYARPASISVKNTKWRCFPLPKVK TNH*NIRICLPPPR |
| 3926 | 11977 | A | 4863 | 448 | 582 | |
| 3927 | 11978 | A | 4864 | 495 | 920 | WRRRDR CASHHFAVSVTTIGSSRDPDAG SLPVHSWRRKERRSALYLHRSRSHRRT YPRRDRRRAFWFVQPRCWLAAILSGH*T GGCT*NIRSHQLGTSQTLRCVQNHRCR RCRSSDRPRLRVLSWHARKYQTPGRCSE R |
| 3928 | 11979 | A | 4865 | 1 | 2799 | |
| 3929 | 11980 | A | 4866 | 3675 | 4064 | VSSDQNRRCNRCYGR LQPGGCFSLWC QFSASKSYLSPSDL**W*/QLSPSASRLPL ASLTISSSLSCAGSASFHSRSHIPGRCTCR YLRVFGVAFWAVW**HVDFLKSQQGKS |

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| | | | | | | AKKRQIAEKGRNYTQNP |
| 3930 | 11981 | B | 4867 | 1 | 2325 | MNLMEQPAKDQYLSTQGLPVLVNSLAR YPQEALPITNYFAASELAPAVARAFNKL KTLRENARSWLLKYPEHALTGLLPAALG KAGEAQDNARAALRMLTENGHQPILLQE IARRYNQPEVTDVAVNALLALDPLDNHPT KIPTLPAFYQPSLWTRPVKANAQSLPDS ALLHLGEMLRFPQEEALYPGLLQVKDVC SADSLAGFAWDLFTAWQTAGAPSKESW AFTAEFSSKRRQTRKEIFLSRMEQILPWQ NMVEVIEFFYPKAGNGRRPYPLETMLRI HCMQHWYNLSDGAMEDALYEIASMRL FARLSLDSALPDRTTIMNFRHLEQHQL ARQLFKTINRWLAEGVMMTQGTLVDA TIEAPSSTKNKEQQRDPEMHQTKKGNQ WHFGMKAHIGVDAKSGLTHSLVTTAAN EHDNLQGNLLHGEKQFVSAMPATKEP QREELAEVDVDLLIAERP GKVKTLKQNP RKNKTAINEYMKASIRARVEHPFRIKR QFGFVKARYKGLLKNDNQLAMLFTLAN LFRVDQMIQLPTYELSSGIGAVRRQAE DGTPAINSKRVYRIMRQNALLERKPAV PPSKRAHTGRVAVKESNQRWCSDGFEE CCDNGERLRVTFALDCCDREALHWAVT TGGFNSETVQDVMLGAVERRFGNDLPSS PVEWLTONGSCYRANETRQFARMLGLE PKNTAVRSPESNGIAESFVKTIKRDYISIM PKPDGLTAAKNLAFAFEHYNEWHPHSA LGYRSPREYLRQRACNGLSDNRCLIEI* |
| 3931 | 11982 | A | 4868 | 82 | 199 | |
| 3932 | 11983 | A | 4869 | 882 | 1091 | VCHAAPPILRTTATSVPVPGAASDSGY AAQFAAYIAC*LRAAFPSGGIHTAASHPS SISPRQVVTAGS |
| 3933 | 11984 | A | 487 | 77 | 199 | SKSRPIASNKIEAIKSLPAKKPGPDGFAT EFYQTFKEEL |
| 3934 | 11985 | A | 4870 | 3 | 274 | |
| 3935 | 11986 | A | 4871 | 2888 | 3076 | KTITNWRCSRWPTCFGR TK*YHWHQL LSMVRQLMVLWSKKISSWFMGPPIIRKSI LAENSI |
| 3936 | 11987 | A | 4872 | 1 | 2043 | |
| 3937 | 11988 | A | 4873 | 222 | 513 | PEGAPRTPGPLPRAPGRTSEGAGRRGGP LGPVVTMCLPRRQLSYPDVG*AEGGLPA LDPWPGHARGSEGPRRQGGAVLAVRLG GRVYVHLHTPGGQ |
| 3938 | 11989 | A | 4874 | 20 | 161 | |

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|------|-------|---|------|------|------|--|
| 3939 | 11990 | A | 4875 | 1 | 2251 | MAGVGAGPLRAMGRQALLLLALSHRRQ GLYFHIGETEKRCFIEEIPDETMVIGNYRT QMWDKQKEVFLPSTPGLGMHVEVKDP DGKVVLSRQYGSEGRFTTSTHTPGDHQI CLHSNSTRMALFAGGKLYREERFRLTSE STNQRLVWWSIAQTVILITGIWQMRHL KSFFEAKLRVRAALLSSAMEDSEALGF EHMGLDPRLLQAVTDLGWSRPTLIQEKA IPLALEGKDLLARARTGSGKTAAYAIPM LQLLLHRKATGPVVEQAVRGLVLVPTKE LARQAQSMIQLATYCARDVRVANVSA AEDSVSQRVLMKEKPDVVVGTPSRILSH LQQDSLKLKRDSELLLVDADLLFSFGF EELKSLCHLPRIYQAFMSATFNEDV QALKELILHNPVTLKLQESQLPGPDQLQ QFQVVCETEEDKFLLYALLKLSLRGKS LLFVNTLERSYRLRLFLEQFSIPTCVLNG ELPLRSRCHISQFNQGFYDCVIATDAEV LGAPVKGKR\GAEGPKGDKASDPEAGV ARGIDFHHVSAVLNFDLPPTPEAYIHRAG R**CDGPGICMTARANNPGIVLTFVLPT QFHLGKIEELLSGENRGPILLPYQFRMEEI EGFRYRCRDAMRSVTKQAIREARLKEIK EELLHSEKLTIFYEDNPRDLQLLRHDL LHPAVVKPHLGHVPDYLESKVPEPTAQL QAQRKEIQTHSQALLRLLGLSGAEHIVE HRLTPFVDRRGSGAYCTA |
| 3940 | 11991 | A | 4876 | 2 | 2318 | |
| 3941 | 11992 | A | 4877 | 866 | 1150 | |
| 3942 | 11993 | A | 4878 | 417 | 872 | |
| 3943 | 11994 | A | 4879 | 3 | 282 | |
| 3944 | 11995 | A | 488 | 29 | 380 | SETPQAPTLPQTQGSLLGEERMEDIRLT VALFTLICCPGSDEKVFEVHVRPKKLAV EPKGSLEVNCSTTCNQPEVGGIETSLD KVFAQTEQAQWKHLLGSSNLSPTVLA HCHFH |
| 3945 | 11996 | A | 4880 | 2 | 437 | |
| 3946 | 11997 | A | 4881 | 336 | 442 | |
| 3947 | 11998 | A | 4882 | 523 | 630 | |
| 3948 | 11999 | A | 4883 | 1 | 1004 | MAPWPHENSSLAPWPDLPNTANTS GLPGVPWEAALAGALLALAVLATVGGN LLVIVAIAWTPRLQTMNVFVTSAAAD LVMGLLVVPPAATLALTGHWPLGATGC ELWTSVDVLCVTASIELCALAVDRYLA VTNPLRYGALVTKRCARTAVVLVWVVS AAVSFAPIMSQWVRVGADAEAQCHSN PRCCAFASNMPYVLLSSVSFYLPPLVM LFVYARVFWVATRQLRLRGELGRFPPE ESPPAPSRSLAP/APGYANSFNLPIYCRS PDRSAFRRLLCRCGRRLPPEPCAAARPA LFPSGVPAARSSPAQPRLCQRLDGERHL |
| 3949 | 12000 | A | 4884 | 144 | 1423 | |
| 3950 | 12001 | A | 4885 | 1309 | 1702 | |
| 3951 | 12002 | A | 4886 | 1 | 648 | |
| 3952 | 12003 | A | 4887 | 1 | 1049 | GGGGTTWPASVPPRHLACLRPAAPRLRP PSPARRAMPVAGSELPRRPLPPAAQERD AEPRPPHGELQYLQIQHILRCGVRKDD RTGTGTLVFGMQARYSLRDEFPLTTK RVFWKGVLEELLWFIKGSTNAKELSSKG VKIWDANGSRDFLDLGFSTREEGDLGP VYGFQWRHFGAEYRDMESDYSQGQVD QLQRVIDTIKTNPDRIIMCAWNPRDLP LMALPPCHALCQFYVNSELSQCLYQRS GDMGLGVFNIAASYALLTYMIAHITGLK PGDFIHTLGDHIIYLNHIEPLKIQLOREPR PFPKLRILRKS*RKLIIDFKAEDFQIEGYN PHPTIKMEMAV |
| 3953 | 12004 | A | 4888 | 437 | 851 | |

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| 3954 | 12005 | A | 4889 | 1 | 1063 | |
| 3955 | 12006 | A | 489 | 27 | 406 | |
| 3956 | 12007 | A | 4890 | 496 | 701 | |
| 3957 | 12008 | A | 4891 | 875 | 1156 | |
| 3958 | 12009 | A | 4892 | 76 | 382 | |
| 3959 | 12010 | A | 4893 | 71 | 228 | |
| 3960 | 12011 | A | 4894 | 69 | 242 | |
| 3961 | 12012 | A | 4895 | 146 | 431 | |
| 3962 | 12013 | A | 4896 | 3 | 262 | |
| 3963 | 12014 | B | 4897 | 185 | 338 | MSTTFMGRSQATGGCVQTDTPGPPTLLQ DTQQLSVVHPDIQLEVGFPGGGGX* |
| 3964 | 12015 | A | 4898 | 69 | 303 | |
| 3965 | 12016 | A | 4899 | 260 | 881 | |
| 3966 | 12017 | A | 49 | 245 | 616 | NPPN*NPPNACVKPEFENQPKLWSQRG VGGPRREGPPAQAPEGTAGRRADKL RVGWRPPPATSQAQSAHSPPLFC*SSRSR GPSSPCLEAPTPGASPST*TITPPRAWRR ACWTWPCSCPTPCG |
| 3967 | 12018 | A | 490 | 191 | 1074 | RLPEMSSFGYRTLTVLFTLACCPGASDE KVFEVHGEAKGSWAVEPKGSLEVNCS TCANQP*SGVGLGDLS*D*GFCWDEQVQ L/WKHYLGFQTFSHDVLQCHFTCSGK QESMNSN/VSALYQPPRQVILDTCPNLL GGFLGKSFHHLKLQGVPTVEPLGQP*PSF LVSVGNETLAHYETFGKAAPAPQEATATF NSTADREDGHRNFSLAVLDLMSRGGNI FHKHSAPKMLEIYEPVSDSQMVIVTVVS VLLSLFVTSVLLCFIFGQHLRQQRMGTY GVRAAWRRLPQAFRP |
| 3968 | 12019 | A | 4900 | 373 | 491 | |
| 3969 | 12020 | A | 4901 | 1 | 232 | |
| 3970 | 12021 | A | 4902 | 3 | 701 | |
| 3971 | 12022 | A | 4903 | 3 | 1622 | |
| 3972 | 12023 | A | 4904 | 26 | 168 | |
| 3973 | 12024 | A | 4905 | 258 | 484 | |
| 3974 | 12025 | A | 4906 | 1121 | 1518 | |
| 3975 | 12026 | A | 4907 | 19 | 541 | |
| 3976 | 12027 | A | 4908 | 288 | 561 | |
| 3977 | 12028 | A | 4909 | 1 | 1857 | |
| 3978 | 12029 | A | 491 | 3 | 403 | SWSGSAAALRMRPVRLMKVFVTRIPA EGANLKVISTMSVGIDHLALDEIKKRGIR VGYPDVL/TRYHRRTRSLPATYHLPV AGGHRGSEEWWTWWSKPLWLCGYGL TQSTVGIIGLGRIGQAIARRLKPGF |
| 3979 | 12030 | A | 4910 | 81 | 414 | |
| 3980 | 12031 | A | 4911 | 1 | 507 | |
| 3981 | 12032 | A | 4912 | 519 | 858 | GLSEILAIGFCPHQVQRGPKVLQSLA AQLPGPFTRLVHRRQSLHAVPKCIHAVP CSFTLFHLPQEGLRPEFLAPWGLHLKA TPVWPFANPRCCSILGAGGYFVQLTGM S |
| 3982 | 12033 | A | 4913 | 67 | 467 | |
| 3983 | 12034 | A | 4914 | 2 | 307 | |
| 3984 | 12035 | A | 4915 | 1 | 2112 | |
| 3985 | 12036 | A | 4916 | 796 | 1018 | |
| 3986 | 12037 | A | 4919 | 512 | 625 | |
| 3987 | 12038 | A | 492 | 2 | 465 | DAAGANLKVISTMSVGIDHLALDEINKR GIRVGYPDVL/TRYHRRTRSLPATYHLP PVAGGHRGSEEWWTWWSKPLWLCGY GLTQSTVGIIGLGRIGEAPTGPLARPGSHS VVCIPGTTCLKAEKTHMLSGHFACSRDIS NEGYSFVKHRQIHK |
| 3988 | 12039 | A | 4920 | 206 | 366 | |
| 3989 | 12040 | A | 4921 | 504 | 690 | |

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|------|-------|---|------|------|------|---|
| 3990 | 12041 | A | 4922 | 3 | 336 | |
| 3991 | 12042 | A | 4923 | 22 | 129 | |
| 3992 | 12043 | A | 4924 | 852 | 1364 | |
| 3993 | 12044 | A | 4925 | 1 | 897 | |
| 3994 | 12045 | B | 4926 | 449 | 2578 | MLLECEEEAVCVIMCASVKYNIRGPALIP RMKTKHRIYYITLFSIVLLGLIATGMFQF WPHSIESSNDWNVEKRSIRDVPVRLPA DSPIPERGDLSCRMHTCFDVYRCGFNPK NKIKVYIYALKKYVDDFGVSVSNTISRE YNELMAISDSDDYTTDDINRACLFVPSID VLNQNTLRIKETAQAMAQLSRWDRGTN HLLFNMLPGGPPDYNTALDVPRDRALL AGGGFSTWYRQGYDVSIPVYSPLSAEV DLPEKGPGPRQYFLLSSQVGLHPEYRED LEALQVKHGESVLVLDKCTNLSEGLSV RKRCHKHQVFDYPQVLQEATFCVVLRG ARLGQAVLSDVLQAGCVPVVIADSYILP FSEVLDWKRASVVVPEEKMSDVYSILQS IPQRQIEEMQRQARWFWEAYFQSIKAI LATLQIINDRIYPYAAISYEEWNPFAVK WGSVSNPLFLPLIPPQSQGFTAIVLTYDR VESLFRVITEVSKVPSLSKLLVVWNNQN KNPPEDSLWPKIRVPLKVVRTAENKLSN RFFPYDEIETEAVLAIDDDIIMLTSDLOF GYEVWREFPDRLVGYPGRHLWDHEM NKWKYESEWTNEVSMVLTGAIFYHKY FNYLYTYKMPGDIKNWVDAHMCEDIA MNFLVANVTGKAVIKVTPRKKFKCPECT AIDGLSLDQTHMVERSECNKFASVFGT MPLKVWEHRA* |
| 3995 | 12046 | A | 4927 | 533 | 804 | |
| 3996 | 12047 | A | 4928 | 965 | 1109 | |
| 3997 | 12048 | A | 493 | 217 | 426 | TLVNMVEADVTTTRCLIRSGIRVGYTPDV LTRYHRRTRSLPATYHLPVAGGHRGSE EVSERRPGAVAHGC |
| 3998 | 12049 | A | 4930 | 507 | 981 | CWRSTATCYQWVIKSANRCTLQVGTTR RTMDNGDERHSRICPGM*EAARSLFIPT/ CQTRH*RPVPQRLRSNTAPIRT/RPRPSV HRPTGRESMPRTPEPEPLQTPLAATKR RSTENASYSDALLRGLGKLGKDRAR RGPRSRPGSRVQTAGAAL |
| 3999 | 12050 | A | 4931 | 1121 | 1272 | |
| 4000 | 12051 | C | 4934 | 178 | 360 | MGQELRHFGTVTWPMHRKMERRXFPRE QGPGXQLLPQWRGNEKTLGSAGRQGED HRLRAE* |
| 4001 | 12052 | A | 4935 | 409 | 516 | |
| 4002 | 12053 | A | 4936 | 288 | 573 | |
| 4003 | 12054 | B | 4937 | 1 | 1152 | MGSEAGCLVRAERFQLIVERDVRSSFPS WKELSMPGFIQKQARVYVQFFLADALI LPVPRCLHSATPSTPQTDPTGPEGPHLG QSRLFLCHKEALMKRNFVPPGASPEV PKPALSFYVLGSLGGTQRKEGTGWGL PEPQGNDDNDQKVHLIFFGSSVRWFEFL HPGQVYRLIAPGPATPMLFEKDGSSCISR RPLELAGCASCLTVQDNWTLLESSQDI QDVLANKSLPESSLTDLSDKSHNVYC CFRSSTYVQVLSFPETTISIPLPHIYLAEL LQGGQSPFQATASCHIVSVFSLQLFWVC AYCTSICRQSSARVDEPMTMFLWTLCTS PSVLRPIVLSFELERKPSKIVPLGTPSRSSS FQFFAARAKGGK* |
| 4004 | 12055 | A | 4938 | 409 | 701 | KEKVKNVWLLNPLPKAQEFGYPSPLPA TLHLKLSRCKLQDH/CCCHMVIHTGH HGFSPILHQEPMGSRKYSRL |
| 4005 | 12056 | A | 4939 | 301 | 573 | |

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|------|-------|---|------|------|------|---|
| 4006 | 12057 | A | 494 | 80 | 1058 | RCSSPAGYPPRCRVALARAADCEVEQW DSDEPIPAKELERGVAGAHGLCLLSDH VDKRILDAAGANLKVISTMSVGIDHLAL DEIKKRGRIVGYTPDVLTRYHRRTRSLPC SYHLA\PLAGGL\QGSEEW\WTSWK LWLCGYGLTQSTVGHGLGRIGPGPLLGV LKPFQVQRFL\YTGRQPRSEEA\EFQAE FVSTPELAAQSDFIVVACSLTPATEGLC NKDFFQKMKETA\VFNISRGDVVNQDDL YQALASGKIAAAGLDVTSPEPL\PTNHP LLTLKNCVILPHIGSATHRTRNTMSLLAA NNLLAGLRGEPMPSELKL |
| 4007 | 12058 | A | 4941 | 339 | 494 | |
| 4008 | 12059 | A | 4942 | 408 | 546 | |
| 4009 | 12060 | A | 4943 | 1421 | 1581 | |
| 4010 | 12061 | A | 4944 | 1 | 1113 | MHQEDLRAWYLDLGLPSHQNAQPTAW KCQRAPSPYTHQDMALIPSPARWLSPE KEPKQGEVGEKSLLPDPTLPLTDPRLTGS TEQAHAEGLAALMSALRVSHLQGRGGV VTLVDSQLGVIAVSSTQFNKGPSYRLLA DVQNRLLPKYDSQKEAELRSWIKGFTGL SIRPDFQKGLKDGILCTLVNKLQPGSVP KINASV*NWH*LENLSNFLKAMVSYGM /NPVDLFEANNLFESGNNMQVRVSLAL AGKAKTKGLRSGVDIRDKYSEKQNFDD TTMKASQCVIRLQITNKCASQSGMTAYG TRRHLYDPKNRILPPMDNSTISLQMGTN KCASQVGMTAPGTQRHIYDTKLGDICE NSSMSLKMGT |
| 4011 | 12062 | A | 4945 | 272 | 902 | |
| 4012 | 12063 | A | 4946 | 281 | 470 | TGWSWQCTPSC*TTMCVYTFMTYTWAW GCPNHNHVQPHA*PVSPTVLLNVGFRKA VFSGHGYL |
| 4013 | 12064 | A | 4947 | 1192 | 2248 | APSKKLRSATLRRPGSSKDTARGPVSVG WCPSQEPLGARCATSCPWLRLPSSVFS PRALAJRLGGGSGSLAGCAARLQGSVP CWPLARLRSASATPLSELRQQPAPPPRC DPGSRLSVPVAPCPAPRAPQPRRLSPGP RFCRCPSLSVCRSLG/PVSPPPQFLPPCLP RWLARSLALGRGETASQANPRNLCKKL AMKFKKFFDFGAIFEWSQSFPLSPRPVRF PLEPEGSPVPASLPERPSRHPASSGRLO DPGLILCSLCHYLFIRTDYAVVTRAGNG GECVWLQKFPVKLASLMSFGLYIGHF LGVPPANPQEA\PRTRSFTPKSVMESAV PGTAERVLHPG |
| 4014 | 12065 | A | 4948 | 654 | 730 | |
| 4015 | 12066 | A | 4949 | 1574 | 1881 | |
| 4016 | 12067 | A | 495 | 3485 | 4056 | DLPSRHRVMEACHVCCVRRGCCV/CAC /ICVCHMCSVWCVRVLCVPQVLCVVH ALCV\CVCLQCARYVWCMCCVCSVLC MRCV/CVCVPRVLCV\CVCCGCSRCSVW CVCCVCRV/CLCV/CACAVWCVCMC/L CVLCV/CACACVCCVCRVCSVWCVRV/ CVCCACSVWCVLWCVC/VCMQVCVY WCMCCVCCVLE |
| 4017 | 12068 | A | 4950 | 207 | 315 | |
| 4018 | 12069 | B | 4951 | 199 | 420 | MSLPIGIYRRAVSYYDDTLEDPA\MTPPPS DMGSVPWKPVIPERKYQHLAKVEEGEA SLPSPAMTLSSAIDSVDK* |
| 4019 | 12070 | A | 4952 | 336 | 594 | |
| 4020 | 12071 | A | 4953 | 401 | 1301 | |
| 4021 | 12072 | A | 4954 | 388 | 681 | |
| 4022 | 12073 | A | 4955 | 272 | 452 | |
| 4023 | 12074 | A | 4956 | 256 | 381 | |
| 4024 | 12075 | A | 4957 | 58 | 301 | |
| 4025 | 12076 | A | 4958 | 562 | 1221 | |

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|------|-------|---|------|------|------|--|
| 4026 | 12077 | A | 4959 | 152 | 358 | |
| 4027 | 12078 | A | 496 | 1 | 858 | |
| 4028 | 12079 | A | 4960 | 184 | 361 | |
| 4029 | 12080 | A | 4961 | 2017 | 2406 | |
| 4030 | 12081 | A | 4968 | 1 | 396 | |
| 4031 | 12082 | A | 4969 | 67 | 180 | |
| 4032 | 12083 | A | 497 | 106 | 542 | GATLGGMSEHVEPAA\PGPGPNGGGGGP AP\ARGPRHPQFSTPTPLINVRDRLFHAIL FFKMAVITYSRLFPAPFRRLFEEFVLLK ALFVLFVLAYIHIVFSR\SPINCLEHVRD KWPREGNPALWKVRHNSSRAPVFLQ\FC DISGGR |
| 4033 | 12084 | A | 4970 | 2 | 415 | |
| 4034 | 12085 | A | 4971 | 1090 | 1203 | |
| 4035 | 12086 | A | 4972 | 3 | 356 | VQNRTLHFSLLYEPKRKSKPESYLYCYKI FQDEPLAP*AFL*IPASLSQIQ*FTSRKGGK ASQNLIIYVIKYSKMSLWPPEPSCKYLPP CLKSNSSQLSWLLWCVLVWGVGWKYC QGWGGPPLHLVSLWGGYSASRWEDIGK QHTSLRGVPKGVIFIIYI |
| 4036 | 12087 | B | 4973 | 148 | 305 | MDNSASVEQLQETLLRALRALVLKNRPL DTSRFTKLLLKLPCGPFISLGHN* |
| 4037 | 12088 | A | 4974 | 484 | 927 | |
| 4038 | 12089 | A | 4975 | 2053 | 2615 | RGCPFGGRKAPFGLLFNVKDQTMFLSR TTYSLQELGAMGMGDLLSAMFDFSEKL NSLALTEEELGLFTAIVLLVSADR\SGME NSASVEQLQETLLRALRALVLKNRPLE TSRFTLLLKLPLDLRTLNNMHSEKLLVLS GWTAPVTPPRAGLSAGCPLCTESELCTS LSFYETEKEKQTRILFILL |
| 4039 | 12090 | A | 4976 | 173 | 520 | |
| 4040 | 12091 | A | 4977 | 44 | 213 | |
| 4041 | 12092 | A | 4978 | 840 | 980 | |
| 4042 | 12093 | A | 4979 | 72 | 464 | |
| 4043 | 12094 | A | 498 | 309 | 586 | NKNLEISFFFETESRCCQPR\AECNGAISV HCNLC\PGSSNSPTS\ASQVAEMTGVC HAQLIFVFLVAMVFHLH/VGQGGLELLT SGGPPASASQ |
| 4044 | 12095 | A | 4980 | 1 | 132 | |
| 4045 | 12096 | A | 4981 | 99 | 212 | |
| 4046 | 12097 | A | 4982 | 84 | 196 | |
| 4047 | 12098 | A | 4983 | 2 | 186 | |
| 4048 | 12099 | A | 4984 | 87 | 347 | SLNFHIGQ*AOPHAGFGLRGS*GPCPPCC QANAC*APEPNDSMEDQAPGVRHPPLSN VKIQGSE |
| 4049 | 12100 | A | 4985 | 176 | 1554 | |
| 4050 | 12101 | A | 4986 | 1 | 1863 | |
| 4051 | 12102 | A | 4987 | 1171 | 2784 | |
| 4052 | 12103 | A | 4988 | 176 | 464 | |
| 4053 | 12104 | A | 499 | 3 | 451 | |
| 4054 | 12105 | A | 4990 | 7 | 394 | HHELQYPIRFCPIKSCCKGRNSLQNKIYD LSLQNFPPATLRQNLALSPRLECSGTISAP CNLHLP\GSSDSPASASRVVAGNAGMHCH KQLIFVFLVETGFHHVAQAQLRTP*PCG SGPPRGPKSAGDLQ |

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|------|-------|---|------|------|------|---|
| 4055 | 12106 | A | 4991 | 1 | 2201 | MTNLMAMVERDSEAGTAASRFPGNHAAK GKAQAHYKVVWRPAEVRCLKLGPWVT LRYTIKHPYKLCGKRQHVFFTSRSDV GFMLTTLKPFGSVSVESKMNNKAGSFF WNLRFSTLSTSRMTMLCCLGLCKPKI VHSNWNILNMFHNRMQSTDIIRYLFQDA FIFKSDVGFQTKGISTLTALRIERLLYAKR LFFDSKQSLVPVDKSDDELKKVNLNHEV SNEDVLTKETKPNRISSRKLSEECNSLSD VLDAFSKAPTFPSSNYFTAMWTIAKRLS DDQKRFEKRLMFSHPAFNQLCEHMMRE AKIMQYKYLLFSLHAIVKLGIPQNTILVQ TLRVTQERINECDEICLSVLSTVLEAME PCKNVHVLRTGFRILVDQQVWKIEDVFT LQVVMKCGKDAPIALKRKLKALREL DRFSVLNSQHMFEVLAAMNHRSLILLDE CSKVVDNIHGCPLRIMINILQSKDLQY HNLDLFKGLADYVAATFDIWKFRKVLFI LILFENLGFPRVGLMDLFMKRIVEDPESL NMKNILSILHTYSSLNHVYKQCNKEQFV EVMASALTGYLHTISSVNLDAVYSFCL MNYFPLAPFNQLLQKDISELLTSDDMK NAYKLHTLDTCLKLDDTVYLRDIALSLP QLPRELPSSHTNAKVAEVLSSLGGEGH FSKDVHLPNHYHIDFEIRMDTNRNQVL PLSLDVGTTSATDIQRLTYISFAGLSEL KS |
| 4056 | 12107 | A | 4992 | 3 | 485 | LHTLDTCLKLDDTVYLRDIALSLPQLPRE LPSSHTNAKGGQRS*AALLGGEGTPPSK DVHLAPHNYHIDFEIQNGTPNRNPSAYP LSDVDTTSCQLQFKE*LCYVFPRSAyclG SSHPRGFLAMKMRHLNAMGFHVILVNN WEDGQTRDGRCQSPFLKT |
| 4057 | 12108 | A | 4993 | 40 | 131 | ATKAFEENEVYKTTLVVYCFKCVILKA SL*FRILLTEWFYMRWLKKYHIVCF/PLG DAKIFCFMYITVLFKTLSDSC*TLVVYCF FKCVILKASL |
| 4058 | 12109 | A | 4994 | 2437 | 2762 | GIILFWAQLFPASFFFFF*DGVSLLCCPG WSAVVRSQLTASSASRVQAILCLSLPSS WDYRHLPPCLANFFVFL/CRDGGFTMLA RLVLNS*AS*VHPPWPPQSAGDY |
| 4059 | 12110 | A | 4995 | 1 | 299 | FSLIKISMMLLMKMEK*NLQFIW/KPRRL QIAKARLNASSSSSSSSSSSSSSSVVW YWHKKRHIDHWNRLSNSNINRHICSQLI LTKVPGANTKDHP |
| 4060 | 12111 | A | 4996 | 3 | 358 | |
| 4061 | 12112 | A | 4997 | 76 | 386 | VLPPSSPALHSPAPPSTCPYLPGA/PPPLL PPCAGRSPPAAAAPHCPAPCAPRH*GSR* LESPAPQGPQSRAARMPAWPLPAPPTD PTAPPAPRSHWPAAPPT |
| 4062 | 12113 | A | 4998 | 66 | 381 | VLPPSSPALHSPAPPSTCPYLPALPPL/EP GPSRRPPRTFIGNPGGQGPGEVSPVILRS PSQPH*PGNQGPCPSSQPPGSPRSEHGC* HRCWALYGOQEKAPPS |
| 4063 | 12114 | C | 4999 | 36 | 236 | MGPTIPDXSFFWRKPITWMPTWEGTSN VGPQPLSSSKSLHSXRGHPAPIPTGQAGP RDSGPGASP* |

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| 4064 | 12115 | A | 5 | 105 | 1711 | VESNTGRKWTEAAGTGDIQCLAWGSSG DGRGGDPRGRVPAALGAAVVAAMAS PDPWAPGPKQPG/LMGRPGSSPALWAQ/ PA*PPY/FPGLTPPCQEVQSFPPG/EQG RVLRGGQNV*TEGGRVPQVCGRRPPCPS LMEPFVYTPASPFPSGQPGTTPGRRQDG EPRLGTGGQTGSPGPGLVSGPRGRAAKP GGTQGGVLRQVPPGEHPTPGEARI*HLG WVGCP*RMGQGNFGVASKPFLDL/PGPM LGSTNCDNLGSFGLS/GPMFPKWPTSTGR LPKGPSAN*GG/PGMERPPGVMPSS/GHQ DPEASGPLDLLVRAALQGG*ALGHKIGG AS*TSQKAESLPQPLGPPGGGCGITQNP LASGPKQWMSMGRPGSFPALWAQNRLT FLTTPRPSPPCQEVQSFPPGSPQGAER RARLSRERGGFLKVCGRPPCPSMMEP SCLHTC*PLSLPASLRQAKEPPSCGLRAP S*HLRRPCLTPPFRPQGLLGTSHCPQKPA PDSGLLHSPNSPRGFSGQCNPRLHPQL NPSNRDR |
| 4065 | 12116 | A | 50 | 96 | 547 | ADPAAPVPWFGPSQPGARAQWPGLLGP AAPPALCSP*TD SGVQDPVSNAPWVN SQQWWRQ/PAATEKPPATKAPGLLVQEK YKVS*QKGW/PSTKKAKGYFP*NCPL QFLPPLSLPPGDISGQCPLPKLIPPS YPAPCPGFCPR |
| 4066 | 12117 | A | 500 | 2 | 493 | GLEFGTSHRLRENPPMVAVSCPTKTNVK GPPGGKVGAGAGYEGSEALERMFLSFP TVTKTYFPHFDLASHGFAQVKGATAKKV A'DALTKAVANVDDMPNGAVRPEATL HAHKLREVPVNFKLLKPLACLVDPGA HLPGRVSLAVARLPWNKVSFAFCGQI |
| 4067 | 12118 | C | 5000 | 231 | 521 | MRAPVCQSQSVYFTQTISLKPTITVPGRC DAFQVITNNKLAQATQSEGVAGASNPDL ESHEPAHGMQREFSGVTAVSQADTVMN YPVSNWENRGSG* |
| 4068 | 12119 | A | 5001 | 46 | 1438 | LSTPTALVWPGHRPP*PIP*WPLCPQEGG PGGLPRGWSSGTVP*S*AGGCEGKIQS YPQGSASWSEPAPSPS/PAFPAPFLMLNC SGPLALSLSGPKWAREQL*CVPPRALAT GLPLEVWL*LRPFWP*CLPPG/PWVQL LHSLSSCWGPPMPRTIRGIPPGSICRLCF CPAAGLPPWWLSSGQLPHPPGTPLCSVS *GGPDQPLLCLSPWAPGLSSTALCHSRL VLPATPIPVVTVWPSGLSTI/PPAPGATPT PAACFQQVPSAPDKPLLVSPPAKHPPVP PPVGLGLRAMDR/PPGPIPETPRDLPCHP TPPKSKLQARGPWGWVD*TTSGWKLK KEALMGPTIPDPKSSSWAGPLVSLPLVL GGNPSPWNALRGKRDPRKCGNPQPPSPK LRKSPPTAPGKTPAPYSPREKAGPQKTL GPRGPPP*SRDPPL*LRTPADPGVTRGA GPPAPRRNP |
| 4069 | 12120 | A | 5002 | 1 | 874 | LDDALESCDEHGYRTASSSCLRKGV MV KSSSNREL*V*SRYTDTI/SGSTSEFPDWA AGQRGSSHPRRWAARQRRSSLHLFYSEP DTDAKHQDDALTEET*G/SRSASCAHW L*SNCCTATGSSTLLPLTSRL*LPRMAVK SSRASAALPSSRFSSWHRACASPAAT AAPSAWGLSSNIPSGPAGCAPRPTSFSL PGALPTTTRRRHSSDRSRSPSRGLTSAR ESGSKSPQ/GTARDSRQALRSAMVTKTS WRMELDRECGRSSCTSTFCVSAASRGFL LQTSFRWE |
| 4070 | 12121 | A | 5003 | 1 | 2487 | |

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| 4071 | 12122 | A | 5004 | 227 | 2119 | RCRKEMFSLCWAYYCI*KLQOIPMLRAP LPTLDPV*SP/GGASTATNSGSSVTSSGVS TATISGSSVTNSGVSIIVTNSEFHTTSSGIS TATNSEFSTASSGSIATNSESSTTSSGAST ATNSESSTPSSGASTATNSDSSTTSSGAST ATNSDSSTTSSEASTATNSESSTTSSGAST ATNSESSTVSSRASTATNSESSTTSSGAST ATNSESRTTNSGAGTATNSESSTTSSGAS TATNSESSTPSSGAGTATNSESSTTSSGA GTATNSESSTVSSGISTVTNSESSTPSSGA NTATNSESSTTSSGANTATNSDSSTTSSG ASTATNSESSTTSSGASTATNSESSTTSSG ASTATNSGSSSTTSSGTSTATNSESSTVSS GASTATNSESSTTSSGASTATNSESSTVSS GASTATNSESSTTSSGANTATNSGSSVTS AGSGTAALTGMHTTSHSASTAVSEAKPG GSLVPWEIFLITLVSVVAAVGLFAGLFFC VVSACVPLCECRDALKMPGGLEQLLTS RIVHWGTEGRPIATAEGWVLLAMKIRL AAEAKIKCFLDGMAGLRSSLSRLGSQ AEALPTSQTMGGQAETLLSSQTGSRPNR GLFSLRRWAAGQRRSLTS |
| 4072 | 12123 | A | 5005 | 124 | 670 | FQRTKLLNGPGDVETGTSITVPQKKWLH VISPIFVQSLTLPFLAKWGDRQLQLLQIEL AAREVSDI*EETV*NETYLLLLSRKTLTD TLKWAHSIPSYARLFYI**FCSLKLAFSQ FLPAPDPYGVAVGGTVGHCLCTGLAVI GGRMIAQKISVRTVTIIGGIVFLAFAFSAL FISPDGSGF |
| 4073 | 12124 | A | 5006 | 3 | 273 | AAAPGNNGRASAPRLLLLFLVPLLWAPAA VRAGPDEDLSHRNKEPPAPAQQLQPQPV IAYQGPEPARVEVSGPGWGERGCRAGC AEYQAPGL |
| 4074 | 12125 | A | 5007 | 2 | 986 | AAAAPGNNGRASAPRLLLLFLVPLLWAPA AVRAGPDEDLSHRNKEPPAPAQQLQPQ PVAVQGPEPARVEKIFTAPAPVHTNTE DPATQVNLGVFIHAFVAAISVIVSELGD RTFVIAAIMAMRYNRPGPCWAGAMLCL/ AGLMTCLFS/VLFGYATTVIPRGLYILMF QPVLFAIFGIRMLREGLKMSPEDEQEEL EEVQAELEKKKDEEFQRTKLLNGPGDV ETGTSITVPQKKWLHFISPIFGQALTLTF LAEWGDRS*LTIVLAAREDPYGVAVG GTVGHCLCTGLAVIGGRMIAQKISVRTV TIIGGIVFLAFAFSALFISP |
| 4075 | 12126 | A | 5008 | 2 | 439 | |
| 4076 | 12127 | A | 5009 | 3 | 366 | RDSVVEILFEQDNKEQSVATLILDSLIQCP IDTRKQLAENLEMMFMDVGKTQPLLKRA FSTEK*KFD*/TINLASYQIFNQL*ANCTK YVGC FVIEDYSGSESILCLLFALIYNSDF VSLV |
| 4077 | 12128 | A | 501 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLLDLKGT AQLSELHCDKLHVDPENFKLLGNVLVTV LAIHFGKEFTPEVQASWQKMTGVASAL LSSRYH |
| 4078 | 12129 | A | 5010 | 387 | 446 | |
| 4079 | 12130 | B | 5011 | 16 | 348 | MVLDCGYRESVLPIYEGIPVLNCWGAL PLGGKALHKELETQLEQCTVDTSVAKE QSLPSVMGSPVEGVLEDIKARTCFVSDL KRGLKJQAAKFNIDGNNERPSPPKPC* |
| 4080 | 12131 | A | 5012 | 1 | 595 | MGCRPVGOAGLELLTSARTCFVSDLR GLKIQAAKFNIDGNNECPIDTRKQLAENL VVIGGTSMLPGFLHRLAEIRYLVEKPKY KKALGKTKFRIHTPPAKANCVAWLG/GK VFVGI*QVEYAMKAVENTSSTAIGIRCKD GVVLGVRKISPF |

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| 4081 | 12132 | A | 5013 | 3 | 461 | YIEDDMNPFQGNLEEQRPKSKTFL*QG AAEQIKHILANFKNYQFFIGENMISDGM VLLLDYVKGWVCPYMIFFKDGLDMD KMLNKCGLFWIYHPVIHNWASALSSH TTTRDLRQNWTDCHPGALPFILDWGFYL GVGGHCFYEKPCPW |
| 4082 | 12133 | A | 5014 | 3 | 325 | RRVSSVTQAGVQWHGLGSLQPPPGFKL FCLSLPRSQDYRCMPRPANFC/IFLVETG FHPAH*DKLVSNS*PCGPPAPASQSAGIT GVTHRAHLPCNV/C*LDLFHHHV |
| 4083 | 12134 | A | 5015 | 1593 | 4449 | PSGLGNTCIYRRGPHLPNSHRHAARGJS ADDRFRHLGHRELHPAPCVPGRGEPHPA PCVPGHGHLPALCVPGRGQLHSVPCIP GRGEPH/RCTLCPRSWA/RCTLHPRDLRF NRIREIQGAFRRRLRNLTLLNNNNQIKRI PSGAFEDLENLKYLYLYKNEIQSIDRQAF KGLASLEQLRLDSNTLHCDCEILWLADL LKTYAESGNAQAAAICEYPRRIQGRSVA TITPEELNCERPRITSEPQDADVTSG |
| 4084 | 12135 | A | 5016 | 1 | 3174 | |
| 4085 | 12136 | A | 5017 | 1 | 4759 | SRPWWLRASERPSAPSAMAYRSRGPGR RCLLALVLFCAWGTAVVAQKPGACGP SRCLCFRTTVRCMHLLLEAVPAVAPQTS ILDRLFRNIREIQGAFRRRLRNLTLLNN NQIKRIPSGAFEDLENLKYLYLYKNEIQSI DRQAFKGLASLEQLYLFHFNQIETLDPDSF QHLPKLERLFLHNNRITHLVPGTFNHLES MKRLRLDSNTLHCDCEILWLADLLKTY AESGNAQAAAICEYPRRIQGRSVATIT |
| 4086 | 12137 | A | 5018 | 2 | 267 | ADLSAEAL*TRREWDDIFKVLKTSS/LGQ PKILYPSKLSLINEASSSSSSSSSS/REFTT RLVL*EMLKGILHMEAQQGYLPS*KHTK V |
| 4087 | 12138 | A | 5019 | 1 | 164 | TRVNNQIESKAAAYALFYKRQDVARRLL SPAGS/SGAPASPACSSPPSSEFMDVN |
| 4088 | 12139 | A | 502 | 38 | 557 | APSPDA\MGHFTTEEDKATITSLWGKVVN EDAGGETLGRLLVVYPWTQRFFDSFGN LSSAFCHPWATPKVKAHGKKVLTSLGD AIKHLADDLKGVTFAQA*SETALVTKLHV GS*RTFKLPGEMLLGDPLGNPIFGKRISP LEVGRLSWAERWVTWSWPVALVLPRLP LKLNCP |
| 4089 | 12140 | A | 5020 | 1 | 712 | EILIIHLKRFSYTKFSREKLDTLVEFPISG ARERMAGGRQKQEGVYQY*PSPHPQDL DFSEFVIQPNESNPELYKYDLIAVSNHY GGMRDGHCMCQAVGGACPGGSGQGGD QDLPSE*LGM*ASGEGSSVVGK*TRSEI WTLSEEARKGRRG*LSFPFRITTFACNKD SGQWHYFDDNSVSPVNNQIESKAAAYV LFYQRQDVARRLLSPAGSSGAPSPACS SPPSSEFMDVN |
| 4090 | 12141 | A | 5021 | 3 | 3090 | IPLLQLLRRLWRRHGRWTEDEPQHEE LPGLDSQWRQIENGESGRERPLRAGESW FLVEKHWYKQWEAYVQGGDQDSSTFPG CINNATLFQDEINWRLKEGLVEGEDYVL LPARAWHYLVSWYGLEHGQPPIERKVIE LPNIQKVEVYPVELLLVRHNDLGKSHTV QFSHTDSIGLVLRARERFLVEPQEDTRL WAKNSEGLDRLYDTHITVLDAALETGQ LIIMETRKKDGTWPSAQLHVMNNNMSE EDED |
| 4091 | 12142 | A | 5022 | 1 | 1584 | |
| 4092 | 12143 | A | 5023 | 1 | 3519 | |
| 4093 | 12144 | A | 5024 | 3 | 673 | |
| 4094 | 12145 | A | 5025 | 3 | 2383 | |
| 4095 | 12146 | A | 5026 | 2 | 2348 | |
| 4096 | 12147 | A | 5027 | 1 | 7338 | |

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| 4097 | 12148 | A | 5028 | 2 | 7106 | KSKRQAQQMVPQSPVAVSQSKPGCYD NGKHYQINQQWERTYLG NVLVCTCYGG SRGFNCEKPEAEETCFDKYTGNTRYVG DTYERPKDSMIWDCTCIGAGRGRISCTIA NRCHEGGQSYKIGDTWRRPHETGGYML ECVCLGNGKGEWTCKPIAEKCFDHAAG TSYVVGETWEKPYQGWMMVDCTCLGE GSGRITCTSRNRCNDQDPRASYRIGDPW SNKVHRGNLLQCUCTGNARGEWK CERH TSVQTTSS |
| 4098 | 12149 | A | 5029 | 1 | 389 | |
| 4099 | 12150 | A | 503 | 318 | 449 | ERKKKKMATVQKGM/PHKYYHGKTGS YNVIQHAVGNAV TNRTGS |
| 4100 | 12151 | A | 5030 | 2 | 554 | ADALGRPTRPASQSRCTRSQSVGPSGFG GGHRGE/SGRAYVWQPPYGSSE/HASGL RYWSRRLRPAAGSFAAVCSRSVASKTPV GFIGLGNMGNPMAKNLMKHGYPLIYD VFPDACEFQDAGEQV VSSPADVAEKA DRIITMLPTSINAIEAYSGANGILKKVKK GSLIDSSTIDPAVSKELA |
| 4101 | 12152 | A | 5031 | 1 | 1123 | MGNPMAKNLMKHGYPLIYDVFPDACK EFQDAGEQLCPNLDVNHFPVQRLHAAD TPWPISHLLAASVIGCCDIACLFSGRVSIS SLCVTISSQADEVRAKENKPIQHPTKIA EMLVVSSPADVAEKADRIITMLPTSINAI EAYSGANGILKKVKKGSLIDSSTIDPAV SKELAKEVEKMGAVFMDAPVSGGVGA ARSGNLTVMVGGVEDEFAAAQELLGC MGSNVVYCGAVGTGQAACICNNMLLAI SMIGTAEAMNLGIK/S*GFDPKLLAKILN MSSIGRCWSK*HFNPVPGVMDGVPSA N*LFRVDFGTTLHWLKDGLAQDSATST KSPILLGSLAHQIYRMMCAKGYSKKDFS SVFQFLREEETF |
| 4102 | 12153 | B | 5032 | 13 | 441 | MEGVEEKKKEVPAVETLKKKRRNFAE LKIKRLRKKFAQKMLRKARRKLIYEKAK HYHKEYRQMYRTEIRMARMARKAGNF YVPAEPKLAFVIRXRGINGVSPKVRKVL QLRLRQIFNGTFVKNKASINMLRDCR AIYCMG* |
| 4103 | 12154 | A | 5033 | 1 | 775 | RRVPAVETLKKKRRNFAELKIKRLRK KFAQQMLARKAR\RKLIYEKAKHYHKEY RQMYRT*NF EWARMGKKLANFYVPA EPQIWR FVIRIRGINGVSPKGSEFFQLL RLRQIFNGNLL*KLNQGRFNMAEDF*S PYIAMGGTPNLKVSKMN*SYKRLWAK SNKKRUAL\TDNALIARSLGKIRHILawe DLIHEIYTVGKRFKIANNFLWPFKLSFS TKVEMKKKTTHFVEGGDAGNRVEDQIN RLIRRMN |
| 4104 | 12155 | A | 5034 | 193 | 384 | |
| 4105 | 12156 | A | 5035 | 96 | 1636 | ARSPAMAPLRPLLILALLAWVALADQES CKGRCTEGFNVDKKCQDELCSYYQSC CTDYTAECKPQVTRGDVFTMPDEYTV YERLGEEKNNATVHEQVGGPSLTSDLQA QSKGNPEQTPVLKPEEEAPAEVVGASKP EGIDSRPETLHPGARQPAPAEELCSGKPF DAFTDLKNGSLFAFRGQYCYELDEKAV RPGYYPKLIRDVWGIEGPI DAAFTIRINLF RGRPYLFKG\QYW/RAFEDGV LGPWIIY PRNISWTAFDGHSPGQTWD\AALGLPCP LAYSGRERVYFFQRGKQYW/ESYQFPG TSPVQEECEGSSL\SAV\EHFAMMQRDS WEDIFELLFWGAERSGWVTR\QPQFHL AGEWHGVPG\QVDAAMG\GRILHLQG MATRPLLWPKKKRFRHNRNRKGYRSIQ RAHSRGR*PETPRRP\SRAMWLSFVLPS EESNLGA\NNYDDYRMDLALCLPTCEPI QECFFSFGDKYYRVNLRTRRVDTVDPP |

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| | | | | | | YPRSIAQYWLGCPAPGHL |
| 4106 | 12157 | C | 5036 | 1 | 300 | MRSFGQLTLCPRNGTVTGKWRGSHVVG LLTTLNFGDGPDRNKTRTFQATVLGSQM GLKGGAGSVWLQAAGLGLLPASLLWPS LLCHCYVLPPAPGVPLV* |
| 4107 | 12158 | A | 5037 | 359 | 1229 | MPQPPTLQEMTGSPQWGTGKGGPLGP* QLRAKAQEVDSHLGRKKIKQQNRSKSC |
| 4108 | 12159 | A | 5038 | 2 | 311 | VRWNSAAPLVTSRGAPASARPRGQALP GGSAPSAPHGQLPGRAQPAPVSGPPPTS GLCHFDPAAPWPPGLGLGMLPPHPQDW PAQP*HPPGLGLFFEIFSAS |
| 4109 | 12160 | A | 5039 | 310 | 415 | SQYFGTLRRVDHLRSGVRDQPGQLGKTP S*PQVIHPPQCPKVLGLQYYHFLFLRRS L/DSVAQAGVQWRDLGSLQRPPPGFTPF SCLSLPSSWDYRRPPRLANFFVFSVETG FTVSARMVIS*PRDPPASASQSAGDTG VSQAPV |
| 4110 | 12161 | A | 504 | 1 | 467 | DHSSSPAREQNWMENEFDELTEVGFR WVITNSSELKKHVLTOCKEAKNLEKRLG ELLTRITSLEKNINDLMELKNTARELHEA YTSINSWINQAEERLSEIEDQLNEIKRED KITEKMKNSTTVRVAASMQSKLLQGVA EEGPLRLTRSASFSA |
| 4111 | 12162 | A | 5040 | 1 | 114 | ARAEMLIQYILPRLTHCAIFTILFIFSLT *VMLLSS |
| 4112 | 12163 | A | 5041 | 335 | 477 | TPASLKIPVE**NTLLAKMVIS*PRDLPA SASQSAGITGVSHRARC |
| 4113 | 12164 | A | 5042 | 135 | 804 | GIDTILTLNQN*SLKTRQ*FTLIIF/IFFFL RWSLALSPRPDCGLQWRDLGSLQAPLPG FTPFSCLSLPSSWDYRCPPRPANFFCNFF FSRDGGFTVLARMVIS*PQ/CDPPTLAS QRAGVTGLSHCTRLFFF*WMESPSVTQA GIQWHDGLSLQPMPPQFR*FSWLSLPSSQ DYRCMPPCQANFICIFSRDEVSPC*PGWS GSPDLVIHLPWPPKVLGLHA |
| 4114 | 12165 | A | 5043 | 63 | 361 | |
| 4115 | 12166 | A | 5044 | 151 | 384 | |
| 4116 | 12167 | B | 5045 | 385 | 479 | MAGAFRRRFASEVRAQGLESLEHGLRC AGSLRGGQSLPTTMWSPVKVGFE* |
| 4117 | 12168 | A | 5046 | 3 | 698 | VFFFFSGCTRGPLFESDFHRAPHRCGQG LAAP*AAGAPQPRAPGETRGPEPAPHWR SASGDKPPGQAAWPPALVPGEGPSWDS PRGHRCSQATLPRVLAPLQP*LS*LSL* DPPELRSL*PPL*LRL*SLLEPP*PPLDS NRFPP*PRSPPLENPRPRPRPRKKPRPP AEPPTYPTESVSDDLPAWSTRISVHLQTS HSWPSWASLASSMFFKVTKPNSRELWSS |
| 4118 | 12169 | A | 5047 | 138 | 550 | FCCCFTSSEHSLAYGSCSPRREVLCAQ QNPSETQAAPLASIMWK*PCNSRLKGP GPGLGEGWPESRMTSGVTVPGGTSPGT RAGGSAPCPGGLSPEALRQ*GAGSGPRVS PGA/PGCGAPAAAYGAASPCQRCGAL |

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| 4119 | 12170 | A | 5048 | 2 | 555 | FFFFFLGAHVLYSNPTFTGLHIVVGKD WPPP*AAGAPQPRAPGETRGPEPAPHWR SASGDKPPGASGCLQLLFQGEVPPGDS*P QRSSLALRPFPRLVLPFGPFQPAKAKQR YSQRPPQGSQALPP/GPPRKQPQLRKVS G*SGGCDLRLRHRPACGRVCTLAQLEP ATRMGWSYVVGQCL |
| 4120 | 12171 | A | 5049 | 1246 | 1379 | RCLFILSFFTGRRTHTP*PPLPGLRTGFPP* PRSPPPSREPTGP/RPRPPREESPGPRQ*PP RVPHGIGLSDDLPAWSYSGS/GRPSTGLPI /PWPSWHP*RRQCSQR*QTQIPEISGSPCL SQPPLQRSVRTLRPPAPATA/PLVSKLSPP TKSLPSSDAMRPLSRAGP*RKQEDSAPQ DPEPPRNRGPGN |
| 4121 | 12172 | A | 505 | 1 | 1140 | |
| 4122 | 12173 | A | 5050 | 207 | 251 | |
| 4123 | 12174 | A | 5051 | 335 | 419 | TFDFPNWRSYFMSNWTSLPTLLSSWD\Y YRHVPLYPAKICIFSRDRVLPYWPQ*SHD FTLFVSMITLTLQIYKMTKLDNYLETIYY |
| 4124 | 12175 | A | 5052 | 68 | 399 | WELLIYFSGHTCSNLSPLLSLFFFF*DS LAVSAPGVQ\WHDLCSLRPLPPRFKRFW CLSLSGWD\YRHVP\QYPAKICIFSRDRV LPILAKASRNVSFLTNLMLGGFS |
| 4125 | 12176 | A | 5053 | 2 | 322 | AAAAFFFF*DGACSVTRLECSGTITAHCN FRHLGSSNFPASTSRVVEITGTCHHT*LIF VFLVETGFHHVGQAGLELLT*VIHPPQS TKVLGLQVVSHCTRPLSDF |
| 4126 | 12177 | A | 5054 | 16 | 357 | TITIGQNFFFFFLEMGCSCSVARLECSGVS AHCNLKLLGSSNLPSTST*VAGTTGVCA TIPSYFYNKISM*NQSLPMLPSLGLLELLG LRPVFLPRPPKVLGITRHEPPHSALK |
| 4127 | 12178 | A | 5055 | 2 | 346 | LRWSL/DSVAQGGVQWHDGSLQPPPPG FKRLSGLSLMSSWDYRRPPRLANFLHF **RRSFTMLARMVLIS*PHDPPASASQSA GITGVSDHAQSQIFLKLQMTKSMGFKTK FLN |
| 4128 | 12179 | A | 5056 | 3 | 401 | FFFWRQSLTLVTQAGVQ*LDHGSLOPPL PGPKGFSLSPSSWDHKKHAPPHLANFF L*RHGFTM/RLVLTSLPQ/CDPPAAASQS AGITGVSHCAQPVIFCKKLDIFSSTDIPTPS NLQPRGFWDLTAPQGEIVST |
| 4129 | 12180 | A | 5057 | 142 | 250 | PPTGSLLTPLWDPQFASLFNGTL*WERE *PLPQNV |
| 4130 | 12181 | A | 5058 | 2 | 775 | RCNSAQQQMTSSQKALMLELKSLOEEP VEGFRITLVEDSLYNWEVAIFGPPNTLY EGGYFKAHIKFPIDYPYSPPTFRFLTKM WHPNIYEEWEMYGISILHPPVDDPQSGE LPSEWNPTQQCEGLILLRC*SHWLNEP QHLSPQPMDSASVMFRKWERQ*REKTK EYGLKFIRETKFSAT*GPKAGKGWGV SPTNPGREYCIKTEVPRNDEQVQSLLYD ELGMMTDIDDER*GRRKAD\CYDDDEF WGMRKP |
| 4131 | 12182 | A | 5059 | 1 | 571 | ALGKAGYID/KYVTAMGIVAFVFFRSGK YNLDFRSRNDP/ARHI/TPEQLVALYKSI REKH*VFPD*GLVQRTLFLVFLVCLKN/ SFDCCDREVWKKFTANACLQEAGNDLT VNLRHIAEAVDENS CNFLQLTVD*ACK LIQSNW*GIMVSHYSLT*NTFIALVKHCT G*/INTGAPC*SEPLARYKELSF |
| 4132 | 12183 | A | 506 | 1 | 2640 | |
| 4133 | 12184 | A | 5060 | 32 | 534 | GRERPLSPYMETLYRVPFLVLECPNLK LKKPPWLHMPSAMTVYALVVVSYFLIT GGIYDVIVEPPSVGSMTEHGHQRPVAF LGLQSKMDNNGKGLCIQAS*FTMGGF RFS*ILDPIECTKYPKTSNDSFFCSIGISSV VLEFFPWARSNSMRNGNCPGLI |

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| 4134 | 12185 | A | 5061 | 1 | 328 | FLKRQRFGLVAQAGL*WHNLGSLQPLPP GFK*FSCLSLSSWDYRHLPPHPNLLF LVETGFYHFGQAGLKLLTDSGDPPALAS QSAGIIGVSHRAGPGLCTFSNHI |
| 4135 | 12186 | A | 5062 | 2 | 687 | GRVGFNVWRDRNDTNLIPNGSSITVNOQT NKRDYVSKYINYIFNDSVKAVYEEFRRG FYKMCDEDIKLFHPEELKDVMLGNTD YDWEINIEKNARYEPGYNSSHTIVMFW KAFHKLTLLEKKKKFLVLTGTDRLOMK DLNNMKITFCCPESWNERDPIRALTC/YP VSLLPSPKYSYNGNS*KKRFKKPINNR GIWLTSLPCPNLILLLLLLLLLLLLLFLY FVLF |
| 4136 | 12187 | A | 5063 | 1 | 525 | ISHDAIAQESKRYWQNLNANVPGAQVLG NQIMPGLNMMKIKFVCRPQCPEKRSKIE PDKNRKYCSAKARHSWTKDRRAMRV MSY*VRKKWMNIRPLPTKKQMPLQFDLC NHIASGKKCQYVGNCFAHSPEEREVWT YMKENGIQDMEQFYELWLKSQKNEKSE DIASQSNKEN |
| 4137 | 12188 | A | 5064 | 735 | 1517 | SYSYFFIQLCNHIASGKKCQYVGNCFA HSPEEREVWTYMKENGIQDMEQFYELW AQESKK*KK*RHRPVSPNKGKWEQI MANRIMAGRLQWDFSLAGMCGGKTGN SEKQWQGHISSEKHKEKVHTEVTDQYC WQHRFPTGYFSICDRYMNGH/AAQEGNS CK/CLHMGNARTFMEWGRKGRRPLKV EASTKHKRDHLIGPKDNDFGKIYSLFK DLN*YAGFYGMIPNQSIDQKNLKCSEAH SRGAARFPACIGVYRSS |
| 4138 | 12189 | A | 5065 | 237 | 381 | LHQPTTQTLAFTSNLRGR*RSAALPDAL DSSKVSEMRFLKRRGVN |
| 4139 | 12190 | A | 5066 | 1 | 876 | |
| 4140 | 12191 | A | 5067 | 1 | 78 | |
| 4141 | 12192 | A | 5068 | 155 | 417 | |
| 4142 | 12193 | B | 5069 | 40 | 411 | MQVTGVRTDSGALNITHKLASSPHSKPF PIFQATFIFSDHIRCIAEQRLAKGRIPGKA HEDAENSCPPWTSQSSPPLKSWGLDSAP PPPLSTCLASATTRGAGAAATPQCSAPCL HRWTRCQ* |
| 4143 | 12194 | A | 507 | 1 | 714 | |
| 4144 | 12195 | A | 5070 | 1 | 987 | |
| 4145 | 12196 | A | 5071 | 111 | 2187 | DERRVGAADMFGRSRSWVGSGHGKTS RNIHSLDHLKYLHVLTNTTVEQNRN LLVETIRSITELIWGDQNDSSVDFDFLEK NMFVFFLNILRQKSGRYVCVQLLQTLNI LFENISHETSLYLLSNNYVNSIIVHKFDF SDEEIMAYYISFLKTLCLKLNNHTVHFFY NEHTNDFALYTEAIKFFNHPESMVRIAV RTITLNVYKVDNQAMLHYIRDKTAVPYF SNLVWFIGSHVIELDDCVQTDDEHRNRG KLSDLVAEHLDDLHYLNDILIINCEFLND VLTDLNRLFLPLYVYSLENQDKVFLII HHAPLVNSLAEVILNGDLSEMYAKTEQD IQRSSVLPTLSSLWQGSLSLNLQSLGH KCSSHLCGAQAADSVTGEIPAIRSLEW LISAGSKARTFFFLKMLIGFWEKVDCEY QRRQVLSTRLQEALPSNRLTDVAHVSS CMLGFGSTAPRGSWIGDPAAVHLPLPGE LAEHLGSKGTTTGTKHQPAKPSIRCFIK PTETLERSLEMNKHKGKRRVQKRPNYK NVGEEDEEKGPTEDAQEDAERAKGTE GGSKGIKTSGESEIEMVIMERSKLSLA ASTSVQEONTTDEEKSAATCSESTQWS RPFLLDMVYHALDSPDDYHALFVLCCL YAMSHNK/GKSPEKEEGLSGTQSHPGKA GTFGKEGAERKRAQV |

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| 4146 | 12197 | A | 5072 | 2 | 2774 | RNLLVETIRSITEILIWGDQNDSSVDFDFL EKNMFVFFLNILRQKSGRYVCVQLLQTL NILFENISHETSLYYLLSNVYVNSIIVHKF DFSDEEIMAYYISFLKTLCLKLNNHTVHF FYNEHTNDFALYTEAIKFFNHPESMVRIA VRTITLNVYKVSLEDNQAMLHYIRDKTAV PYFSNLVWFIGSHVIELDDCVQTDDEHR NRGKLSDLVAEHLDDLHYLNDILIINCE LNDVLTDLHLNRLFLPLYVYSLEN |
| 4147 | 12198 | A | 5073 | 2 | 1802 | |
| 4148 | 12199 | A | 5074 | 546 | 802 | GQAGRARQVRSVPSSALITLPPLA*QKH G/ISRWWVIGDENYGECSREHALEPR HLGGRAITKSFARIHGELESVPRPSSSH |
| 4149 | 12200 | A | 5075 | 3 | 2380 | SLSVHKMAPYSLLVTRLQKALGVRQYH VASVLCQRAKVAMTHFEPNEYIHYDLLE KNINIVRKRLNRPLTLSEKIVYGHLLDDPA SQEIERGKSYLRRLPDRVAMQDATAQM AMLQFISSGLSKVAVPSTIHCDHLIEAQV GDEKDLRRAKDINQEVYNFLATAGDKY GVGFWSFGSGIHHQILENYAYPGVLLIGT DSHTPNGGGLGGICIGVGGADAVDVMA GIPWELKCPKVIGVKLTGSLSGWTS PKD VILKVAGILTVKGGTGAIVEYHGPVDS MSCTGMATICNMGAIEGATTSVFPYNHR MKKYLSKTGREDIANLADEFKDLVPDP GCHYDQLEINLSELKPHINGPFTPDLAH PVAEVGKVAEKEGWPLDIRVGLIGSCTN SSYEDMGRSAAVAKQALAHGLKCKSQF TITPGSEQIRATIERDGYRQILRDLGGIVL ANACGPCIGQWDRKDIKKGKNTIVTSY NRNFTGRNDANPETHAFVTSPEIVTALAI AGTLKFNPETNYLTGTDGKKFRLEAPDA DELPKGEFDPGQDQTYQHPPKSSGQHVD VSPTSQRLQLLEPFDKWDGKDLEDLQILI KVKGKCTTDHISAAAGPWLFGRHLDNIS NNLLIGAINIENGKANSVGNVAVTQEFGP VPDTARYYKKGIRWVWVIGDENYGECS SREHALEPRHLGGRAITKSFARDPRD EPGRKQGLLPFGPFADPADYNKIHPVD KLTIQGLKDFTPG/RSPKCIKHPNGTQ ETILLNHTFNETQIEWFRAGSALQK*RN LQQ |
| 4150 | 12201 | A | 5076 | 3 | 203 | |
| 4151 | 12202 | A | 5077 | 52 | 393 | EASAWPAPRGSWMVVAEDPACSVTLCP ESLSGYLPGSGGQGPSPAAGTSPSPPPRS LPGLEKLRSFGRESRLSSSAPRAPSIAK AQLQCQAEEDPEIVNNV*FSSVTCLSL |
| 4152 | 12203 | C | 5078 | 121 | 396 | MALPGRPLPHRKLAGGTLEAPWPGIPSGA VRRHQPOPPTTLXXWLGKVKPLRKRIE AKFLCAEGPEHIRQGSAAVPGGGGRSRN CEQCLI** |
| 4153 | 12204 | A | 5079 | 3 | 755 | FVVDFDRPHETRVLQVSCGRAHSLVLT REGVFSMGNNSYGQGRKVVENEIYSES HTVHRMHDQVQVQVACGQDHSFLT DKGKVYSCGWADGQTGLGHYNITSSP TKLGGDLAGVNVIVATYGDCLAVSA DGDIFGWGNLEYLQLA/APVTDSTQVN VPRCLHFGVGKVRQ/CLHAVARAVQC* TGEHGVFVWGYGILGK/GPNLSGKCPSL KMIPPTLFGDFGQPRNPGFPAFRCGIQA TLLH |
| 4154 | 12205 | B | 508 | 1 | 546 | MKQPNRKRKLNMDSKERLDQDGRLVK MSFFVFCCVVSSESEHEETQDLMCSELF WVLLHMWSDQHQHLEDHNSSPAR GQHWMESEDELTEVGFRRWVITNSSSEL KEHALTQCKEAKNLEKRLDKLLTRIISLE KNINELMELKSTARELREAYTSINSQIDQ VEKGYQLKINLMK* |

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| 4155 | 12206 | A | 5082 | 7 | 279 | GQVCIAETGVQWYHLSSLQPLPPGFKRF LCSASRRAPPCANF*FLVEMGFHHVG QAGLQLLTLGDPPTSASQSAGITGVSHH ALPAWL |
| 4156 | 12207 | A | 5083 | 5164 | 5586 | FTAALNSWVIKLSSCFSLSSWDCMYMP PCPASFFFFFLR*SFALVAQAGVQWCDL GSLPPPPSGFERFSCGLPSSWDYRPP/P TPG*FFFFVFLVEMGFHYVGQAGLELLT SSDLPTSASQSAGITGVSHHALPSLYK |
| 4157 | 12208 | A | 5084 | 2 | 5438 | |
| 4158 | 12209 | A | 5085 | 1 | 4294 | WAVFDGNYYYLPAHTKPVVTLTSY WEDISHRLDAVNALLAMAERLQTNIEAL KSGIQGKIPANQLAELWLKLIDEVIEDTR YTLPLTEGKANVTVLDTQIRKLRSRSLSQ IHEAAVRMRSEATDVKSTLAEIEDWLDK LMQLTEEPQNSMPDIIHWMIRGEKRLAY ARIPAHQVLYSTGENASGKYCGKTQTI FLKYPQEKNNGPVPVELRVNIWGLLSA VEKKFNSFAEGTFTVFAEMYENQALMF GKWG |
| 4159 | 12210 | A | 5086 | 444 | 797 | FHSLSPGASKPMLEPGLDWEPCCKLNDV KRAKSVPLTRHLH*VYLLMLSLPPPTPQ QAPVYDVPLPVSKCSHCQFPLWF*FAFL* WPVMMSVFSCVWLHKCLLRVCSYP LPTF |
| 4160 | 12211 | A | 5087 | 489 | 611 | SPCPLCPEWYCLGFLGFLWFLV*HLSL *SILNYFLYKV |
| 4161 | 12212 | A | 5088 | 1 | 336 | |
| 4162 | 12213 | A | 5089 | 1 | 1581 | |
| 4163 | 12214 | A | 509 | 1 | 732 | |
| 4164 | 12215 | A | 5090 | 235 | 583 | |
| 4165 | 12216 | A | 5091 | 1 | 430 | MGKDFMTKTPKAMATKAKIDKWDVIKL KSFCTAKETTIRVNRQTEWEKFFATYSS DKGLISRIHKELTQIYKKKTNNPIKKWAK DMNRHFSKEDIYAANKHMEKCPSSLAIK EMQIKTTMRYHLMPPVRMAIJKSGKNR WELNNENTWTQEGEHHTLGPVVGWVK GGGKALGDTPNVNDELMAFSTTRPTFFP RSDPTTTRPMAVPPHEEKDDHLETHRPL RPRTTLPHAPDGRWLLTLTHTSTPGKT GLRTYRCLSRTEKVQTAGARPSHPHSS AAFTTWAKGPTGRRPGHMRSESATQKE VTMSPCTALRGQKADSKAHGQQGTWA ARGMHITESGTCKASRGFPSLLSPRTRIPK VFVAERKGLRGFVLSLTLFSCIQKHWE QTVPMSPLVEDVSE*TGNLQNGRNFLQP THLTGK*YPESTKNSHKFTRKKQTPSKS GQRI*TDTSQKKTQMPTNTWKNAHHH WPSKKCKSKPQ*DTT*QLEWQSLKSQE KTGGN |
| 4166 | 12217 | A | 5092 | 65 | 163 | LEASKFSLVPTGPSV*CSPPCVHVFSLFNS HL |
| 4167 | 12218 | A | 5093 | 175 | 495 | PQFFGNVLGHLLYSFLGPFQCDENIRYLS *CSPSSCPPCTNRQYVMFSLCPCVLMV QLPPMSENMWCLVFCSCDSLLRMMVSS FIHVYPYFCYCNLVVYFEVRCH |
| 4168 | 12219 | A | 5094 | 67 | 351 | LHTRKSVFNCVKLFLHCISSVLINQLYDR PWCVMFPTLCPSVFIVQFPMSSENMWCL VFCPCDTLLRMMVSSFIHVPPERHKSCH HDTRG*CSNM |
| 4169 | 12220 | A | 5095 | 2 | 431 | QVFGSIVRIHQGEWFPLLYGILLPRVQNC LTN*LDLCWSQHQTTPHVLTHRWELNNE NTWTQEGEHHTLGPVVGWEGGGIALG DIPNVNDKLMGAAHQHDFLVSPKITGIV LSISQVRVPFIDHRRKARYSADLTSFLIAI PG |
| 4170 | 12221 | A | 5096 | 75 | 173 | |

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| 4171 | 12222 | A | 5097 | 1 | 2349 | MLEDRDGEDEGEDRLDNAVRGPGPK GPVGTVSEAQLARRLTKVKNSRRMLSN KPQDFQVATAWRSASLFNLYIAHLLAIA VMFQWTSNGQWLNRPALNDFIPTAAL GLYNPTVPILGMLTGGSTQLVAPGIAQS CPGLVLAILIGEGNEATPEDPKDPTCWER LGNHPPSVLQIRVRVIEGRQLSGNNIRPV VKVHVCQQTHTRIKRGNNPFFDEV LW LQPGDHTPASYSRAGLNDYHNCCCKNM QGVVLTHKWELNNENTWTQDGEHHTL GPVVGLWPQCLTDEPGFEETWASTQPF AGVTCKALYLLHFTPTAIGSHCLDHCFS DFLGIKNYRKEKVGLRDLGICRRPGEGR LGKHILRNVLGDDAEALIGTATVALKD LTGDQSRSLPYKLISLLNEKGQDTGIYNC ELENVAEFEGLTDFSDTFKLYRGKSDEN EDPSVVGEFKGKLQMWVDVFPKSLGPP GPPFNITPRKAKKYLRVWNTKDVILA EKSITGEEMSDIYVKGWIPGNEENKQKT DVHYRSLDGEENFNWRFVFPFDYLP AE QLCIVAKKEHFWSIDQTEFRIPPRLIQIW VNDKFSLADDYLGFPRLTLRHTIHFLQ KSPGGNC/RGLDMISGTFKAMNPLKAKT AFLFEQKFMN*WWPCYAEKDGARVMA GKVENTLEILNEKEADERPAGKGRDEPN MNPKLDLPNRPETSFLWFTNPCKTMKF IVWRGFWWVIIIGLLFLLILLFVGRAPLT LLPNYFVQWKIVKPNVLTGKGGFISRVIQ Q |
| 4172 | 12223 | A | 5098 | 1 | 296 | RRSAPSTSLRTTCVSSCCWPRRRAPSMTP GAGYPSGSSAGP/PTHSP*PPWTRPS/SAQ RYLRK*QPQGPALLPLLPAP/PKAWLS GLGPVVLDSGPQ |
| 4173 | 12224 | A | 5099 | 26 | 253 | RWLSPWPL/SCPQPGWTARNPQPTRELPP HPQAGKPFPLPVVPFQPTSPSLLPVMGGL SRPGSFSPVSVASLRCTH |
| 4174 | 12225 | A | 51 | 702 | 1107 | LQERYSDPGLLASFHGESSQDRLDTVQQ EK*NAGSASPPGPPHNTCQPRDGRGFT RLPCHRMWGTPGIRWKMLPQ*AAAGPPH AA*WPGSLMPPCL*PSASAWTRQQ**PG SLPTLTSPG*DPGAHILLWRKQSY |
| 4175 | 12226 | A | 510 | 2 | 1601 | |
| 4176 | 12227 | A | 5100 | 274 | 2462 | RRSAPSTSLRTTCVSSCCWPRRRAPSMTP GAGYPSGSSAAHHRCDGWATTHSP*PP WTRPSWRSAYLRK*QPQPGPTQHCCPLP SQPPAKGVAVRAGPCSAGLSRATIGTGQ G/PG/TSPGHTWGQRYHEATFWG*LLD CLVFKSEKPR*LILLITMF*STSVSLTML SLD*ARGRREPAHPTPGSPAATN*PGAL LPTVQIS*KCSSLQAPERASPPPCSPR/PPA TASFRPSLSDGPS/APSGKPSPHLKPN NIFIFLPYQLLSHL*VAQSMATPCPQPGW TARNPQPTRELPPHPQAGKPLLPVPVFPQ PTSPSLLPVMGGLSRPGSISLPSQWLL*G AVHAR*VPFSLPRGTELTWTPSAKGPM GWAAGLAASGGCLHSSR*PTLVFRGWW EHIPVPLPHNRCGDSPPGR*QGSSMVVR DSGEL*GLGDPGLPGFENKPCCF*AEIL KWNARLARNVLTQNA SPCPYWTWP CLMPKDPYPEAYPPYVLR EAECPLQAV MGPEAPPAWPCSPVG/SVTVPF/TSVSRSP PPKKLTHCE*PWAS/SPNLLVPQFPHLEK MGPPASSRAAHAPFSP/SPHPALGR LM PLPQWALWEPTGSPALTPPEASEACVMS QLSSR*GPRVLCWWGWGMP SFLYLFHR KSPAGAEMQSGGLPSP*PVLL*GPEAGP GPVAAEPSPQEVKLVP SGRLPVRGLSPSF QNSRRGLQSPVRQTGPFPPVKPCV |

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| 4177 | 12228 | A | 5101 | 1 | 545 | DFPRQSS*NLNITGKCGISP/GTPLNA\AHF VPGQY/VDVTTKTMCKGFQGVMKRWG LKAQPAATHGQSKSTGRPGA\IATGDIGR VWPGTKMPGKWGNIYRQEYGLKVWRI NTKPPIN\YVKWSGPGP*KWLR*RSKDFK LPA\FKDLGKNLPIPIYIFFLEGDEGGTAQ KIGMDEKRVSSPGAPSN |
| 4178 | 12229 | A | 5102 | 2 | 202 | LFGYLPK*VDNMSTKKPCTWIFTLALCIT ARTWKQPRCPLVGKWI/QLCCI*KMKYY SDFKKSCQAMK |
| 4179 | 12230 | A | 5103 | 1 | 422 | FFFFLRSFTLVA*A*VQWRDLNSLQPP PPRFKRFSCLSLPSSWDYRRASPCSANFL DF/HFLVETRFHHVCQAGLELLMSGDLP ASASQSAGIIGVSHCARPLASFLIHIFNK CISGVRLCSRWPWRYSAQAQSLDLAY |
| 4180 | 12231 | A | 5104 | 2 | 375 | DGSCFVAQTGVQVWHNLGSLQLPPRFK* FSCLSLPSSWDLRQVPPHPANF*FLV*P GFHDVGQAGLELLTSGDPPILATRSVGIT GVSHCARPGSIYKQRLDKKLRSVAART NRCPLWSLPI |
| 4181 | 12232 | A | 5105 | 1 | 293 | RRLFFSFLRQSLVLVIQAGVQWGDLSL RPLPAGFKRFSCLSLPSG*DYRHGPPRLA NFWIFTREGM/FAMLARLVSNS*PQGDPP ASASQSSGDYRA |
| 4182 | 12233 | A | 5106 | 3 | 305 | ETETCSVAQAGVQWPILSSLQPLPPRLKR FSCLSLNSWDYRCLPPHAANF*FLVET GFPHVGQSGKLKLTSGDLPTSGSQSAGIT GVSHCTWAGKSYIF |
| 4183 | 12234 | A | 5107 | 1 | 485 | ARRDAAEVFLVSDPSGRMVKFSLQRILN SHCFAREKEGDKPSATIHASRTMPLLSLH SRGGSSE/SDRLNVTEELTSNDKTRIL NVQSRLTDAKRINWRTVLSGGSLEYIEIPG GALPEGSKDSFAVLLEFAEEQLRADHVF CFHKNREDRAALLRTFSFL |
| 4184 | 12235 | A | 5108 | 1 | 506 | FGVSVYLHDYNMRTNPGEMSESTVPTH PADKGWPQGPDAQPRGGPTPPPLKTL RTCRPMKQASGLLGTGCPGLTISKPKK LKVRSKAAAGEKPSEPLPTRTPRPHPPP QGDRAQLRMKGRRRHPHAPYCRRYGS PTSVLAVLVEANEDMVGSQLLLSELQEN WQAVLAPLGQRAARDLDVEAAATQHCS PNWRTVLSGGSLEYIEIPGGALPEGSKDS LPVLEFAEEQLRADHVFICFHKNREDR GR*PVSPAUGCVCVGPAPPLHSQAGTVS LRGWGVRAGGSGRQGF*RLLPRAALLR TFSFLGFEIVRPGHPLVPKRPDACFMAY TFERESSGEEEE |
| 4185 | 12236 | A | 5109 | 1 | 996 | MVKSSLQRLNSHCFAREKEGDKPSATIH ASRTMPLLSLHSGGSSESESVWMARD APGEAAH/CRRHPG/PSRPGPGSWGWR TPTARQRPKTPAASREDASFRGRGCQ LRLWGS/HAGSRSSFPDCVPRGRRSAP DREDDRLNVNRGN*RSNRQDGGFFNVQ SRLATEAQTALNWRNNC*SGGSFLNIKPA GRRWPEGSKGQLLQFLLEFAE/EKQLR ADHVVFICSHKNRE\DRSCLAPKLSAFLG LKILRPGHPLVPKETPDACFMALQRSRE SLPGEEEEVGARLRGWAIPPPWGHFVS RVGRNRRLAHLAWVCPHVIVQINAHS Q |
| 4186 | 12237 | A | 511 | 1374 | 2220 | QAENSHINNKDVHSETPSEGHQKRKP KDHSSSPAREQNWMEFDELTEVGFR RWVITNSSELKKHVLTOCKEAKNLEKRL GELLTRITSLEKNNDLMELKNTARELHE AYTSINSWINQAEERLSEIEDQLNEIKRE DKITEKMKNSTTVLVSTWGSQLEQNNLP HIISPLFHSTHDNISFYGGCLLQACSSKL LQGLAEGGPLRLTRSASFFAAKLCLTKH FLPTMILIKSRKTTPTDTPRRLYLLQGV |

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| | | | | | | VDQTSRKGPTALNIRQKTFAAAPPHR |
| 4187 | 12238 | A | 5110 | 1 | 125 | FFFEMESHSVIRLECSGVNSAYCNL/TLP GSSGSPASAPPPQVGTTGTHHHAQLIFV FLVETGFHHVGQDGLDLL/NLVIRPPQPP KVLG*QAVLLPQHRPPK |
| 4188 | 12239 | A | 5111 | 2 | 280 | FFFFGDRVPLHSAQAQGVKWCNLGSLQ PPAP/GLKPFSCSLPSS*DYRSLPPCPTHF CIFSRDEVSPSWPGWSPTDLMNHPPRPP KVLGIQV |
| 4189 | 12240 | A | 5112 | 2 | 291 | FLEMESHVAQAGVQWRDLGSLQPPPP GFKRFSCLSFPSSWDYRRPQPRPA/NFFV FLVETGFVILARLVSNS*PRDPPASASQS AGITGVTYRARP |
| 4190 | 12241 | A | 5113 | 3 | 690 | FFFFFLRQSL/DSVTQAEVQW/RRILGSLR P/LQLPGLK*CCCLSLSS*DYSYNPLPRL ANFF/VFCIF**RRGFTMLARLLSNS*PCD LPTSASQSAGITGVSH/HAPGLASPSLNN KVQSSVGAQRRHDEDNGSRA*VFCCFF FKRFALVA*AGVQWRDLSSLOPLPLRFM *FSCSLPSS*DHRCPVPPHANFFVFI*RD. GVSPCQPG*SRSPDLAIRPPRPPKVLGLQ A |
| 4191 | 12242 | A | 5114 | 3 | 282 | FFFETESHLSLSPRECNGTISAHCNLR PGPRDCPASAS*VAGITGVCHHAWLIFVF LVETGFHHVGQAGLELL/NLVIRLPQPPK VLGLQA |
| 4192 | 12243 | A | 5115 | 3 | 198 | LSLNWCILYIYICIYVV/CVVLFCHSCLS NMGT*FFLAGLLFRICLCIFIFYELL***L LFIMI |
| 4193 | 12244 | A | 5116 | 1 | 854 | MNKLFSILLGEKVDTPQNVLHNDPHARH SDDNGQNHLEGQMNFNADSSQFKDENT DIAEKLEEKVRILCWVMTGPQWLEKKA KHVKATWAQRCNKVLFMSSEENKDFPA VGLKTKEGRDQLYWKTIFQYVHEHY L*DADWFLKADDDTYVILDNLRWLLSK YDPEEPIYFGRRFKPYVKQGYMSGGAG YVLTREPLKRFVDALKTVKCTHSSSIED LALGRCMEIMNVEAGDSRDTIGKGNFFH PFVPEWHFNLKGYLPRTFWYWNYY PPVEGPGLLL |
| 4194 | 12245 | A | 5117 | 13 | 290 | ECRRQRGVQ*CNHS*QQL*PPGLMQSSL LSSPGSSDYRQVLLHSAEF*VFNLVEMG SYYVVQAGLKFLASSDPPALTSQWARIT GMSHITRA |
| 4195 | 12246 | A | 5118 | 1 | 595 | MGIHHVGQASLELLTSGDLPASASQGRG VRLYYINEGRSSQSASVTALFLSSLPTVTS AMAGTRPPSARSHQTLQACRAQKTKTR MSSI*GTGAKHQASSPGKAPLSTPSPYFW KPSLQTPCSGSRSLWASLPSPLAALFLC FWQDAT*RSSTTRSSLPSWPSRSTRALRL STS*PECAPSA*ASSKAGERSTGDRL |
| 4196 | 12247 | A | 5119 | 3 | 496 | FFFLRCSV/NSTAKAGVQCHNLSSLPLP PGFKQFPCFSLPSS*DYGCAPPHANFYIP SRISQAWWRVPVIPATQEARSFNFAQ VGVQWHNLSSPQAFPAFGK*FSCSLSPTS WDYRHMPPCPDNFCIFSRGGVSPYWPS WSRTLDIMIHIPRPPNVLGLQA |

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| 4197 | 12248 | B | 512 | 1 | 765 | MLAGQOREFPVGVGSADPALGAAGWP QRPQARDLQLAMPEPPISMGSCAAGA SPTSTAPCSKAPSPIDHPRAAECRRRARD WQAAPPAAPVRDPLGEASRAPESVKDV CIYDIMFDGGAGRFAAATLTGISELPAPF EERKSWKPKRQAPGALV* |
| 4198 | 12249 | A | 5120 | 3 | 329 | ETVSHSVAQAGVHWHHVGSQQPPSPGS KQFSNLSLPGGWYRHPPPHPANFIFLV ETGSHYVAKADLQLLASNDPPTSASQHA GIIGRSHCTRPRYI*WSNKL*YKIT |
| 4199 | 12250 | A | 5121 | 1 | 537 | ERQSCSVARAGVQWHDLGSPQP/LPPRL KRFS\CLNLLSSWDYRRALPHPG*FLYF* *RQGFTMLVRL/VLNS*PCDPPTSASQSA GITGVSHRARPVLRF*QNYYYFETGSGS AAQAGMQWPIAMAMQPQPRLKQASNL SLLSSWDHGMQPHANTTVCKTERKQV FRMHLLNNTNYREQ |
| 4200 | 12251 | A | 5122 | 1 | 197 | EAGSHSVAHAGEQWCDYGSLLQHQPVPV LKQFSLSLPSS*DYRCVPPCPANFLILM ISVSIRGSV |
| 4201 | 12252 | A | 5123 | 809 | 1472 | KTLLLSCLYLSKLWPVDYLRSSRLRRRAA SSFSGSWRFALQRTPTTTRRLSRSSKAVQ TAFPRRSPSSRHRCGSSSRATTTTCRMSFL SSLTTCAQQLAGWVTLKRSIGLRKRMS LMALKKWPCLMWKKRRSLPRYPQQRRT RGKKRSGSKIMIRRLNGQMGPRTVPAPA MKEVQI/TKLKKSKRRSCSHCSSKVCDS KS/VQEQGAP*VGGQPPPRG*SYAWC |
| 4202 | 12253 | A | 5124 | 1 | 504 | DSEPCSVAQAGEQ*RDLSLQPLSLGLK QFSCCLPSSRDYRRPPCLANFCYF*YR WGFTTSARPV*NSWPCDPPTSASQSAGT TGVSHQARLLLFFKAFKVWSGDSI*CVN EFNIISKISSFPHFTSTPQSCPMHSSQIKY K*F*DYP*CSKQAGGISIDTY |
| 4203 | 12254 | A | 5125 | 2 | 351 | KQGIIMTYVLRPPFFSRWSL/DSVSQAG VQWRVFGSLQAPPPGFLPFSCGT/RQPPS PANFFLYFLVETGFLF**RQGFTVLDRMV SIS*PRDPPALASQSAGITGVSPRTREQH S |
| 4204 | 12255 | A | 5126 | 1 | 1047 | MVSISWPRDLPASASQSAGITGLIGALVL SVGIYAEVER/HEI*NP*KCLPGSSHHHP PGRRHVHGLLHWCAGVPP*QPELLASL RLSRGYGLVLSWLEPRYEKMISGMYLG EIVRNILIDFTKKGFLFRGQISETLKTGIF ETKFLSQIESDRLALLQVRAILQQLGLNS TCDDSVLVKTVCGVVSRRAAQLCGAGM AAVVDKIRENRGLDRLNVTVGVDGTL KLHPHFSRIMHQTVKELSPKCNVSFLLSE DGSCKGAALITAVGVRLRTEASS |
| 4205 | 12256 | A | 5127 | 116 | 498 | YNFALKSELKFNQAIIVSLNKFFFFFLR WSLRPVAQAGVQWRDLGSLQPPPPGLT PSSCLSLPSSWNRPPPCPAKSFWM/M* RRGFTVLARMVVIS*PRDLPASASQSAGI TGVSHRTRQEGHS |
| 4206 | 12257 | A | 5128 | 3 | 490 | GIYHTLRTGQEGRSGSIKQQRLLQRLPYF FLFIFPSFLYMIEIKH*LSFYILLFAFNIVS* PFSYFIFFF/RF*DSVLLCGPWSTVA*S*L TAASTSDQDQDSPTSGPLKVTDRCVGH T*ANFYIFCGGWGGLTILLRRIPNSWAQ GIFPPWPPKVLGLQA |
| 4207 | 12258 | A | 5129 | 423 | 495 | |
| 4208 | 12259 | A | 513 | 594 | 1300 | LGASEPWQPRSQETPKHSWPSHP/PANQS KEVPENPNYALKCTLVGHTEAVSSVKFS PN/CENGLASSADRLIIWGAIDGKYEK TLYGHNLEISDVAWSSDSSRLVSASDDK TLKLWDVRSKGCLKTLKGHSNYVFCCN FNPPSNLIISGSFDETVKIWEVKTKCLK TLSAHSDPVSAVHFNCSGSLIVSGSYDGL CBIWDAASGOC1KTLVDDNDPVSSEVKE |

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| | | | | | | CRIWDAASGQCLKTLVDDDNPPVSFVKF SPNGKYILTAT |
| 4209 | 12260 | C | 5130 | 628 | 849 | MCGSVYSTIWSLIASRREETIRVIVLYIQS PNINTRHISKRGLNKGVNQFHKEDWNLL KRVCSHSGAEAGIFS* |
| 4210 | 12261 | A | 5131 | 350 | 412 | NFELKLSPYQKKSIVWGAAQVMPVAVG KPSSEWPPGSHMDNSQIRGNPVCIGIK*FS CPSLQCSWDYRCMTPCLANLFFFKLEGG FCHVAQTSKLLGSSSPFILASRSTGITG MNHHAIRQLLN*SIRE*HSITHRLTHSRE KSCECNLYGKTLSSNFPPTKKKVSTGELP R |
| 4211 | 12262 | A | 5132 | 3 | 189 | HERKAQPAGEGRTHMTKSDSLPSFRVST LPLESHHPDPNTMGGASHRDRALSGTAT VRDTRGIDPAPVHASPTRNRNEGRHVF KRFPDILTDRSISIYTDHHSIQIRTLRALS QL*TTPTQTPWAGPATGTGLSRGLPPYG TPEG |
| 4212 | 12263 | A | 5133 | 32 | 800 | FKTIKVRFLCIRVYSLCCKLLTYCDHFH SLDFEECAHKLLKMEFPESQTKELCNMI LDCCAQQRTEYKFFGLLAGRFCMLKKE YMESFEGIFKEQYDTHRLETNKLNRVA KMFAHLLYTDSLPSWSVLECIKLESETTTS SSRIFVKIFFQELCEYMGLF*/SLIARLKD GNLAPFF*/RIFPRDDPRITRVANSFFPSIA SGCLTYCPVSALSSIPRLPLVVALLLPIPIF HHDLLLELFLRPFYNDTLVLPFV |
| 4213 | 12264 | A | 5134 | 2 | 706 | RCNSAQQMTSSQKALMLELKSLOEEP VEGFRITLVDES DLYNWEVAIFGPPNTLY EGGYFKAHIKFPIDYPYSPPY/TFRFLTKM WHPNIYENG DVCISILHPPVDDPQSGAEL PSERWNPTQQCEGLILLRC*SHWLNBPQ HLSQPMSDASVMFRKWRDSKGKDKKE YGLKFIRETKFSATKARRQEKGG*RF TTLGNTCIKTEVPARNDEQVQSLLYDEL GMMTDIDDER*GRRKDAD\CYDD\DDSG E*GSPQPWAGIPASKLRPCNDEQVQSL LYDELGMMTDIDDER |
| 4214 | 12265 | A | 5135 | 7 | 219 | EGV*VSRDW*QWS/DIGSWRHSMTGSGD SLASAF*VSGGTGESHHKQLIAVNMVEM GSHRAGQAGNELSTL |
| 4215 | 12266 | A | 5136 | 2 | 309 | DGVSLLLSPRLQWHNLGLLQPPPP*FKGF SCLSLPGSWDYRHV/PPCLANFVFLVETG FRHVGQTGLELLTSGDPPASASQRAGIT GVSHRTWQKMYFLSQKYF |
| 4216 | 12267 | A | 5137 | 1 | 309 | SCLSLSSWDHRRVPAHPANFVFLVETG FHHVSQV/GLELLTSSNPPASASHSAGIT GVNHRAWLPGLNLR*FKMIIRRLRLLK NKFHSTILRKSETSNSCE |
| 4217 | 12268 | A | 5138 | 2 | 625 | TYGEMAKIVDVPTKQLRAPDPIDSMCH FCHNVSPCTRNGCVDMEHFKVIKTHQI EDERERREKKLYFGYSLGAHPILNQITIG RMQRATEGRKEELFALYSAHDVTLSPVL SALGLSEARFPRFAARLIFELWQDREKPS *TFVIRILYNGVDVTFHTSFCQDHHKRSS KPMFPLENLVRFVVRDMFLALGGSCNTN YYDACHREGF |
| 4218 | 12269 | A | 5139 | 167 | 688 | |
| 4219 | 12270 | A | 514 | 188 | 478 | QRGVLLKTANVLVPEDLGREMRIFFSVK TWKTFTCIFTKGTNIHLFLFYFFETASLS EAQAGAQLGSLQPPPPGGSSDPPASASPI AGITGACHH |

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| 4220 | 12271 | A | 5140 | 3 | 1230 | QRDSYAREFTTTVVSCCSAELQT/GEGAT ARNIFLSGFQVVLEDTVLFPEGGGQDD RGTINDISVLRVTRRGEQADHFTQPLDP GSQVLVRVDWERRFDHMQQHSQHLIT VAVADHLFKLETTSEWVGRFRSAIELDTP SMTAEQVAAIEQSVNEKIRDRLPVNVRE LSLDDPEVEQVSGRGLPDDHAGPIRVVN IEGVDSNMCCGTHVSNLSDLQVV*VLGT EKGKKNRTNLIFLSGNRVLKWERSHG TEKALTGLKCGAEDHVEAVKKLQNST KILQKNNLKSQAQ/RT*AVHIAHSLKEQSR LGRCGHITQEGG*FRVHEYHCQ*RLGQR RPSLFLTCCR*ERWWTLLYWQGHRLW RPWGPGLRSWEGKGACKKGRFQGKA TKLSRRMEAQALSPGLHQHAEC |
| 4221 | 12272 | A | 5141 | 3 | 306 | SRQWTLFADGQHSGPAAPCPCGEV*RTG ALNPKTFFQG/LPSAPGPCPVPHGASHP*T PQKLQPGNKSQMKPVKPGFPPSGAGGA WASL*PSSLPPFDLQYLL |
| 4222 | 12273 | A | 5142 | 1 | 306 | FFFFFL*QSCSVAQAGVQWYDPSQKP PPPRFERFSCNLNLPSS*DYRRPPSLPAUFV FLVETGFHHIGQDSLKLLASSDLPISASQS AGITGMSHCTWPV |
| 4223 | 12274 | A | 5143 | 81 | 657 | TAEKGGEETKSGELGRSQRTLSQVGATR GTSEEITLIVQMRDAGGSALCSGIGGGEK WSVLGVILKKDDRIVLAYCMGHEIKRGI EDDSKVFFFFFLEMKSCSVVQAGVQWH DLSSLQPALPRYK*FCSLSLPGSWDYRH VLLRLVNF*FLVEIGFHHVVQAGLKLLT SSDLPHSASRSAGITGVSHRARP |
| 4224 | 12275 | A | 5144 | 3 | 494 | ETEDLALSPQAGVHVAR/SLSSLQPPPPG VFKQILCLSLSSWDYRG/PCHPHAKFL AF*VETGVSPSWAR/LFLNS*PRDPPASAS QSAGEPPRWASVCNSVKMLSSAFNWCV CRLHKEKWMRRQKTHVMIPHSNRCSS RHFSRIPSSIETYNLRLHTLLAGRF |
| 4225 | 12276 | A | 5145 | 3 | 123 | ESGSHSLPKL*CSGAITAHCNLKLGSR DPPTSASGVAGT |
| 4226 | 12277 | A | 5146 | 3 | 292 | RQRLNSVTHSGVQWRNPGSLQPLPPGF KHFSCLSLSSWDYRHTPQCPAUFVFLV ETGFRHARLVSN*PHNLPVSASQ/SAWI TGLSHHARPCVSF |
| 4227 | 12278 | A | 5147 | 2 | 303 | FLGWSFTLVVQAGVQWRDLGSPHPLPP GFKQFFCLSLPSS*DYRHAPPHLANFVFL GEMDFLHAWQAGLELLTSGDPPTLASQ SAGITGVRHCSRPFVSE |
| 4228 | 12279 | A | 5148 | 2 | 613 | PRVRTYRFGSVGHDTQLCLWDLTEDILF PHQPLSRARTHNTVMNATSPAGSNGNS VTPGNSVPPPLPRSNLPHSAVSNAGSK SSVMDGAIASGVSKFATLSLHDKRKEKAP RERSQSRNHSNGHNF*QEASDKLESS/SP KPKPDPAKTLGTPLCPMEDVPLEPLIC KKIAHERLTVLIFLEDICIVTACQEGFICT WGRPG |
| 4229 | 12280 | A | 5149 | 2 | 393 | IGFQPQLTEFQVSLQDLEKLSGLVFFPHL DRTSDIRNICSVDTCLLDFQEFTLYLST RKIEGARSVLRDLKIMDHLKNV*NEPYD YPMRRYYKKLQELTAIDLSTHISQPSLL SYTCLISGATPPFT |
| 4230 | 12281 | A | 515 | 355 | 612 | SFSISGFSASIALVCQLLAVKGSVFEVG GISYCPLNVFLDLQVAPEEDERKKRRR ERNKIAAAKCRNKKKEKTECLQKVSFAF |
| 4231 | 12282 | A | 5150 | 644 | 962 | NASSLAWTVLLKLLVGFGAGQCMGNFF FCWGGAMESPSVAQAGVQWRNLGSLQ PPPPGFKRFSCLSPSSWDYRHPVPPHAN FACFSRDGVSRCPGWS*TPDLR |

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| 4232 | 12283 | A | 5151 | 3 | 321 | RRCLCAGYFKNVARRSCWRTFCTMDGR GSPVHHHPSSALHEQETKLEWIFHEVLV TTKVYARIVCPIRYEYVVRDLLPKLHEFN AHGFEQCGPT*SERRCKKEMDK |
| 4233 | 12284 | A | 5152 | 237 | 602 | LLITGRQYSLTFRFYIHLRNKILNSGLG KPPLKLHFYTEAFFARNPDQMEFHSVAQ AGVQWHDLG*LQPLPAGFKQFFCLRFLS SWDYK\GTPPCLAGFCIFSRDEVSPRWG WS*TPDLK |
| 4234 | 12285 | C | 5153 | 166 | 417 | |
| 4235 | 12286 | A | 5154 | 282 | 1112 | FLKRENLLKNVCRNKLDLRPNRASPTGS QEWQRHGVQSEVQFVHSLKPGPPADS CRTAA/GDPGGTETADPGHTGLELRFPEP PKPTLPLALSEAPVP/PERGENTGPRSLPS TPMPSWGPLLSSPPRPATSPSPQAN*PP PPRPSSHPTTVPPTRPQWQPGCCAQPP RPCLH*RGGN*VY*GMQLHQKSVSWPH SQWPQKREGNGSSHEIHPSCPPSGFHGPS PEGRMPTQAGALHSWVPGLSLSHSGSP HPPPRWTATVQAARPRVPLTNL |
| 4236 | 12287 | A | 5155 | 69 | 734 | SRLGRDHVGPGLGGVG/VRR/RENDIGEY EGGRNEAGERHGRGRARLPNGDTYEGS YEFGRKHGQGIYKFKNGARYIGEYVRN KKHGQGTFIYPDGSRYEGEWANDLRHG HGVYYYINNDTYTGEWFAHQRHGQGTY LYAETGSKYVGTWVNGQEGTAEIHL NHRYYQKFLNKNPVGP/AKVCI*CWV*T TW*ISFNRYGKRRRGRGRISNCCSKME SYPNH |
| 4237 | 12288 | A | 5156 | 4 | 674 | GVQRGHFQEAKGSGRCLSSLNVPHPSP SAGMDPSSPVNPPEEAGGPLAQVPSAAL AQVAPGPVPISSLLEGTPTSLPF*ERGNSS HKQASGPERGARPPALLGPQEIIGSSK/Y PPPGPGSTLGKGLLASPRCGPPQVLGWG LRDPTRELEGPWWSL/GNTPREPSIKCSP* MGRMGAQPLPKAEGAPPPTQLPPTHSR RILGPLGASPERPPPRVVPGGEG |
| 4238 | 12289 | A | 5157 | 3 | 342 | NFFFLRQSF/NSVTQAGVQWRDLGSLQ LPSGFTPFSCLSLLSSWDYRHPPHPANF LYF**RRGFTLLARMVLIS*PHDPPTSASQ SAGITGVSHGAWPKSIFFLNAEVMLEY |
| 4239 | 12290 | A | 5158 | 1 | 251 | VCVCGFCFVLETESRSVTQAGLQRHHL SLQPPPPGFKGFSCLSLPSSWDYRCP LANF*FLVEMGFHHVGQAGLKLVA PPASVSQSAEMTGVSHHALPG*SRVTQ AGLQRHHLCSLQPPPPGFKGFSCLSLP WDYRCPPRLANFCIFSRDGVSPRW SGW SQTRGLK |
| 4240 | 12291 | C | 5159 | 24 | 362 | MGITVFRXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXS* |
| 4241 | 12292 | A | 516 | 3 | 853 | SQARTACLSSLAARAHPARAPAVSPR CSPAGQTNSPPDPVPTLAAPSGAWSKM MLQHFGQVSASEVSASAIVCLSPPGSLV FEDFANLTPFVKEELRFAIQNKLCHRM SSALESVTVSDRPLGVSTKAEVAPEEDE RKK\RRRERNKIAAAKCRNKKKEKTEC LQLQY*QSHRPPLWHHQGFSEEEGLHFP KPSAALPSIFLSQLDEPRCV\QSEKLES VNAELKAQIEELKNEKQHLYMLNLH TCIVRAQNGRTPEDERNLFIQIKEGT LS |
| 4242 | 12293 | A | 5160 | 1 | 287 | FFFF*DIRVSAQSPRLECSGAILAHCNLCL PGSSDSCASTSPVAGITGMCHHTQLIFFV FLVETGVHHVGRAGLELRLQVHPPQP PKVLGLQA |

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| 4243 | 12294 | A | 5161 | 1 | 1672 | QTGLQATTKHSGFPVRMDNAVPIVPQAP AAQPLQIQSGVLTQGSCTPLMVATLHPQ VATITPQYAVPFTLSAAGRPAIVEQDC RCTAGVAWKGLKQILLPSNFGQQLAWG *ALHNSVQPTAMIEAMSGGQQLADWR NAHSHGNQYSTIMQQPSLLTNHVTLATA QPLNVGVAVHVRQQQSSSLPSKRNKIQS APVSSKSSLDVLPQVYSLVGSSPLRTTS SYNSLVVPVQDQHQPPIPDTPSPVSVITI RSDTDEEEDNKYKPSSSLKPRSNVISYV TVNDSPDSDDLSSPYSTDLSALRGNSSG SVLEGPGRVVADGTGTRTIVPLKTQLG DCTVATQASGLLSNKTGPVAVSVGSSG CCITPTGYRAQRGGTAAQPLNLSQNNQ SSAAPTQERSNPAPRRQAFVAPLSQA PYTFQHGSPHSTGPHLAPAPAHLPSPQ AHLYTYAAPTSAALGSTSSIAHLFSPQG SSRHAAAYTTHPSTLVHQVPVSVGPSLL TSASVAPAQYQQQVATQSYIGSFRGST IYTGYPSPKISQCYL |
| 4244 | 12295 | A | 5162 | 1 | 111 | ELRYKRWPGWKADTPQAQTVKWVGV GKSRESMIQLF |
| 4245 | 12296 | A | 5163 | 2 | 1034 | DRAHLVDFHQAQVDGLQEVQRAQEGK NIGTTKKGIGPTYSSKAARTGLRICDLLS DFDEFSSRFKNLAHQHQSMPFTLEIDIEG QLKRLKGFAERIRPMVRDGVYFMYEAL HGPPKKILVEGANAALLDIDFGTYPFVTS SNCTVGGVCTGLGIPPQIGDVYGVVKA YTTRVGIGAFPTQINEIGLLQTRGHEW GVTTGRKRRCGWLGSMILRYAHMVNG FTALALTKLDLVDLGEVKVGVSYKLN GKIRIPYFPG*PGRCFKKGRKLKYETLPG WKVADTTGRPGRWEDLPPQAQTYIRFVE NHVGSRSYHYQSFLVSVKWVGVGQ VQESPMIQLF |
| 4246 | 12297 | A | 5164 | 3 | 148 | LLSSRDHRHVPPHPANFFCRD/RGLAMLP RLALNSWA*AIHPPWPPKVL |
| 4247 | 12298 | A | 5165 | 3 | 325 | YVFSGDLAHQILNVSLGIRRLHADSV GICLAKLRIAPVPPHNSVFNWRCPYS SCSYVHLITSHQFQPSSEIKYWNHLQHN KHNAACANAA*EKAGMYRHRRLH |
| 4248 | 12299 | A | 5166 | 373 | 950 | SRGVFFFLRQSFTLVA*AGVQWCDLGS QPLPPRFKQFSCPASLVSWDYRHAPHP ANFFIFLVEDKGFSMLVRLGLELPTSGDL PASASQSPGITGVSHHARP*MILFIFMFSF GRRDGVSVTQAGVQWHDLSLQASPSG FMPFSCSLSPSSWDYRHV*PCQANFLYF* *ANLSRVSPCWGWSRTPNLK |
| 4249 | 12300 | A | 5167 | 2 | 334 | VRHRTLVLPQAGVQ*CSLG*QOSPPWF KQFSCSLSPRSWDYRHLPPHPANFFVF/V EKTGFHHVGGAGLELLTSVDPASASQS AGLTGLSHHAQLSFNLSAKKSFTKTRS |
| 4250 | 12301 | A | 5168 | 35 | 437 | |
| 4251 | 12302 | A | 5169 | 1 | 1845 | |
| 4252 | 12303 | A | 5170 | 1 | 212 | |
| 4253 | 12304 | A | 5171 | 371 | 915 | |
| 4254 | 12305 | A | 5172 | 1 | 2460 | |
| 4255 | 12306 | A | 5173 | 1 | 933 | LESMIGIDPGNRGIGHLLCKDELLKASLS LSHARSVLITTFPTHFNHEPPEETDGP GAVALVAFLQALGRRSP*SLTREPVLH QKIVEDALSKVF*RRRSRY*LTQVDQW KLLRHSCAKIGDPQTLRFDHLVAIERAG RAADGNYYNARKMEHQAL/RLTPFDDL FLASAKKIPGISSIGVGDGNGELGMKV EA/DEEAHTARGCHRLATWKAFAVIAG VSNWGGYALACALYILYSCAVHSQYLR KAVGPSRAPGRFRPGLRPSRRSLRKKKC |

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| | | | | | | WASWCSTKSGVASRASWAWRWMGCPS TTPTPR |
| 4256 | 12307 | A | 5177 | 1 | 439 | |
| 4257 | 12308 | A | 5178 | 1 | 552 | GNEFSILKSPGSSVFRNGNWPIPERIPD VAALSMGFSVKEDLSWPGLAVGNLFHR PRGYPSWVMVKGSGTKLALTPQAVVIS YPLENRVYMVGKANSVFEDLSVTLRQ LRNRLFQENSVLSSLPLNSLSRNNEVDLL FLSELQVLHDISSLLSRHKHLAKDHSPDL YSLELAGLDEIGKRY |
| 4258 | 12309 | A | 5179 | 3 | 1111 | ILKSPVGSVFRNGNWPIPRERDPPDVA ALSHGLPL*KKDLSWPGLAVGNLFHRP RATVMVNVNGVKNKLDLPPAGSGISYPL ENAVPFLDSVANSUHSLSFSEETPVVLQ LAPSEERVYV/VKGRANSVFEDLSVTLR HSRNRLVFKKTLFLSFTPPQILLSRNNEV DLLFLSELQVLHDISSLPSRPKHLVARDH SPDLYFTGSWAGLDEIGKALLGEDSEQ FRDASKILVDALQKFADDDHVPVFMVGN PVVELVHCPSHLNTSPPLGKTRDLPLRPK QAQEPQQVPYNLA\YKYNFEYSVVFNM VLWIMIALALA\VIITSYNIWNMDPGYD SIYRMTNQKISEWIECYLWPRIKRGFG NWLFC |
| 4259 | 12310 | C | 518 | 512 | 739 | MAEHHWAFPIPSXASXGFAXLQPTKATL KKXEGFKXFXKKKKKKKTPEGGAXGTX IXXPXGGAGXNKXPXGXXXG* |
| 4260 | 12311 | A | 5180 | 18 | 594 | NVAGTAICSFAPGRRQTPCHTREPQDGR PRARLTAWTRARGTCRVAHTHTGRQNH PMPLWGFSRHHRAFSEHLSLGCAPPSAT WT*TRSPAAAAAGP/PVPRKPNPSPPSRS PAGLRPPGRAGPLTSPRCGPPASQASDT VGPVRHKQRGPTSDVSGAWDGPATAAS GPVVRLYPSTLGGGRGRQITRSADKT |
| 4261 | 12312 | A | 5181 | 68 | 446 | RLTSELAQTLAVHPSKSARPRP*AGEKP GKKPPLQVNGAWD**PRVGADPGHSPD SLDPSTGQDVQGGSSYSYWEGRITIMPLW GFPDRAGLLGSPGSSGPGKRRPILAGQPY KLELQARFLGPGH |
| 4262 | 12313 | A | 5182 | 2 | 512 | APPSATWT*TRSPAAAAAGP/PVPRKPNP SPPSRSPAGLRPPGRAGPLTSPRCGPPAS PGIGHCGCRQTQAAWPRRTYQGRGMG PRPRPRRPVVPVGGERSHSHPSGPPLRSP GPEWGLTSSSCPARG/PGGCLCPQNQLPN PGP/SGPASPNNLPSRLHPTDTSGBPFPRA |

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| 4263 | 12314 | A | 5183 | 14 | 720 | RNFDPDRPTRPRTRGRTRGRTRVTFGPG PVASAGCSRGDGRFGEAGPTALDSGADS GVRDTLPVHEPGSCLRYRTPRPRSRRAH PTPLIRPTSGPRCFGSDGTHSVRCPVNAG RPGHLGLGG/AKSSGFAGQKGRLLAAG TCGVHVQGPLRAARPQEVLFQGGPLQP AAVEQPPATGAWLQPRLCSEKAL*LP* GAP/SQSPPRPMQIPITVPASG*NAGGPGA SGGTRVPG*KLPDTGGP/SAQHPLSPTGL PHDARP/PSSCPTGRSCVHCPQLNAVHL* E*PANSELSRPLESDTGP*AAPTRPGSAG PISDPHSVPPSSPSSSGTPALPGHMSS/GG KWYQHQPASACPVLGL/PPDPGAEKAGSQ PSPGHLVQAPGHPGPPGHTPAVTPSFPN SRAALPSFSR*PCQSPKPKQSGCDPRPR KPKPWKFQGS*GLPLQKNRPPFSPRTG ATPGEPPGAL/PLSGNPPKSHRDGSALPS MSMSHPARPSVLGSKLSGFLPSSWPGPC TF*WMKCGRTRSIRGHSCAWLKA |
| 4264 | 12315 | A | 5184 | 2 | 1558 | RRSRDSGYRAPPASHSRPGQAARAFAPR PARREVCCPRPGVPRRARTTRKTPTWAA VATGTRGASAEGGPTGLAHG/SGLAAAA GLMGCEPASGWGPGRQSGGARTAAAGS SGSSSGGPSAPTSSSVLGSLVAPVSPY KPGQTVFPLPPAGMTYPGSLAGAYAGYP PQFLPHGVALDPTKPSLVGAQLAAAA AGSLGCSKPAGSSPLAGASPPSVMTASL CRDPYCLSYHCASHLAGAAAASASCAH DPAAAAAALKSGYPLVYPTHPLHGVHSS LTAAAAAGATPPSLAGHPLYPYGFMLPN DPLPTSATGCRPTGRATSASPRKSC*AT /SRHTAFPGTDKLLSGYPSSSSLASAAA AAMACHMHIPTSGATGQPWDAGAAQPP PRGWDSAAATTPTPRA/ALPTPGAPVVPV AATGPYYSPYALYGQRLTTASAAGVSV RGGREGERGIGRKRGRGGVQGEAASRT RLLTARGEGLGPRKERNVLPYISYPTAA TETRWDTPLLPTFTSHTQTL |
| 4265 | 12316 | A | 5185 | 6 | 56 | VVAWRGSDSFGLTSKLVQRQVFHHQL LKTVPHQAHFY*LPRAALQQIHRC*LPR/ DTSQVAASLLASKSSSQTSGSLVSKSTSL ASVSQLASKSSSQTSTSQLPSKSTSQSSS SVKFSCKLTNEDVKHEATFF/LIRLYKTV AWKLVAVGGFSPNVNHGELLNAAIEAL KATLDVFFVPLKELADLPQNKSSQESIVC ELRCKSVYLTGCGKSKENAKAVASRE ALKLFLKKKVVKICKRKYRGSEIEDLV LLDEESRPVNLPPALKHPQELL*CVQNIT AYNIWYLKRKTDFCIV*N |
| 4266 | 12317 | B | 5186 | 133 | 345 | RLSERRNWTQAMLYLKGAQGRRYLLR PEPANGPLRPAHCRIDHAPISTYYILRRPE PSYRSSSYFPDDD* |

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| 4267 | 12318 | A | 5187 | 2 | 2168 | KESRRTVRRMLRGRSLSVTSLGGLPQWE VEELPVEELLLEFEVAWEVTNKVGGIYTV IQTKAKTTADEWGENYFLIGPYFEHNMK TQVEQCEPVNDAVRRAVDAMNKHGCQ VHFGRWLIEGSPYVVLFDIGYSAWNLDL WKGDLEACSVGIPYHDREANDMLIFG SLTAWFLKEVTDHADGKYVVAQFHEW QAGIGLILSRARKLPATIFTTHATLLGRY LCAANIDFYNHLDKFNIDKEAGERQIYH RYCMERASVHCAHVFTTVSEITAIEAEH MLKRKPDVVTPNGLNVKKFSAVHEFQN LHAMYKARIQDFVRGHFYGHLDLDFLEK TLFLFIAGRYEFFKTKGADIFLDSLSRLNF LLRMHKS DITVVVFFIMPACTNNFNVET LKGQAVRKQLWDVAHSVKEKFGKKLY DALLRGEIPDLNDILDRDDLTIMKRAIFS TQRQSLAPVTTHNMIDDSTDPISTIRRI LFNNRTDRVKVILHPEFLSSTSPLLPMDY EEFVRGCHLGVPFSYYPWGYTPAECTV MGIPSVTTNLSGFGCFMQEHVADPTAYG IYIVDRRFRSPDDSCNQLTKFLYGFCNMS RRQRFIQNRNTERLSDDLWDWRYLGARY YQHARHLTLRQSFSKINFHVGTHAPPT DRKDFKYPR/PCSYPPFSFGSSGPSSP QSSDVEDEVEDERYDEEEEAERDRLNIK SPFSLSHVPHGKKKLHGEYKN |
| 4268 | 12319 | A | 5188 | 1 | 1347 | |
| 4269 | 12320 | A | 5189 | 1 | 272 | QTEGFKYRRPSSVPPSPSGSQASSPQSSD VEDEVEDERYDEEEEAAGFG/RVV*ESPSI LYAVPYSDSCCQVTPSLHCSHFILFPKT DKSS |
| 4270 | 12321 | A | 519 | 1 | 760 | |
| 4271 | 12322 | A | 5191 | 225 | 430 | |
| 4272 | 12323 | A | 5192 | 16 | 1420 | PSVRRNQRF*SCKDFDYWHN*RKQEGC YT/VLEKKVLSNRKQRF/DGSSGKLTGS TSSLNKL SVQSSGNRRSQSSSLDMGNM SASDL DVADRTKFDKIFEQVLESEPLCL AEQDFISKFFKHSNIKVCLELWAGSRGP GMGGTITAT*LLGTPLPVSEKDMIRQM MIKIFRCIEPELNNLIALGDKIDSFNLYM LVKMSHHV* LQONVDPASFLSTTLGNV LVTVKRNFDCISNQIRQMEEVKISKKS KVGILPFVAEFEEFAGLAESIFKNAER/RG DLDKAYTKLIRGVFNVEKVANESQKT PRDVVM MENFHHIFATLSRLKISCLEAE KKEAKQKYTDHLQSYVIYSLGQPLEKLN HFFEGVEARVAQGIREEEVSQYLA FNK QELRKVIKEYPGKEVKGLDNLKYKKVD KHLCEEENLLQVWWHSMQDEFIRQYKH FEGLIARCPGSGVTEFT |
| 4273 | 12324 | A | 5193 | 2 | 391 | FFFFLRWSLA/SV/TQAGVQWRGLGSWQ RPPPGFKSFCLSLSSWDYRRPPHAQLI FVFLVETSFTMLAGMVIS*PRDPPASAS QSAGITGVSHRARLTLLIFKRCIRDESFE VFLVYVLFKTNILLKA |
| 4274 | 12325 | A | 5194 | 2 | 302 | KTLQSGCPRLEVQWCNLGSLQPL/PFPGS K*FSCLSLPGSWDYRSVPPRSANF*FLV ETAFHHVGGAGLELSTSGDPPVSASQSA GITGVSHSARQ*RAF |
| 4275 | 12326 | A | 5195 | 2 | 388 | RATPRHIVRFTKVEMKEKMLRAAREKG RVTLKGKPIRLTADLSAETLQSRREWG /FNILKEKNFQPRISYPAKVSFISER*IKYF TDKQMLRDFLT SRPALKELLKEALNMER NNRYQPLQNHAKM |

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| 4276 | 12327 | A | 5196 | 1 | 578 | VAAKCMHKDAKKGFIRLDMS*FQERHE VAKFIGSPPGYVGHEEGQLTKKLKQCP NAVVLFDVVDKAHPDVLTIMLQLFDEGR LTDGKGKTIDCKDAIFIMTSNVASDEIAQ HALQLRQEALEMSRNRIENLGDVQISD KITISKNFKENVIRPILKAHFRDEFLGRI NEIVYFLPFCHSELIQLVNKEC |
| 4277 | 12328 | A | 5197 | 3 | 1618 | |
| 4278 | 12329 | A | 5198 | 495 | 653 | MTLTSIDPVLTTFFNLECPL/VFTATASSG LGEVE*AIALN |
| 4279 | 12330 | A | 5199 | 1 | 1433 | MPESNCSLTWRHSVGRAVAAQGGHSS QGASLVLGEPGGSSWLLGLEGDTGLW GGLLEKGRITDGGKGTIDCKDAIFIMTS NVASDEIAQHALQLRQEALEMSRNRIAE NLGDVQISDKITISKNFKENVIRPILKVR GLSWHFLLEPKAHFRDEFLGRUGEIVY FLPFCHSELIQLVNKELNFWAKRAKQR HNITLLWDREVADVLVDGYNVHYGA RSUKHEVERVRVNNQLAAAL*SRTLLP GCTLRITVEDSDKQLKSPPELSPQAEKR LPKLRLIIDKDSKTRRLDIRAPLHPEKG RLTDGKGKTIDCKDAIFIMTSNVASDEIA QHALQLRQEALEMSRNRIENLGDVQIS DKITISKNFKENVIRPILKVRGLSWHFLLE PKVLTFFNLVLYLHGNSIQLGEVNKL AVLPRLRSLTLHGPNMEEKGYYRRARG HSLHQGIEKYICESDDIFRKYCNNQFL |
| 4280 | 12331 | A | 520 | 669 | 823 | |
| 4281 | 12332 | A | 5200 | 1823 | 4712 | FFKNLCSAHYY/TWCVLPFFFLRQG LNSIGQAGVQWCNHSSLQPCPRLKLSL HLSLPSSWDHRHAPLRMT/NFFKYLRRG LPVLPRLVSNSWAQVVLPS/SASQSIGITD MSH*PAQLPNSLPFFKRQFRSISPLGM Q*CDHSSL*PQTLGLKQFSHQPPFFVQ MGSCYVAPSW*TPKENTTIQHHPMYT LKTTVTFLYTELYSDIA |
| 4282 | 12333 | A | 5201 | 3 | 298 | RQSCSVA*AAVQWRDLSSLQPPPLGFKR FSCLSLSSWDYRPPRPNVNF*KIFLIET GFHHLGQAGVERLTSVDPGASQSAGII GISHCTWPELFK |
| 4283 | 12334 | A | 5202 | 1 | 422 | APMPAATMTARSGPAAISTRCPWRPRSP STPRPSWSGTCCAPTRSLRAATASQGPS PATNTPSPRAASPP*RVWAPRTETIKGHT AHSRLTGATTGPKLSAP/VATESGHPDSQ KPPTHPGTSDTILPPETASHPSTRRP*LPP ETASHPSTRRP |
| 4284 | 12335 | A | 5203 | 123 | 201 | KRGFCWVPQVGGQGHDFGLWQSPFPGL RQFSGFFLWKSWDYGHPPPC*ISSSSSSS SVFSSSSSSSLKLWT*GDPLA*VSQRVGIP GLSHWP*PRLGGRGTILVYGNLHFRD |
| 4285 | 12336 | A | 5204 | 88 | 167 | KINMGILLKLVYRFNINPVKTPAGLFSSS SHE/ITEIDKRILKFIWKCTEHRIAKQSLK RTKLEDFLLNFKTYEATEIKTS*YRFNI NPVKTPAGLF |
| 4286 | 12337 | A | 5205 | 179 | 474 | FGFQINVFKDPVADPNKRSKKGRSLHR TPVAGNFVTL*GKGDLLEYGQDLLHTV *KNGKVTKAYSFDEIRKNAQLNIELEAA RSLGLMDWVCVCM |
| 4287 | 12338 | A | 5206 | 195 | 351 | |

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| 4288 | 12339 | A | 5207 | 1 | 1080 | ERCTMPDEPLVRAPDKGTDSPSPPLEET SNGGRMLHESLRHAVPITRMQSSDTEA GWPAYSEDEYEDIEPRTLNEITTVTDKT SPWSSVISDTSEVISQPDEVQREGPSCPS PGPFCEELMVKSSFLSSPERAVNPHLPR QD'SPSQSLVACECEASKARVGGESASA NPQIPCPITLSGAQQSSITVGVSSPQTDQ NKEPKSEAPAIEELKVATS*GSVDSA*LA FKKLPLNLASQSRRENHKGPPIDSSDIRQ RQVTTGSETSTKQSLLLPGPIVVPNFFLPP QQLEASLRMLSLSATLPPAATTDQDKSE ATRGALSQRPCRPRPNSLPLNLPPEETLR IARIFSSQYSQKD |
| 4289 | 12340 | A | 5208 | 1 | 1140 | AIVEDKHSGRSYDITSDLGNVLTSTSIK TVNG*AESSDSGAESDEEDAQEDLMGA YHSDIDKKMMKIVADHKNLEVIVTNGY DKDGFVHDIQNDIHASSSLNGRSTVHVK PIDENLGQTGKSACVCIHQDINDDHVEDV TGIQHLTSDSDSEVYCDSEOFQGEESL DSFTSNNGPFFQYYLGVHSSPPMENSGR EDIQGPNGNIGNMQVVAVEGKGEVK HGGEDGRNNSGAPVHREKRAGETDEFSN VRRGRGHRMQHLSNEGTKGRQVGSAGD GERWGS DRGSRGSLNEQIALVLMRLQE DMQNVLQRLQKLEMLTALQAKSSTSTL QTAPQTSQRPSWWPFEMSPGVLTFAH WPFIAQWL VYLYYQRRRRKLN |
| 4290 | 12341 | C | 5209 | 68 | 331 | MLKNVLMRCKGVHDREKFLVLDYFCQS SVLAVLYLILSLCYFPYQDVASECEVKC MPTFOFFKKGQKVGEFGANKEKLEATI NELV* |
| 4291 | 12342 | A | 521 | 3 | 108 | VCREREHPQKVFNKMPK*SYRTVPVTP GIVLSL |
| 4292 | 12343 | A | 5210 | 935 | 1036 | |
| 4293 | 12344 | A | 5211 | 1 | 3270 | MRPKTFPATTYSGNSRQRLQEIREGLKQ PSKSSVQGLPAGPNSDTSIDAKVLGSKD ATRQQQMMRATPKFGPYQKALREIRYSL LPFANESGTSAAAENVNRQMLQELVNAG CDQEMAGRALKQTGSRSEAALEYISKM GYLDPNEQIVRVIKQTS PGKGLMPTPV TRRPSFEGTGDSFASYHQLSGTPYEGPSF GADGPTALEEMP/PAVRGLPFRSRPPRA RPPAPAPTQGLRCQRRGSRGTLPAAGRA LR |
| 4294 | 12345 | A | 5212 | 3 | 274 | LERLIFVGG LGQFFPPKLRFFPKIPQLVF FSPFRKIFPCPPRLSLGPPRVLLKGPPS SSSSSSSSKKC*PLMFYCHRRWPTGVYV LP |
| 4295 | 12346 | A | 5213 | 403 | 776 | QGP DHFSLFWHLLQAPGLSPCLKWATA LETTPSPNGLPIVPVFGSSRMAGMIEISH IIEIGFLPNKEKKKGCPPLFRNFGFKF APSGLKVGYLKVFEPLKNYS DHDVIKW VR*VGRASGIY |
| 4296 | 12347 | A | 5214 | 165 | 439 | PPRQAKMQNLAAPGSHSQSPW/TLRPA L*LTPSQIFSA*RLKTDARS PRKPPSFQ PVSLASITVVGDGQASKPLKTPQLWCQ LRQYSFK |
| 4297 | 12348 | A | 5215 | 2 | 525 | AAED*HCPIASETYKTITLWVTL PVEG KSVPFLLINTEATHSTLPSFQGPVSLASITV VGIDSQAYKPLKSSQLWCQLGQYSFMH SFLVIPTCPVLLGQDILT KLSASLTIPGL QPHLIATLFP SLKPPSHPLVSPHLNPHIW DMSTPSLVTDHAPLTIPLKPNHPYPVQC |
| 4298 | 12349 | A | 5216 | 1 | 425 | PGNEIYR/KGTISFFEIDGRKNKSYSQNL LLAKCFLDHKTLYYDTDPFLFYVMTEYD CKGFHIVGYFSKEKESTEDYNVACILTL PYQR/ RGY/GKLLIEFSYELSKVEGKTGP EKPLSDLGLLSYRSYWSQTINEISEITS |

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| 4299 | 12350 | A | 5217 | 25 | 193 | LGGCEDSRRKGAAPRCFLSRGDHSWEPRD *PPPWLFPNSC**LAAGRPSPVRSSPS |
| 4300 | 12351 | A | 5218 | 1 | 1383 | |
| 4301 | 12352 | A | 5219 | 1 | 1617 | MAEVGEIIEGCRLPVLRNQNEDDEWPL AEILSVKDISGRKLFYVHYIDFNKRLDEW VTHERLDLKKIQFPKKEAKTPTKNGLPG SRPGSPEREVPASQAQSGKTLPIPVQITLR FNLPKEREAIPEGGEDQPLSSSSCLQPNH RSTKRKVEVVPATPVSETAPASVFPQN GAARRAVAAQGRKRKSNCLGTDSDSQ DSSDGIPSAPRMTGSLVSDRSHDDIVTR MKNIECIELGRHRLKPWFYFSPYQELTTL PVLYLCEFLKYGRSLKCLQRHLTKCDL RHPPGNEIYRKGTISFFEIDGRKNKYSQ NLCLLAKCFLDHKTLYYDTPFLFYVMT EYDCKGFHIVGYFSKEKESTEDYNVACI LTLPPYQRRGYRKLLIEFSEYELSKVEG KTGTPEKPLSDLGLLSYRSYWSQTILEIL MGLKSKSGERPQITSNDISEITSIKKEDVI STLQYLNLYYKQGYILTSEDIVDGN ERPMLKRLLRIDSKCLHFSQRTWSQE VDSGDQDTCPHCKCORPASQDLGAD |
| 4302 | 12353 | A | 522 | 383 | 542 | LWSPPNISNLDTTTAGEPTEQDLNRERER EKE/RERERERERERERERERERERERES |
| 4303 | 12354 | A | 5220 | 890 | 1537 | MLLMFICDLLLLTLSCSIALGYELSKVEGK TGTPEKPLSDLGLLSYRSYWSQTILEILM GLKSESGERPQITIK*AWRCLPGGTWHG LSVPGLSLGSLGTDKGPQGT*PVLSHSE ISEITSIKKEDVISTLQYLNLYY/KGRE GRGDRCVGCRVQSSVG*PPAEPISSAQG QYILTSEDIVDGERAMLRLLRIDSCK LHFTPKDWSKRGKW |
| 4304 | 12355 | A | 5221 | 2 | 434 | LRDGVLLCHPGWSTVAQS*LTAALNFW VRGSSCLSL*LVLRNSPLHPANLFFYFC R/DKHLTILTRLVLNFWAQVILRPWLPKG LGITGMSHCTQPNFKNQKGYCQVNFN NQTKTSLAGNTYFTPIFFGNKHVTSY NFPSM |
| 4305 | 12356 | A | 5222 | 3 | 384 | VVAAEVPSEFFFFLRTESCFVTQAGLQW HDLGSATSI/SPGSSDSPASASQVAGITGR HHYALA*FFVFLVDMGIHHVSGWSRN SLNLVNLPLCLGPPQYWGLQGMSPMPRP LKCPSLKGKMPNSHP |
| 4306 | 12357 | A | 5223 | 2 | 322 | LYFFSFETESCSVTQAGVQ/WWCDLGSL ATPPP/GSSNSCASAS*VARITGVHHHAQ LMFVFLVETGFHHFGQSLKPLSDPPAS ASQSAGINRCEPPGTGHYIFSK |

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| 4307 | 12358 | A | 5224 | 1 | 2535 | MQPLDFSSGSDPNISLSEKIRDQLVVGQ LIPDCYVELEKILSERKNVPIEPVIDRKR LLQLVRENQLQDENELPHAVHFLNESG VLLHFQDPALQSDLYFVEPKWLCKIMA QDVSSIFGLYIRDILTVKVEGCPKHPKGII SRRDVEKFLSKKRKFKNYMSQYFKLLE KFQIALPIGEEYLLVPSSLSDRPVIELPH CENSEIIRLYEMPYFPMGFW SRLINRLL ISPYMLSGRGICLLGQVVDHIDSLMEEW FPGLEIDICGEGETLLKKWALYSFNDGE EHQKILLDDLMKKAEGDLLVNPDPQRL TIPISQIAPDLILADPPRNMMLNDELEFEQ APEFLLDCFVCIHLYPSSDYISRHYMRTI NIVQTGFAKCRWRVTVHGADHGDGSFG SVYRAAYEGEEVAVKIFNKHTSLRLLRQ ELVVLCHLHHPSLISLLAAGIRPRMLVM ELASKGSLDRLLQQDKASLTRLQHRIA LHVADGLRYLHSAMIIYRDLKPHNVLLF TLYPNAIIAKIADYGIAQ/SLL*NGD*KTI QRGTPGFRAPEVARGNVIYNQADVYSF GLLLYDILTGGRIVEGLKFPNEFDELEIQ GKLPDPVKEYGCAPWPMVEKLIKQCLK ENPQERPTSAQVFDILNSAELVCLTRIL LPKNVIVECMVATHHNSRNASIWLGCG HTRDQGLSFLDLNTEGYTSEEVADSRILC LALVHLPVEKESWIVSGTQSGTLLVINTE DGKKRHTLEKMTDSVTCLYCNSFSKQS KQKNFLLVGTADGKLAIFEDKTVKLG AAPLKILNIGNVSTPLMCLSESTNSTERN VMWGRMWHKDFLLF |
| 4308 | 12359 | A | 5225 | 2 | 223 | LGVAFCFCFFCFWVELFGFVGLQLLSNL EKFQPLCLQIFFLSPCPIRSLYI/C*SSKVV SQLTVTLVFPVFFSL |
| 4309 | 12360 | A | 5226 | 236 | 1626 | LAAAAHPLAGLVGGEAWIGGAKSWLSF SAGSSCMAEMATATRLGWRVASWRL RPPLAGFVSQRAHSLLPVDDAINGLSEEQ RQLRQTMALFLOEHLAPKAQEIDRSNEF KNLREFWKQGLNGLVGLITAPVQYGGG GLGYLEHVLVMEEISRASGAVGLSYGAH SNLCINQLVRNGNEAQKEKYL PKLISGE YIGALAMSEPNA GFWMVSMKLKAEKK GNHYILNGNKFWITNGPDADVLIVYAKT DLA AVPAISRGITAFIVEKGMPGFSTSKK LDKLGMRGSNTCELIFEDCKIPAANILGH ENKGVYVLM SGLDLAERLVLAGGLGLA MQAVLADHTIPYLHVREAFGQKIGHFQL MQGKMADMYTRLHGLFGQYVYNVAK ACDEGWHIIPKDCAGVILYAAECATQVAL DGIQCFGGNGYINDFPMGRFLDAKLYE IGAGTSEVRRLVIGRAFNADFH |
| 4310 | 12361 | A | 5227 | 1 | 867 | MATATRLGWRVASWRLRPPLAGFVS QRAHSLLPVDDAIKGVLR/ESQRQLRQT MAKFLQENLAPKA REIDRSNEFKNLRE FWKQLGEPWAVFGASQPLVQYGGFRP GAYLGSMLLG*WEEISPSFSGAVGLSYG AHSNLSHQPSLLRNWEFRAQKEKYLPEG *FSGEYIGALAMSKPHAGSDVVSMLK AEKKGEATNLGAKMGRGNHYILNGNK FWITNGPDADVLIVYAKTDLA AVPASRG ITAFIVEKGMPGFSTSKKLDKLGMRGSN TCELIFEDCKIPGK |
| 4311 | 12362 | A | 5228 | 3 | 391 | SHHHPLAAPSLGEAISRSFQSLACSPGL PAADRLSYSGRPGSRQAGLGRAGDSAV LVLPSPGPRSSRPSMDEGGSLLEDSDS EVFKMLQENREGRAAPRQSSSFRLQEA LEAEERGOTPAFLASSLSPQSFLARLQ/ GLATPPKLHTCEKCSSTIANQAVRIQGR YRHPGICYTCADCGNLKRRGHFWVG DELYCEKHARQRY SAPATLSSRA*APFG |

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| | | | | | | SCRKPWKLRREVARQPSWPAH |
| 4312 | 12363 | A | 5229 | 2 | 384 | FVHFQSKKTMRKICLFFFSSETGSRSVS QAGVQ/WARVIAHCNKLKLLDSSDLPALA LAS*VARTVGMYHRGLACVYFIQINLIL YFLAQMNLLKKHQTLFYEMLNLIASQA GKIYSSNRNIKVFWPQ |
| 4313 | 12364 | A | 523 | 389 | 549 | ERKRPSRKQ/RERNRKNQNERKSRGDW QRANVGAGQKEEMKCLAVELEIGSQPR S |
| 4314 | 12365 | C | 5230 | 301 | 369 | MPTLYNHCFLQLFTIISKLISY* |
| 4315 | 12366 | C | 5231 | 210 | 329 | MWNLCIWRVNCTINNTNMPTLYNHCFL QLFTIISKLISY* |
| 4316 | 12367 | A | 5232 | 2 | 268 | FFFLKRDVRSFCHPGLSAVAQL*LTVAL NS*VKGSSYLSFQS/SWHYRYVLPYLAN FKNFFFKRRELTFLRLILTSWAQVSFLL OPPK |
| 4317 | 12368 | A | 5233 | 1 | 415 | LFAGPSAMFYLAADVDFYVPVSEMPEH /KIQSSGGPLQITMKMVPKLLSPLVKDW APKAFIISFKLETDPAINRARKALEIYQ HQVVVANILESRQSFVIVTKDSETKLVS THSFYR*QKLL*KALIGSKIVQGS |
| 4318 | 12369 | A | 5234 | 3 | 705 | PVRFLDNFSSGRRGATSAAFLAAGYGV LFLYRARSAPFYAHRFPQTWLSALRPS GPALSGLLSLEAEENALPGFAEALRSYQ EAAAAGTFLAVEFTTLADYLHLLQAAA QALNPLGPSAMFYLAADVDFYVPVSE MPEHKIQSSGGPLQITMKMVPKLLSPLV KDWAPKAFIISFKLETDPAINRARKAL EIQHQVVVANILESRQSFVIVTKDSET KLLLSEKKK |
| 4319 | 12370 | A | 5235 | 200 | 636 | GPCAMFYLAADVDFYVPVSEMPEHKIQ SSGGPLQITMKMVPKLLSPLVKDWAPK AFIISFKLET*PR/LIVINRARKALEIQHQ VVVANILGVKDSPLCLL*PKDSEPKLL SEEEIEKGVEIEEKIVDNLQSRHTAFIGDR N |
| 4320 | 12371 | A | 5236 | 17 | 424 | |
| 4321 | 12372 | A | 5237 | 1 | 338 | SDRQLDC/ALDLMR/RLPPQIQGNLSNLI DLVPSLCEDLSSVDQPLKIARDKVVAK DYLLCDYNRDGDSYRSPWSNKYDPPLE DGAMP SARLRKLQVEACFCHTSLSVLST FP |
| 4322 | 12373 | A | 5238 | 2 | 160 | |
| 4323 | 12374 | B | 5239 | 46 | 426 | MSDQQLDCALDLMRRLPPQIEKNLSDL IDLVPSLCEDLSSVDQPLKIARDKVVGK DYLLCDYNRDGDSYRSPMEVTKYDPSL GRMGNAVKLRAEKSLEVKGANKWPF DQYPKTLLELLDPG* |
| 4324 | 12375 | A | 524 | 1 | 495 | EELVPIFLTFHKIEKEGTLPSNFYEASTL IPKPGKDITKENYRWISLMNIDAKILNK ILANQIQITKKIHHQVGFIPGMQGW NMHKSINVIHHVNRIKKNHMIISIDAEK AFDKIQHPMIKTLK/MGIQGTYSVIK AIYDKPTANIKQTFIQD |

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| 4325 | 12376 | A | 5240 | 2 | 938 | PRVR*APGPAAGGRATDAGTGTAATAAT TMSDQHLDICALDLKRRRLRPQQIEKNLS LIDLVPSLCEDLLSSVDQPLKIARDKVVG QDYLLCDYNIDGDSYRSPWSNKDDPPLE DGAMP SARLRKLEVEANNAFDQYRDL YF*KVGVSSVYLWDLDHGFGLS/VILH KRKGWEDGIKRRSKGCWDSIHVVEVQ EKSSGRTPHYKLTSTVMLWLQTNKSGS CTMNLGGSLTRQMEKDETVSDCSPQIS/ ATIGRLVEDMENKIRSTLNEIYFGKNKG YRSMGLRSVQTFADNSKQEALEELTLV GGFERESKQC |
| 4326 | 12377 | A | 5241 | 1 | 1911 | |
| 4327 | 12378 | A | 5242 | 3 | 803 | ESVAAALSPLGIEVDIDVEHGGKRSRLT PVSPEVSATGEKSSSQSSCCSDPSKPG GNVEGATQSLAEQMRKIALESEGRPEAS LCPFPPTGTTGQPSDLWPAPPHSQHLCS PTYKPEGAGCWLAVDVCCHLKSRWEP RTL*LLGLCEWPLFPLDPCSLNCTCACVL PDCLPGARAMVRLGLLRVSPVCSW*VLF QEOMESDNCSSGDDDDWTHLSSKEVDPS TGELQSLQMPSESGPSSLDPSQEGPTGLK EAALYPHLPFGK |
| 4328 | 12379 | A | 5243 | 2 | 1511 | RGGCDRDGPFSASSPLAMASLTVKAYLL GKEDAAREIRRFSCCSPEPEAEAEAAAG PGPCERLLSRVAALFPALRPGGFQAHYR DEDGDLVAFSSDEELTMAMSYVKDDIFR IYIKEKKECRDRHRPPCAQEAPRNMVHP NVICDGCNGPVVGTRYKCSVCPDYDLCS VCEGKGLHRGHTKLAFSPFGHLSEGFS HSRWLRKVKHGFGWPGWEMGPPGN WSPRPPRAGEARPGPTAESASGPSEDPSV NFLKNVGSVAAALSPLGIEVDIDVEHG GKRSRLTPVSPSSSTEESQSSQSSCCS DPSKPGGNVEGATQSLAEQMRKIALES EGRPEEQMESDNC/SQGGDDDDWTHLSS KEVDPSSTGELQSLQMPSESGPKLSGTP PREGPTGLERKLPLYHLPPEVDPRLDL SPFSQIACSMGLSS*LKGGLGSTRVPGRP KNY*HSERLWDTIQYSKHPPAVVDHFL PTFFLRAPLLVFIVVFKLCVELAGLL |
| 4329 | 12380 | A | 5244 | 24 | 493 | HWQVLPVRVKRLSPLKTHNCALPSTKLS AVRDYLFYSENLFNPQLNKDS*RG*QA LK/SPTAVFVLSLSHSFSAVSEGCFFHR ERQVASTSMEQLLSLAGIPFVEDSCPLQ KELSKTLP LTLEVLGVSMFFKFSWLPVI WVFGFISQLSGLES |
| 4330 | 12381 | A | 5245 | 1 | 4547 | MRNPVHSHIGATVSHQTDGANVPNMP ALQSQILTSDTYSMQMIPSNSTRLPV AYQGNQGLNQSFSEQVDWTQCISKG LTPDYRPPPKLYRSPQSFLPDSTIQKQ NFIPHTSLQVKSQLLNSVLTLP SRQTS VPSQYATQTDKRPPPPYNCRYGSQPL QSTQHITKHLMEVPQSREMLSEIRTSF QQQWQNPENNVSTIGNFTNLK VNTNSK QPFNSPIRSSVDGVQTLAQTNEEKIMDSC NP |
| 4331 | 12382 | C | 5246 | 191 | 397 | MLPRAGLLCGKLPNNFSQPSRQILLCL GCDSPHLTVGHEGWKTTLPGAGATPYRI GPFSLLQRGVS* |
| 4332 | 12383 | C | 5247 | 598 | 744 | MSKVLNQSTYITVQCGYVSINSFYVSFY YSIKLAKRHLGTFRTVLVI* |
| 4333 | 12384 | A | 5248 | 164 | 355 | NGSTGCGIQANQYFNYSLSFESGKFV KCTEQLVPGENIH*LLEGSKKLT/LK NLFRNM |
| 4334 | 12385 | A | 5249 | 1 | 308 | KVQSFFIFYLFIYF*DG*V*LF RPGWSAVV LSRLTATSAFRFKQFSLSPSSWDYRC PPLHLANFCIF**RRGFTMLARLVIS*PQ VIRPPWPPKVLGLQM |

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| 4335 | 12386 | A | 525 | 219 | 471 | INFKKKNRLFNK WY\WTCVATLEKNKM NSFLMIYPKSNK*FKNPVNRGKKL*NLFI LLYFKF |
| 4336 | 12387 | A | 5250 | 67 | 367 | SDELRTPGRESLPAENISL*DRVNHQPAIE SCTA*NYLYSINAKTKGEMLEAEGMRV VTNSVYHWRLCEKQQTVLMKAGCWRT DKLCLPPEGMLWAVMSR |
| 4337 | 12388 | A | 5251 | 1429 | 1621 | IPWIPPVSRSMVTHTWRAPTRFVHLPFFQ TDPFVVFISAFVLLRLVQKQP*QVVPDQ GPERGR |
| 4338 | 12389 | A | 5252 | 180 | 411 | IPWIPPV/CPFHGHTHLE/VHPHGLSISLYS PPADSPVQGFVVRLLISFTFSALADLPRSG PWSDDTCHGCFTVAASSEL |
| 4339 | 12390 | A | 5253 | 288 | 530 | |
| 4340 | 12391 | A | 5254 | 9 | 257 | IFTAVAFUISESWKQPQCL*TNE*/IKLWYI HTMQYYSAIKRNEKLIHATTWMNSEN VQW*KARHKKPHIV*LHLYEGSQKRQI |
| 4341 | 12392 | A | 5255 | 6215 | 7038 | RTVTTFLSKDSHGVCYCAQGGKIPDHQNP QCNRKQHPVSTILMLDKASFQRLKRKH NLSVNCINRNPMSLKNTSWHSSLSVTQ RHQQSKLHFQGSILLH*PSQNIL/SNI*K CINYC*HCSSVLLSYLFIETESYSVAQAG VQWHDGLLLQLLPLRFKQFSCFSLPSSW DYRSAPSCPANFCILVEMGFCHVGQAGL KLLASSDPPALASQSAGITGVSHYTQPCS PFLKSTGLFSCKVLSPYHKGRIYLGRM CFLNSTWHLVKSTLFCPLFI |
| 4342 | 12393 | A | 5256 | 2 | 513 | VLIQLVWIALLLVDPSRPVLTKDEPASS TSSFTSQSQKKGQSQGFLQSRN*GCIALC E/VFQREEIY*VGMD*DSFRJWFFNFIFH LTVITSSDLHIHGEIWWVPNTDHCVRFF FVYDDCLVYAYINTLL*GFY*YILLVIV NYTGSVHWFIYYLLVLNVLCFLLYI |
| 4343 | 12394 | A | 5257 | 1 | 274 | STPPHSSQRACEPLPSFAQCPR*APSPAP HCALICPIPKMEERP/PM*IGR*RRHLLST YCARSCTEQAPCIILLNPHNVLDLSRLW VKGQ |
| 4344 | 12395 | A | 5258 | 3 | 436 | GYLSEVVEENTPPKMEKEGLEIMIGKKK GIQGHYNCSYLDSTLFCFAFSSVLDTVL LRPKEKNDVEYYSETQELLRTIENVPLRI YGYVCATKIMLRKILEKVEAASGFTSE EKD/PAGQKVQDCYFYQIFMEKNEKVG VPTIQ |
| 4345 | 12396 | A | 5259 | 1 | 340 | |
| 4346 | 12397 | A | 526 | 1 | 1423 | MNPNQEEISDLPERIQETEKEGTLPSFY EASITLIPKL GKDKTKKENYRPISMMNIE ANILNKILANQIQHIKKIHHHDQVGFISQ MOGWFNHRSINVIHHINRIKKNHMIISI DAEKAFDKIQHHFMIKTLKIGIQGAYLN VIKAIYDKPTANIILNGKKVEAFPLRTGT RQGYPLSQLFFNIALEVLARAIRQENEIK GIHIGKEKVKLSL FAGDMIFYLENPKDSS KKLLELIKELSKVSRWELNNENTWTQGG EHHTPGPVVGSGEERGIALGDTPNVNDK PLTGAALASTLGVWENENKFTHLFNIHS QFCLPSQGIFFLCGTSTYVCLTTNWTSTC TLIFLSPKIDIAFGNQTLPPVRAQVHQH RAVQIIPLLIGLVNTATGTGIAGLSPSLS YYHTLSKDLSDSLQDIKSTLTLSQSDS LAAVTLQNHRLRPPNRRKRWAMHLFR GRLFFHQPVWD |
| 4347 | 12398 | A | 5260 | 215 | 384 | |

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|------|-------|---|------|-----|------|--|
| 4348 | 12399 | B | 5261 | 347 | 1742 | MPNTNGSIGHSPLSLSAQSVMEELNTAP. VQESPLAMPNGSHGLEVGS LAEVKEN PPFYGVIRWIGQPPGLNEVLAGELEDEC AGWYGNLQEGTRYFTCALKKALFVK LKSCRPDSSSVLDTVLLRPKEKNDVEYY SETQELLRTEIVNPLRISAGQKVQDCYFY QIFMEKNEKVGVP TIQQLLEWSFINSNLK FAEAPSCLIQMPRFGKDFLFFKKIFPSLE LNITDLEDTPRQCRICGGLAMYECRE YDDPDISAGKIKQFCKTCNTQVHLHPKR LNHKYNPVS LPKDLPDWDWRHGCIPCQ NMELFAVLCIETSHYVAFVKY GKDDSA WLFFDSMADRDESNEFVQITGVIGK GK ETEGRVLT LHLIRAGSSVHVHCRQWMSL W* |
| 4349 | 12400 | A | 5262 | 1 | 1547 | PVQESPLAMPNGSHGLEVGS LAEVKE NPPFYGVIRWIGQPPGLNEVLAGELEDE CAGCTDGTFRGTRYFTCALKKALFVKL KSCRPD SRFASLQPVSNQIERCNSLAIWE AYLSEVVEENTPTQKWEKEGLEIMIGKK KGIQGHYNSCYLDSTLFC LFAFSSVLDTV LLRPKEKNDVEYYSETQELLRTEIVNPLR IYGYVCATKIMKLRLKILEKVEAASGFTSE EKDPEEFLNLFHHLRVEPLLKIRSAGQK VQDCYFYQIFMGKK*GKLGVP TISGSC*E WSFINSNLKFAEAPSCLIQMPRFGKDF KLFKKIFPSLELNITDLEDTPRQCRICG GLAMYECRECYDDPDISAGKIKQFCKTC NTQVHLHPKRLN HKYNPVS LPKDLPDWD EIARHGCIPCQNMELFAVLCIETSHYVAF VKY GKDDSAWLFFDSMADR DGGQNG FNIPQVTPCEVGEYLEDVSWKTLHSLG LPGESQGCARRLLCDAIYVPCTQSPTMS LYK |
| 4350 | 12401 | A | 5263 | 29 | 258 | LRKYHATDLIS*GSVVGEFDCCFSFLDG SLEDAVDGLLALALOPHKEQYKEFQDLN QEVMLNDDILKVSTFSQKLD |
| 4351 | 12402 | A | 5264 | 98 | 497 | THENNYNEKKDEIKIFKISLQISAQEEFPF FRRWKSCLCCPRLGVQWHD LGSLOPPT SP/GFKRFSGLKLP/RAAWIYRYVPITSG* FLYFQ*RRGFTHVGQADL DLTSGDPPV WASQSAGITGVSHHAQPPYC |
| 4352 | 12403 | A | 5265 | 156 | 1047 | VPAGEARVQWHD LGSLOPPPGSSDSP ASSSRVAGITGIKTNTICKKCAQNVQLYG TPKPCQYCNIIAFIGNKCQRCTNSEKKY GPPYSCEQCKQCAFDRKDDRKKVDGK LLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSQKTLSTS SIQNEIPKKKSKFESITNGDSFSPDLALD SPGTDHFVIIAQLKEEVATLKKMLHQKD QMLEKEKKITELKADFQYQESQMRK MNQMEKTHKEVTEQLQAKNRELLKQA AALSKSKKSEKSGAITSP |
| 4353 | 12404 | A | 5266 | 156 | 960 | VPAGEARVQWHD LGSLOPPPGSSDSP ASSSRVAGITGIKTNTICKKCAQNVQLYG TPKPCQYCNIIAFIGNKCQRCTNSEKKY GPPYSCEQCKQCAFDRKDDRKKVDGK LLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSFSPDLAL DSPGTDHFVIIAQLKEEVATLKKMLHQK DQMLEKEKKITELKADFQYQESQMRK MNQMEKTHKEVTEQLQAKNRELLKQA AALSKSKKSEKSGAITSP |
| 4354 | 12405 | A | 5267 | 4 | 496 | DGFPSCCQAGVQ*HDLGSRQPPPGSSD SPASASRVAGTTGMHH*SRDVLIRILELE EGLELCPHFVRKLPKTGQILTLMLSLAP VKLAPQPKLSWMELTRTQQAVPSPFGR WGGIGRKLVP IADGWASGQARGLL GGSGKGEGKATGCEREGTCLLQG |

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| 4355 | 12406 | C | 5268 | 190 | 435 | |
| 4356 | 12407 | A | 5269 | 114 | 267 | QLYINHTPPPLSKSKEREMDKKDLKSR TLKQKQKPLVNVVHNSWF*DHSN |
| 4357 | 12408 | A | 527 | 31 | 332 | |
| 4358 | 12409 | A | 5270 | 1 | 1071 | |
| 4359 | 12410 | A | 5271 | 1 | 1231 | GRFLCCMLETVTRWHS DRATYEKECGN YPGFLTILRATGFDGKNKADQLDYENFR HVVHKWHYKLTAKSVHCLETGEYTHIR NILIVLTKILPWYPKVLNLGQALERRVHK ICQEEKEKRPDLALAMGYKIIF*CDLQ D*MTGEF*RL*NVLQC*SLSSAFRLWEI MRSCFHRLVRVTSDYQLPVYTG**FF*S HV*YFLIGRKYNFIIIVNRSSRVKKKPS* FKD*FIGKL*FLRKLGLV*KPSRTY*KWV FFNSLEPHSRMNNLLILFLKTSCLCLIW VCIFKHVRLSSYSGQLKK*EKSIP*YPEN EFPQRPPPPRNASVQNGP/GGGPSSS SIGSASKSDESSTEETDKSRERSQCGVKA VNKASSTTPKGNSSNGNSGNSNSNAVKE NDKEKGKEK |
| 4360 | 12411 | A | 5272 | 2 | 3383 | ITDQVLLPSLSLMDCNACMSEELWGMF KTFPYQHRYLRYGQWKNETYNSHPLL KVKAQTIDRAKYIMKRLTKENVKPSGRQ IGKLSHNPILFDYVCFEILSQIQKYDNL ITPVVDSLKYLTSLNYDVLACILSNCHIEA LANPEKERMKHDDTISSWLQSLASFCG AVFRKYPIDLAGLLQYVANQLKAGKSF DLLILKEVVQKMAGIEITEEMTMEQLEA MTGGEQLKAEGGYFGQIRNTKKSSQRL KDA |
| 4361 | 12412 | A | 5273 | 442 | 1457 | KHFLYIYAQMNCFSRLRKKKKKNQLL LQVFSSADE*GSSSSSSSSGHKRHKHK RNRSESSRRHSSRASSNQIDQNRER* VLPSSS*YFSIFSFP*TRSGRKLKGQDR LQYEKTQIKEKDRCPSSSLEIPDDFGG RSEDPRDFYNSYKTQAGSSKTEKPYKSE DIFPARRNSSDSFCRNSEAKIYGYRFEK DIEGRKEHYRRWEPGSVRHSTSPASSEY SWKSVEKYKKYAHSGSRDFSREQRYS LNTNQGEYEREDNYGEDIKTEVPEEDAL SSKEHSESSVK/NKFTSEFTEYI*SDS*I*K RKRK*GQKINTPKDIGHPLPQNAH |
| 4362 | 12413 | A | 5274 | 2 | 457 | KLIFFPRKPSAPQEGRFQFC*KIGNRPTQL TGPVMPVRNVYKKEKARVITEKEKNF QSPCLVFVMARAKARLFGIRAKKSPRK PQNQDVEKEKIKTLPGNFEISLAVMPGSP TWCVSVGTTWALGWGFTACDFLLPRGF GAFLKRQVQAPG |
| 4363 | 12414 | C | 5275 | 27 | 158 | MHSKPTGQVSWLGMTTASLPGTNASSM WMPWRLEDHSNLDALP* |
| 4364 | 12415 | A | 5276 | 1 | 320 | |
| 4365 | 12416 | A | 5277 | 100 | 659 | CPLVIRSCSSALWDIETGQQTITFTGHTG DVMSLSLAPDTRLFVSGACDASAKLWD VYSQCFFLSVYMMS*FAFSQFFPNNGNA FATGSDDATCRLFDLRADQELMTLTPHD NIICGITSVSFSKSGRLLLAGYDDFNCNV WDALKADRAGVLAGVHDNRVSLGVTD DGMATGWSWDSFLKIWN |
| 4366 | 12417 | A | 5278 | 16 | 495 | AFSAPDTRLFVSGVACNASAKLWN/VGE GMCQTFTGHESDINAVICFFPNNGNAFAT GSDDATCRLFDLRADQELMTYPHDNII CGITSVSFSKSGRLPPGMGTTFNFCNVW DALKSRTGQVFLAGVHDNRQPAWGV DVGMA/VATGWSWDSFPQDLGN |
| 4367 | 12418 | A | 5279 | 5 | 108 | SRGFTLLARLVLS*PQ/CDPPLPLASQSA GI/TRLGMSYHA*PIIIFETRSRSVTQDG/G VQ*CNHGLLQPWHPGLKESSCLSLPG/G HAPPHLANFICRNRVSLCCSGWS*TSSD |

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| | | | | | | PPLPLASQSAGHGWV |
| 4368 | 12419 | A | 528 | 27 | 178 | |
| 4369 | 12420 | A | 5280 | 1 | 458 | |
| 4370 | 12421 | B | 5281 | 403 | 629 | XVHLVKASCQACGQLDRVRKQVNNIPS FIVRLDSQKHIDFSLRSPYGGGRPGRVKR KNAKKGQGGAGAGDDEED* |
| 4371 | 12422 | A | 5282 | 1 | 637 | PVARSWVCRKTYGDPGRGPFEEKSRLDQ VELKLIGGVWGSQTKREVLARVKFTLAQD SAKAAPGNWLTALDEKDPTGVLFERQTP LLR/RGLVPQLGCWDEGQKMKLADYIPG P*RLEDFRETTPCKTQVFQSLGLAKSIHQ PRFACLSRQRHVRKQVNNIPSFIVR LDSQKHIDFSLRSPYGGGRPAVRKRKN AKKGQGGAGAGDDEED |
| 4372 | 12423 | A | 5283 | 3 | 295 | VCIGVLLCCLGCGVRWHDHASL*P*PPG LKRSSHLSLLSTWDHRHMLTHPLNFFIV EPRSHYVAQTGLKLLGSSSPPASASQSAR ITGVSHHTQSKK*FLFVEPRSHYVAQTGL KLLGSSSPPASASQSARITGVSHHTQSKK |
| 4373 | 12424 | A | 5284 | 2 | 284 | |
| 4374 | 12425 | A | 5285 | 1 | 785 | MTGLALLYSGVFAFWACALAVACWV NSGTDWAGGIWLERLLPRSRLGFLAGG DPACAGVCYTIFDLGFRFDVAWFLTETS PFMWNSNLGUGLAISLSVVGAAWGHSLT GSSIHVVEGS*KAPRDSKTKNLVSIIFCE AVAIYGIIMGNCSLSNMTVEPFSATEPQG HRQFGN*PWQGYSHGLGAGLHRKPCLN LFCGVVCVIGVTWGPCWQMPQNPTASL CKRFSIVEIFWQAPLALFGVIGRKFFKTS MSERWVTR |
| 4375 | 12426 | A | 5286 | 2 | 350 | |
| 4376 | 12427 | A | 5287 | 1 | 999 | NLLKTHKFLLGQDEDSLHVPVAQMGN YQEYLKTLASPLREIDPDQPKRLHTFGNP FKQDKKGMIDEADEFVAGQNKVKRP GEPNMSYVTKRRRSMSLLLRKPQTPPTC NNHVGGKGPPSASWFPSPNLKPTLVH TDATIIHDGHEEKMEENGQITPDGFLSKSA PSELINMTGDLMPNPQVDSLDDFTSLSK DGLIQNLVVTHL*EEPKTAASP*MTKKT Q*HLLWELCQIHYKSLLWHKE/VNADI KHQLMKEVRKFGRKYERIFILLEEVQGP LEMKKQFVEFTIKEAARFKRRVLIQYLE KVEKINSHHLHNNISHINSRSC |
| 4377 | 12428 | A | 5288 | 329 | 661 | ITLSLLSFFNLRPSFALLAQAGVHWRDL SLQPPPLRFK*FSYLKSPRSWDYGHAPP RPANSVLLVETGSLHVSQGGILPTSGDP PASASQSAGITGVTCARPPSLFS |
| 4378 | 12429 | A | 5289 | 46 | 554 | NKTRKDPFPPTPAHGHTPPTPSLPG/C SAHGLKPRGSHCDQPPSTCRPPVQSPV AHASQVAGRTWA*KRALHLPGGGVKRK GTGSPKAPRSGCLPYKLGSTARAAGSC SPAE/EPETFSQGGQLPVNKGKLRVVGQ PSFQCAPRDCSRYPQFGEQGRAIEHQI P |
| 4379 | 12430 | B | 529 | 110 | 719 | XGRQQHQRWHETPDIKLFGKWSTRDDVQ INDISLDYIAVKEYAKYLPHSAGRYA AKRFRKAQCPIVERLTNSMMMHGRNNG QEAHDCAHRQAACLRDHNTCSQAKNLE VRGTAINSGPREDSTRIGRAGTVRRQAV DVSPLRRVNQAIWLLCTGAREAAFRNIK TIAECLADELINAAGSSNSYAINKKDEL ERVAKSNR* |
| 4380 | 12431 | A | 5290 | 228 | 386 | |

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| 4381 | 12432 | A | 5291 | 3 | 257 | GPRERETGRTATAVEPDSCEERTYSNDT KRWCSHPGNGGVPERQHLG*ATGSW GAKPLRLAAATRASGNPGHRSCLKCLETI F |
| 4382 | 12433 | A | 5292 | 3 | 1379 | NEFFGEGKTLQAARHFAAMKALQALQN EPIPERSPONGESGKMDDDDKDANKSEI SLVFEIALKRNPVSFEVIKESGPPHMK FVTRVSVGEFSAEGEGNSKKLSKKRAAT TVLQELKKLPPLPVVEKPKHFFKKRPKT IVKAGPEYGGQMNPISRLAQIQAKKEK EPDYVLLSERGMP*RREFVMQVKVGN VATGTGPNKKAKKKKNVAVAMLLQLG YKASINLQDQLEKTGENKGWSDPTGFP EPTNNTPKGILHLSPDVYQEMEASHHKV TS/GHYSRLFVTQRYEPTFKLFSSVYLPH RIVQSTFARHLLMNGTSSTAEGIKGSS PIPLVPPVQPSKQLGIFSKGFAFRVHYC DRQKWQRVCDLSDISPCADGL/SHAIGSS IEASHDQAALSALKQFSEQGLDPIDGSM NIEKGSLEKQAKHLIKVDHNPAPPGSIA HDCKISNSAV |
| 4383 | 12434 | A | 5293 | 7 | 351 | SSTSLIRKMQIKTTRYQNIPNRMKIKNA DNTKL/WSRILTNYWWEYRHLHK*KYV HKKTCNFMLIAALFIKFLKWKFKHSST GE*IKL*DRHMTYYY*AIKKAQATDRM QHE |
| 4384 | 12435 | A | 5294 | 3 | 1585 | GEPLI/LHHTTCH/NSKALIAFLAFLIIVTSI ALLVVLNIIYDLHRKRCNVDEQQELVE RYDESNLNMVQPIHADIMLETYHRRIA/D EGRFLAEFQSIPRVFSKFPKEARKTHN QNKNNRYVDILPYDYNRVELSEINGDAGS NYINASYIDGFKEPRKYIAAQGPRDET DDFWRMWEQKATVIVMVRCEEGRNRN KCAEYWPSMEEGTRAFGECCCKDLTKH KRCPDYIIQKLNIVNKKKATGREVTHI QFTSWPDHGVPEDPHLLKLRRRVNAFS NFFSGPIVVHCSAGVGRTGTIYIGIDAMLE GLEAENKVDVYGYVVKLRRQRCLMVQ VEVCSNL*DYSHFGFLDLNLFQVIMIFF KNPNSSQPQTVDLTKTKTW*SPWPML CIW |
| 4385 | 12436 | A | 5295 | 1 | 1323 | MEDSRKAQKRDTKIEREEQLYWPSRKS GKSKGDLVLHTTYKPSHSGGRAVSGFLG SPIPSLGSWTAFLDPPWARVEPIALKGLT QRSPNGGGHRVCFVIPPAPDGEQKKR LCSFRKEQSLPGNLENSFGSCPRLSRQY VYESARTTALMRLGCPLKQIQLISQDLSP FEYRESLPMKDKQNKHQIRISLINTIQUETI ISPNELSKSPGTNSGETEIHDLSDREFKIA VLRTLKEIQDNTEKEFKLYQINLTKRIEII KKNQAEILELRNAIGIQKNASQSFNSRNG REEEIISELENRLFENTQRRQNKRIKNNK ACLQDLEYRLKRANLRVIGLKEEVEKAI GVESLFGIITENFPSLEQDINIQQVEGYG TPSRFPNPKKTTSRHLIVKLPKIRDKERILK VTRENKQVT*NGTHICLAADFSVVAL*A RREWH |
| 4386 | 12437 | A | 5297 | 3 | 226 | GSCEQGCPPGRYGPGEQLCGCLNGGS CDAATGACRCPTGFLGTDNLTCPQGRF GPNCTHVCGGQGAACDPVTGTCLCPP GRAGVRCERGCPQNRFGVGCEHTCSCR NGGLCHASNGSCSGLGWTGRHCELAC PPGRYGAACHLECSCHNNSTCEPATGTC RCGPGFYGQACEHPCPPGFHGAGCQGL CRCQHGAAPCDPISGRCLCPAGFHGFCE RGCEPGSFGEGCHQRCDGCGGAPCDPV TGLCLCPPGRSGATCNLDCCRGGQFGPSC TLHCDCGGGADCDPVSGQCHCVDGYM GPTCREVGPSPRTRP*PRGPAAAPLGS |

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| | | | | | | SGRTATSPVRRASAPTAPTCVGVGRGR PATL |
| 4387 | 12438 | A | 5298 | 152 | 990 | LLIHSEEKPFEDNLYGKALSSNSHLHGP RRLCT/GENPEE/CEQL*KAFSAISRDCD SSH*GRKPVKVSEGFSDSHPLRHTGNHT MEQHSEMRNTLQQKCSHY*ANYSVVFC S*LWESLECSIGF*GDLRINSGENAPFEHH QYWRAFWFSTFVKET/W*SIHTTEK/PWK F*EEKAFSDASVLGK/HMELLPGCKTYE YINIGKFFSDSSLSCI/WRELTWRNP*ECN QC*DA/FSLNSSLSG/HQFSLGTKKYNHC FECGISFIQCLICRLDCWLINFFSLFFF |
| 4388 | 12439 | A | 5299 | 1 | 181 | EIEDLN*TITQLYLT*HLYRTLHRTTPPAYK FFSSVHETFSRIDHVLEHKTSLNEF*RLK |
| 4389 | 12440 | A | 530 | 443 | 565 | QPGFGAGARAPNILTHKHLG/LLEFKTTG AQQQGF*LNESSF |
| 4390 | 12441 | A | 5300 | 1 | 170 | PPPPFPLIPD*G*PPSPSPGQLQSAPPP VLP CPDITLSYPGRRPVGLSLMD |
| 4391 | 12442 | A | 5301 | 846 | 1094 | IPAL/*FYFIVYLNILKYLFFFD/DGVL LCCPAWSAVA*SRLTATFASQVKRFSC SLLSSWYYSVP/SSLANFCIFSRDG/SFIV LAMLVLNS*PQVILLPWPKVL*LPIMEC SSLTIAHCSLNLPGTSPNPASASK |
| 4392 | 12443 | A | 5302 | 19 | 391 | AYPLRGGGRDFLRGGPSRSVSLSVVPAR V*RRRRRLREEARGAMTSASTKVGEIFS AAGAAFTKLGLTMOQLHPVADSSPAGA KWTETEIELRAAVKRFGDDLNHISCVI KGPDKGHCETQGI |
| 4393 | 12444 | A | 5303 | 1 | 338 | SLIFSDSLSSISGTNTLAAFLSWMLPYIPW ILQARPALGLLHLLAACNVVVGQSAT*PS PSLPLGLCSSSHSQ*GLF*PPVFKISPLTD NPNPFDLHLMDFIQKTIKISL |
| 4394 | 12445 | A | 5304 | 3 | 180 | |
| 4395 | 12446 | A | 5305 | 1 | 518 | RAAQSPCSPWSRLACSGGGGVIREEARG AMTSASTKVGEIFSAAGAAFTKLGLT QLHPVADSSPAGAKWTETEIE/PEGCC EAIWGRS*SHQLCHQGTDSGPDKGHC*N ARYIEDFWASPPA*V/IPRKGPRRWASG VFVHLLQLAPPPKQLPVFPEGRGSPPIKE TERLM |
| 4396 | 12447 | A | 5306 | 1 | 705 | GAKFQRTSVPRTTGPGQLKCLEDKVS LETDELDEEKNTEVELTDRNLNRGRDQVD QLRTELMQERS/SSGRTWKCDKISLERQ NKDLKTRLASSEG/SPESLVPASLSLPRI SCCRERLPAEQRVKTVLRSTNRKLERKV N*LSLQIEDERHHVSDTKDQLSLRVKAL KRQVDEAKEEIERLDGLRKKQAQREVEE QHEVNEQLQARIKSLEKDSWRK/GFPLS C*VSSQKRRAELR |
| 4397 | 12448 | A | 5307 | 831 | 1159 | DVKSksFFFFLRWSL/NPFAQAGV*WHD LSSLQPLPHRFKQFSCLSLLSS*DYRRVPP *LANFLYF**RQGFTMLARLASNS*PHDP PASASQSAGITGMSHRTQKKQIS |
| 4398 | 12449 | A | 5308 | 296 | 526 | FNCCEEKFKKKPCFVSFLEGLERG*VK CQEHIPDTH***LLGLSEQINSDSRLRKL NHFILFLEQLTCPPHSRER |

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| 4399 | 12450 | A | 5309 | 5424 | 5957 | YNFFLNEMGSCSVAQAGVQWHNHSSLQ P*TLG*SSYHPASAS*VAGTVCTCHHVQL VF/IFFFLR*SFALVAQAGVQWCDLGSLLP PPPSGFERFSCGLPSSWDYRRPPLHLVN FFFLYF**RWGFTMLARLVSN*PHDHP ASASQSAGITGMSHHVWLNFFFNCKSLI FSNVFRN |
| 4400 | 12451 | A | 531 | 82 | 986 | TMNTRNRGVNSGLGASPASRPTRDPODP SGRQGELSPVEDQREGLEAAPKGPSRES VVHAGQRRTSAYTLIAPNINRRNEIQRIA ELELANLEKWEQNRAKPVHLVPRRLG GSQSETEVRQKQQLQLMQSKYKQKLKR EESVRIKKEAEEAELQKMKAIQREKSNK LEKKRLQENLRREAFREHQYKTAEFL /RQTEHRIARQKCLSKCCLWPTILNMGQ KLGLO\DSLKAENRKLQKMKDEQHOK SELLELKRQQEQERAKIHQTEHRRVNN AFLDRL/RRQKSTRWPRAIWRLEYE |
| 4401 | 12452 | A | 5310 | 2 | 237 | IKRFSYLSLPNSWDYKVPSSMPG*FLYF* LR*GFTNVGQAGFEIP*PQNDNPLSSQS AGITGMSHHNRPLFYFLK |
| 4402 | 12453 | A | 5311 | 36 | 386 | LNHRKFMLLYYH*LLLFL\FHF*DRVSV CHPGWSTV\VNSQGFTAALTYWVK*SS CFNPPCVSWEPRGACHHALANFLIFCKN QVSLCLPRLVSN\WVQAILPSWPPRA GIYGV |
| 4403 | 12454 | A | 5312 | 1 | 310 | FFFFET/ESHVAQAGVQWGDGLL*SSP P\GSSDSPASAS*ASGTTGA/QHHAQLIFV FSVETGFHPVSQDGLDLLTS*SARLSLPK SWDYRHEPLAPGLGFTF |
| 4404 | 12455 | A | 5313 | 598 | 882 | LIFFLSF\FFFFS\FFFFFFFFFFFFFFFFFFFF FFFFFFFFLLLLLLLLLLLLFFFFFFFFFFFF LRQSL\DSVAQAGVQWRHLGSLQALPPR FAP |
| 4405 | 12456 | A | 5314 | 439 | 1169 | QSGHRYLYNIIHQVLCFTIFLRLQDLAV L/TQAGVQWC/DSWQPRPPGLK\GTP\TSA AQVAGTTGMCHH\TR*IFFFFFFFFFFFFFF FFFFFFFFFFFFLRLQSL\DSVAQAGVQWR NLGSLQPLPPRFKRFSCGLPSSWDYRN APPHPANCCIF/M*RRGFTMLAKLVLNSG DSPASASQAGIIGVSHHARPPRYFKKYI FCRDGGLTMLLGWS*TPGLKQSSHLGFP NFWDYRCEPPCLATFIL |
| 4406 | 12457 | A | 5315 | 1 | 222 | ETGSHFVTQAGV*WCNLGLLQPLTPGLK QFSLSPSSWDHCKVPSPCANSTLGL K*RRVSTMLPPGWS\QTP |
| 4407 | 12458 | A | 5316 | 1 | 234 | LRQSFAGWPRLECNGTIPAYCNLHLLGS SNPPASSPRRLIFVVLVEMRFLYA*AG LELLSSDLPPWHRKVLGLQA |
| 4408 | 12459 | A | 5317 | 1 | 196 | FFLINLTLLIVTAQFIN*LDFIDSYSTICPK PPEYTFFSRA/PNGTFTTKDHILGFKISLN KYKSI |
| 4409 | 12460 | A | 5318 | 1 | 477 | SCWSPV\WGHPPRDREPPPS*LGIQSSPG VPQAALPPWSPASHQASATWAVLPLPP LQGPAREPPCPHLLRRHVQPTKTS\VSIL SAPPLPPPG*DLPEASFSQWACKGINKCL QGLGLVCRRTEHKDLGLGLFGLVLAM VEVRGVDLTENNSGASVPRGR |
| 4410 | 12461 | A | 5319 | 139 | 398 | FYFFFYF\FLRQSCSVNQAGVQ*/HCLNSL QPPPPGFKRFSCSLSPSRWDYKCPPPCTP NFCVFS/EMGFLHVGQAGLELMTSGDPP GFG |

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| 4411 | 12462 | A | 532 | 122 | 1340 | EAASKTTKDNICSWKDDTIGCKEMPTSE NCPSFALHQKISDRNHGECREYGKTLCCQ DSKPVQHERIHSSEKPNRCKECCGNFSN GHQLTIHQRLHVGEKPYKYEKCGKAFIS GSAFVKHGRIHTGEKPLKCKQCGKTISG SYQLTVHKSHTGKKPYECGECGKAFLV YGKLTRHQSTHTGEKPGCEECGKAFTS FSYLVQHQRHTSEKPYECKECCGKAFTS SPLAKHQRIHTGEKPYECKECCGKSFTVY GQLTRHQSIHTGEKPFESIHAEIKPYRCK ECGRITFSRASYLVQHGRHTGEKPYECK ECGKAFTSGSYLVQHQRHTGEKPYECK ECGKAFTSRHQLTVHQRVHTGEKPYECK ECGKAFTRVHVHLTQHRKIHTDVKPYEC KECGITFSRASYL |
| 4412 | 12463 | A | 5320 | 11 | 137 | RWGFTKLPRLVSNWPQAILSPWLKVL NNHREALYFSLYYISKYTEGQFRNRLYP GTICQDYLWRYLLFLFIFETESCTVIRLEC SGSLQPPPPRFKQFTCLRLHSSWDYRARP PWPWPFNCISRVTGFHHVGGGLDLV DLCDPPASASQSAGITGREHPAPGTYLW EGFKKSFKSRA*RTLFFPLLH |
| 4413 | 12464 | A | 5321 | 1 | 293 | LERMSFGHIQTKEDILQENTIFATEVQIQ PNPD*TPEAKAFNRCLSYRKEDRIDVH QLTCDPYLMPHMRMSVSTCSPAGAAIAS TSGASSSSSSN |
| 4414 | 12465 | A | 5322 | 3 | 291 | |
| 4415 | 12466 | A | 5323 | 14 | 943 | HRILEPLIFHHFFFSSAPPQPELly/PASL TLPASPGREEVYPLPARLPSLPRWEPLQV WLALGAVKLPLSPWSPGPNGLGKPPGT PKRRGALFCHMPGILTP/WMPGARWTKP PANPPST/TSVPPKDG*KLQPGGLRGKP GPERGWNPPCP/RSRPPYLLC*PQTLPR A*CFPIPKMSFTGHSPCRASLGHLE/VGH GIPLWPRVCQRRKSRAFFVLFFKGACLF NVNNRKP*YLCNTE*YFNHVHLDVHNI FITKQQUEST*PWLPRGVSWLGAGGGYQG AWDREAPPPRPIKLPPTLASRMRSCHL |
| 4416 | 12467 | A | 5324 | 12 | 486 | |
| 4417 | 12468 | A | 5325 | 51 | 390 | DGVLPSLLGWEVMCGSSAPLLRSPVDRL DGMWGVCHPWGSIVAQSQFTAASNLL ASRAT/LSLPSSWDYRRVPPHSAHFKFL *KWGLAMLPRVLNWSQVILLPQPPKV LEL |
| 4418 | 12469 | A | 5326 | 279 | 380 | |
| 4419 | 12470 | A | 5327 | 618 | 818 | |
| 4420 | 12471 | A | 5328 | 1 | 197 | |
| 4421 | 12472 | A | 5329 | 2 | 498 | CPRMTPKDFQ*PVL/VVTNLLGHVIDIKW MSIAFINDRAWPSAFVSDENHARIQCDG QHRFEVSVSELPEDETDSSTVLDLDHOG LGPPPPPAEPDPLQLLLQQLFGLGQLSCV VGPGPWRLSSARDKQNMVSIHKKVKR PQSPLRVYWPRLRYCILPSRRATVN |
| 4422 | 12473 | A | 533 | 456 | 824 | DRVSLSPRLECSGVILAAQCNLHLP/GFNR FSVTLGLPSRLGITGHAPLCGQFFVFLVE DGGFHHVGQAGLELLTSSDPPTSAPVKC RDYRHEPLRLACCSFLKQENIHNCWVRI YIRIFQTN |
| 4423 | 12474 | A | 5330 | 600 | 811 | PIWLSLSPWHFINQRKEKKK**DIVKREK PLMGLSTLTSI*MQSKPRKEHQINLKSEI K*LQDLSQYFGR |
| 4424 | 12475 | A | 5331 | 1 | 75 | FFFFFFFFFKLAMFVFFLFFFSK*KEIVLS QFLVFL/TYLFYVFTSLKVALKISRDIKST FLRVALFFFLNNSWEFCGSTAFPSVSML CMF*LLL*FFFFFFFFFKLAMFVFFLFFIF SK |

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| 4425 | 12476 | A | 5332 | 949 | 1711 | VTIPLIPDLKGSSCVGPPKP*DCRHWTPC LTLIYFFFFKVESPSVAHAGVQWHDSSL LTLSPDQV/HSPVSAF*VAGIQG/MHHHA RL/FFFFFFFLRQSL/SSVAQAREQWCYH GSLQPPPSGFKRFSCLSLPSSWDYRCPPP HLA/DFVFLIEMGFTMLTRLVSNS*PQ/C DLPASASQTAWITGLSHRAWLNFFCIFI YGVSPCWPGWSLTPDLK*SACLSLP*CW DYKCEPPCPAQFTFIRKDSFADVYCSVS |
| 4426 | 12477 | C | 5333 | 11 | 154 | MESRSVARLECNGAISAHCNLHLLGSND SPASASRVAGTTGTATTPG* |
| 4427 | 12478 | C | 5334 | 163 | 270 | MNKMESLFYCFNADILIKQDYFHHQHHL YIYTKPV* |
| 4428 | 12479 | A | 5335 | 92 | 404 | WLQICVSGCICT*AMALYICINVVVVVKVV LFYEDVCIKAVK*AFHFIHNLMCVYICM CVCVWNIEGLYIPQRYIHMAVLLHRSN SQTPGSIRYKFKISFIGFI |
| 4429 | 12480 | A | 5336 | 2 | 1100 | FALAARLQEFGRKYFTESGLVGLLEQA AASFMSMAGMYEAVNEVYKVLPIHEANR DAKKLSTIHGKLQEAFSKIVHQSTGWER MFGTYFRVGFYGTKFGDLDEQEFVYKE PAITKLAEISHRLEGFYGERFGEDVVEVI KDSNPVDKCKLDPNKAYIQITYVEPYFD TYEMKDRITYFRQKLQSSVRFMYCTPFT LDGRAHGGTSMEQFQKGRPNLDYVSCL FPYIKTRG/PMSLIKRRSSLHPFEVAIED MQKKTQELAFATHQDPADPKMLQMV QGSVGHQVNQGPLGSCPGFFCSGNT** PKALSDIH*KLATLAFKDFTKRCEDALR KNKSLIGPDQKEYQRELGEKLSSALKRA LPAT |
| 4430 | 12481 | A | 5337 | 48 | 1057 | RCWENCTSTCKTMKSDPYLR/PYTTINSK WIKDLNVRPETIENIGEFLD/MTLGN FLDITPKAQSTKTK/DKWDYIKPKSF/CTV KETVNKMKQ*PTD/W*KIFVRHIYKGL VSKIYKEFIQLNF*KWAKDLKRHFSEDD TQMANRYIKGCST*LIKEMHFKNHSKY YLSPVRLAVIKKNKNNKC/W*WCGIKGT L/LHCWWECLVQPLWKTEWKFLARKIK LPYDPAIPLGIYSK*MKSPCKYICS/RV FIAALFIVA/K/TWRQLKCPLT/V*IRKLCI YMPYTPMEYYPPLKTKKNPTISCHLLPT WMGLKDTVLEISQTEKKILHNFTIYVES KKKI |
| 4431 | 12482 | A | 5338 | 2 | 409 | PLALALAMAYPSCPGDAHGP RPPLSP PS*PASVP/TSP/PQSSA*FLCPQSYVEGL TPRILPAGGGHVPCSRPSSSPLASVSAP RWGALLPGPCPTSLSSGCRKGRASPRA HPPPTASLCTALWPPCFSP*PGVGLGNG LSLLPRRCTWPAARSTVSSLLACLPNS PLNLLRDSSVLSHTQLRGSPHGFYPLEGA MFPAPALPPHQALPRYQPPGGELCCCLD HALLPSPRDVGKGPPALELTHPPQACV LRSGHLASRLHNL |
| 4432 | 12483 | A | 5339 | 32 | 323 | KFHLGGGGWFPLFPGGARGVGS*VR GFRPPWAPPLNPPFFPKQNSPGLVVFAF RPSSSGG/PGPGNSPHPGGQGFG*QKFRP CPSAWGTKGGFP |
| 4433 | 12484 | A | 534 | 1 | 2278 | |
| 4434 | 12485 | A | 5341 | 4 | 329 | IIAHCKLKRPSNDPPQPPSSWDCRHAPP HPAN*FFF*EMGSCHVAQTSSQTPALNPS RYPPTSASQGAETVMSHCAQLYPCFLT KEK/FSHS*IRRLLSETSNGEY |
| 4435 | 12486 | A | 5342 | 3 | 274 | FQSQNIKLNLMGVLCFETEHSVT*AG LQWLDLSSLQPPPPGFKQ/FSCLSLSSW DYRSPPRGPNFCIFSGDEVSPYWSGWS QTSCLK |

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| 4436 | 12487 | A | 5343 | 1 | 1075 | MVDGTL L L L L L S E A L A L T Q T W A G S H S L K Y F H T S V S R P G R G E P R F I S V G Y V D D T Q F V R F D N D A A S P R M V P R A P W M E Q E G S E Y W D R E T R S A R D T A Q I F R V N L R T L A R L Y * Q S E R R P G S H T L A Q W M H G C E L G P D N A S F R G Y E Q F A Y D G K D Y L T L N E D L R S W T A V D T A A Q I S E Q K S N D A S E A D H Q R P Y L Q A T F V D S F P K * L Y E G K E T F L H L E P P K T H V L H H P I S D H E A T L R C W A L G F Y P A E I T L T W Q Q D G E G H T Q D T E L V E T R P A G D G T F Q K W A A V V V P S G E E Q R Y T C H V Q H E G L P E P V T L R W E A R F P S P P I L P S W A S L L G L V L L G S V S E A V V A A V I W R K K S S G H F L P T G G K G S Y F K G |
| 4437 | 12488 | A | 5344 | 58 | 426 | K L Q L L * F F F W F F F C L F T Y F L E T V E C S G A I I A H C S L K L L G S S H P P A S A S L V A K I T G A C H P A W L I * V V L I V L F K R K W Q S H L K L M V E K R F L S E G Q I L S V Y H F R V P L L Q N D R N L A Q I I L G R K R E M Y |
| 4438 | 12489 | A | 5345 | 3 | 284 | K K I L R K K I L R K S S V * I * D * S S Q P E N I P * K Q F L S N H P K C I T I L S M R N M S I M K K G G R I S E D F I K L F F P S L L S H L L V I E W G L Y I E I Y L T P P N N T F |
| 4439 | 12490 | A | 5346 | 2 | 225 | T L P C T L S T S T P W S A S S Q E R E M S F G D G * P V G * P P L T A V P C C S V W G L R R L * G E R T K L G I G A A G G F H S Y D G N T Q T |
| 4440 | 12491 | A | 5347 | 3 | 104 | W S T V A R S * L T A T S C S F C L S P P S S W D C R R V P P C L A / S F H F Q Y I A L N N * A * A I I L P Q P S K V L G L * A S A L Q V A G T A G V Y H H A W |
| 4441 | 12492 | A | 5348 | 2 | 392 | T G K N E I Y C I C F I D L E Y Q * K I G L L L H I G D K E E Y S / W N S G Y F I G Y C L E L P C P V V K V S G N * N D S I E A A V L M T T P S K I K I * V T L Q S K E A S P I K V L T Q V I G D I K G I L E N G H Y K Y Q L * Q F K L Q K G N D N H |
| 4442 | 12493 | A | 5349 | 2 | 67 | A A E D * H C P I A S E T Y K T I T E L W V T L P V E G K S V P P L I N T E A T H S T L P S F Q G C V S L A S I T V V G I D G Q A S K P L K T P Q L W C Q L G Q H S F M H S F L V I R T F P A P L L G R D I L T N L S A S L T I P G L E P H L I A A F C S S S K P P S H P P L V S L H L K P Q V * D R L G N L Q D H H R C F G |
| 4443 | 12494 | A | 535 | 750 | 1053 | P S T L S S L I S R H D D E A T R T S T S E G L E E G E V E I G E T L L I V E S E D Q A S V D L S H D Q S G G I S L N S D E G D V S W M E E Q L S Y F C D K C Q K W I P A S K E L L K S F D L S I P V |
| 4444 | 12495 | A | 5350 | 2 | 275 | E T E S C S V A R L E C S G M I S A H C N L C L P D T G N S P A S A S * V A G I I G A C H H A Q L I F V L V E T E F H H V F H H V G Q A S L E F L N L V I P P P R P P K A L G L Q G |
| 4445 | 12496 | A | 5351 | 3 | 1031 | S S A P E A A K K P T P C H R C R G L V D K F N Q G M V D T A K K N F G G G N T A W E E K T L S K Y E S S E I R L L E I L E G L C E S S D F E C N Q M L E A Q E H L E A W W L Q L K S E Y P D L F E W F C V K T L K V C C V P G T Y G P D C L A C Q G G S Q R P C S G N G H C S G D G S R Q G D G S C R C H M G Y Q G P L C I D C M D R L L Q L R S R N E T H S I C T A C D E S C K I T C F G P * P T G L R R S C E V G W V L D E G A C V D V E K C A A Q T P P C S A A Q F C K N A N G S Y T C E V E G D S S W V G C P G K G P G N C K Q C I S G Y A R E H G Q C A D V E R V P H * P E K T L C E E K T K C Y N T P G S Y V C V C P D G F E E T / R R C L C A A G R R L K P Q K G E S P T Q L P L P |
| 4446 | 12497 | A | 5352 | 206 | 330 | K M L Q L A L Q S C I K V R T L N S R H L G A G V T A H E E * C P C C H P M I K Q |
| 4447 | 12498 | A | 5353 | 1 | 8271 | |
| 4448 | 12499 | A | 5354 | 2 | 10028 | |

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| 4449 | 12500 | A | 5355 | 2 | 5217 | APLDGEVELLQQKLREKLDEFNELAIQK ESADRQVLMQEEEEIKRLEEMNINIRKKV AQLQEEVEKQKNIVKGLEQDKEVLKKQ QMSLLLASTLQSTLDAGRCPEPPSGSP EGPEIQLEVTQRALLRRESEVLDLKEQLE KMKGDLESKNEEILHLNLKLDMQNSQT AVSLRELEENTSLKVIYTRSSEIEELKAT IENLQENQKRLQKEKAEIEQLHEVIEKL QHLSLMGPVVHEVSDSQAGSLQSELLC |
| 4450 | 12501 | B | 5356 | 224 | 326 | XSSSDGNLRPEAJTAHVFSLLAALLLAV GLALL* |
| 4451 | 12502 | A | 5357 | 87 | 558 | STFFPAIKHWVDLTAQRGHCLSPRSHSN EGRQMQUERGPRWAGSPAPSPWSPEGPG PRLHGRTERKERGLWGLDTRQKVGSA SRGVGPEPQHT*AAGTAKQRQHAQAQSP HGCPQPLTPSPPESEAGVSVAAYKPA ATRSPGQCWWLQQAFAFR |
| 4452 | 12503 | A | 5358 | 3 | 713 | TDRGCRGRDTFHEPELG/PKTPGPGAPLQ VPLAGDAVGGASARSPLGAGNPPPIPW RTPAGAASGAGPAAPAGPLGSLG/RKY RPLLRMRIALFCLHPPAPAPMATCVHKP SLLSSRSSTS/SAALLLAVGAGTVGAE/RF GRSGRRRAPTPVARSSSPMQPRPGPLR TPRRRCRAACPSRSPLLHLSPIAV*PWG KAVPSLGSQIHPVLNSREEGTSKTLPLRS REDGAIHFYIFI |
| 4453 | 12504 | A | 5359 | 2 | 807 | RPQGFPWRLPSRRGATPGRLPRLS*PRPH PRPEPGVRVGPWVHIESVR/HQDCSGRSP GQTPTCEDRAPSGKGSALGRSLGPWTL IGSGRG/RSPGKLGSPGPAKAF*RRRRA SKVAPGPLDGWPRIAQAWAREKGKHLA WGTGGSWPPSHAPGHQLGFQKQPLGN QREWGQNLGIQDL*GQVDPNRPPLSGP GDRHLTGKPSGREGALSQGPQGRHSPGR PQQQASSCCERSHPGLPVVTHCPGVQ WASCPGWGCLARCSPPRA |
| 4454 | 12505 | A | 536 | 426 | 634 | VFCYSRTNWNKTEINRKKFGKLPISWKL SSTLLNNQ/L/VSEENKREIKKYPDINENE DTTYQNLWNLKQC |
| 4455 | 12506 | A | 5360 | 1 | 412 | FFFFLRWSL/NSV/SQAGVQWWDLSSLQP LLPGFKQFSCLSLLSSWDYGCPRPANFL HF**RQGFTMLFRLVSNS*PHDSPISASQS AGUIGVSHRAPSCLLAYFSEFVSKWK QSSTKALPCGFRMLCPVLTPEK |
| 4456 | 12507 | A | 5361 | 3 | 884 | YLSIHQVYGKEACIPCGPGSKNNQDHSV CYSDCFFYHEKENQSLHYDFSNLSSVGS LMNGPSFTSKGTKYFHFFNISLCGHEGK KMALCTNNITDFNVKEIVAGSDDYTNL VGAFVCQSTIIPSES/TGVSEQPYHNPIL ADTFIGVTVETTLKNINIKEDMFPVPTSQI PDVHFFYKSSTATTSCINGRSTAVKMRC NPTKSGAGVISVPIKCPAGTCDGCTFYFL WESAEACPLCTEHDFFEIEGACKRGFQE TLYVWNEPKWCIKGISLPEKKLATCETV DFWLKVGAGV |

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| 4457 | 12508 | A | 5362 | 3 | 2697 | CSVKECLQASAKLPSAPASVSLCLLVA KVWRRRLRWQEAASFSCASGEYLEMKNQ VCSKCGEGTYSLSGSIKFDEWDELPAF SNIATFMDTVVGPDSRDPDGCNNSSWIP RGNIESNRDDCTVSLIYAVHLKKSgyv FFEYQYVDNNIFFEFIGNDQCQEMDTT DKWVKLTDNGEWGSHSVMLKSGTNILY WRTTGILMGSKAVKPVLVKNITIEGVAY TSECFPCKPGTFSNKPFSNQCSCKIIDPF LKRFFYVAEGSSECTERPPCTTKDYFQI HTPCDEEGKTQIMYKWIEPKICREDLTD AIRLPPSGEKKDCPPCNPFGYNNGSSSCH PCPPGTFSDDGTKECRPCPAGTEPALGFY KWWNVLPGNMKTSCFNVGNSKCDGMN GWEVAGDHIQSGAGGSDNDYLILNLHIP GFKPPTSMTGATGSELGRITFVFETLCSA DCVLYFMVDINRKSTNVVESWGGTKEK QAYTHIIFKNATFTFTWAFPEN*FRVQD NRRFINDMVKIYSITATNAVDGVASSCR ACALGSEQSGSSCVPCPPGHYIEKETNQC KECPPDTYLSIHQVYGKEACIPCGPGSKN NQGKKMALCTNNITDFTVKEIVAGSDDY TNLVGAFVCQSTIIPSESKGFRAALSSQSI ILADTFIGVTVETTLKNINIKEDMFPVPTS QIPDVHFFYKTIYRQIHDIKCPAGTCDGCT FYFLWESAECPLCTEHDFHEIEGACKR GFQETLYVWNEPKWCIKISLPEKKLAT CETVDFWLKVGAGVGAFVALLVALTC YFWKKNQKLEYKYSKLVMTTNSKECEL PAADSCAIMEGEDNEEEVVYSNKQSLLG KLKSLATKTAIGVFGGPWSLGYVISCQY SETRSSCIISVHAKNEILAJEEE |
| 4458 | 12509 | A | 5363 | 1 | 1146 | NFDSKRITVRNLRREDIAKYLRNLDPN SAHYDPKTRAMRENPYANAGKNPDEVS YAGDNFVRYTGDITISMAQTQLSVSSMS SHFISAHKTFGIV*SLFSRSIQ*CSCQLTK MFRITLVFAWEA\YDKGSEVHL\QADPVT KLELLYKS\FKVK\EDFKEQKESILEK YGGQEHLDAPPAELLLAQTEDYVEYSR HGTVIKGQERAVACSKYEEDVKIHNHHTH IWGSYWKEGRRGNKCCHSFFKYSYCTG EAGKEIVNSEECINEITGEESVKKPQTLN ELHQEKLKEEKKKKKKKKKKHRKSSSD SDDEKMGHVKSNAKALNA*EAIRLLHVKE TMQ\NDERKRPVNSMY*TSRPVEEEMEA YRMK\RQRPDDPMASFLGQ |
| 4459 | 12510 | A | 5364 | 3 | 1589 | APALKVILRYT*TDAPAIWWLDPELTG CAKPFVFTQGHVSVNRSFFPCFDTPAAK CTYSVVVKAPSGVQELMSATRSAYMEE EGVFHFHMEHPVPAYLVALVAGDLKPG DIGPTSRVWAEPCLPTATSKLSGAVEQ WLSAAERLYGPYMWGRYDIVFLPPSFPI VAMENPCLTFIISSEDEFVIDVIHEVA HSWFGNAVNTATWEEMWLSEGLATYA QRRITTETYGAFTCLETAFRLDALHRQ MKLLGEDSPVSKLQVKLEPGVNPShLRN LFTYEKGycfVYYLSQLCGDPQRFDDFL RAYVGEYKFTSVVAQDLDSFLSFFPEL KEQSVDCRAGLEFERWLNATGPPLAEPD LSQGSSLTRPVEGLFQLWTAEPDQAAA SASAIISKWRTFQTALFLDRLLDGSPLP QEVVMSLSKCYSSLLDSMNAEIRIRWLQ IVVRNDYYSLT/FHRVRRFPGRARCHAC YTIPLYEDLCTGALKSFALEVfyQTQGR HPNLRRAIQILSQGLGFQHRARP |

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| 4460 | 12511 | A | 5365 | 1 | 418 | FMGGVNRADENIDKYRASIRGKKWYSS PLLFCFELVLQNAWQLHKTYPVDFL EFRRRVVCHYLETHGHPPEPGQKGRPQK RNIDSRYEGP*IQVDSNPQGIQTRCAEC HKNTTFRCEKCDVALHVKCSVEYHTE |
| 4461 | 12512 | A | 5366 | 1 | 205 | KKFSCGLKKIFHEKNCQST*QISLLSYFK KLQPPQLSSTTL/SQQPSTLRQNPAPAK RL*LIEGSADG |
| 4462 | 12513 | A | 5367 | 1 | 389 | CRFNAISSKITADFTVFGGFLEVHKVIL KCKWKYYYKSRIKTKGFKKTQLS/GLILH NNKT*YTSIIKTELTKYRHRMENPEIDL HRFDQMIFDEGIKVIQ*GKERLFNQWCW SRLRCICLKFSITNGQ |
| 4463 | 12514 | A | 5368 | 2 | 300 | TFPNLMTNMNLQIQEAQ*IPSWKNSE/RS Q/SRHLIKLLKIKGKERILKEQKLITYKG CSIRLRGDFSPETTEARK*WDDIFKVLKE QVSTKNLIFSITVL |
| 4464 | 12515 | A | 5369 | 199 | 494 | |
| 4465 | 12516 | A | 537 | 1190 | 2097 | SSCLKILNITLAKSLLL/CLDISVCYLLD TGICYCLLDISVCYCLLDISICYCLLDTSV CYCLLDISVCYCLLNISICYLLDTGICYC LLDISVCYCLLDISVCYCLLDISVCYCLL DISVCYLLDISVCYCLLDISVCCCLLDIS VCYCLLDISVCYLLDISICYCLLDISVCY CLLDISVCYCLLDISICYCLLDISVCYCLL DISVCNCLLDISFCYLLDISVCYCLLDIS VCYCLLGISVCYLLDISVCYCLLDISVC YCLLDISVCYLLDNSVCYCLLDISICCC LLDISH |
| 4466 | 12517 | A | 5370 | 256 | 514 | |
| 4467 | 12518 | A | 5371 | 2 | 1340 | SLDLGGISTVVVNGYDVVKECLVHQSEI FADRPCPLFMKMTKMGGLLKISRYGR GWVDHRRRLAVNSFRYFGYGQKSFSKIL /EKETKFFNGCYWKHTKVGPFDF*TV**R MLFSNITNLHIFWEERFHFMQGHRFRH MDWSYFRWKMWNAASASVFLYNAFP W/IWA/FLPFGKHQQLFRK/WTAVVYDFL SRLIEKASVNRKPQLPQHFDVAYLDEMD QKNDPSSSTFSKENLIFSVGELIAGTETT TNVLRWAILFMALYPNIQGOVQKEIDLI MGPNKGPSLGR/RNAKCPYTEAVLHEVL RFIGNIVPLGIFHATSEDA/SLRGYSIPKGT TMITKP*FLYHLGWKKVPGEDPQKVFP ERFPGTSSGIFWPQEGKLWVPFFPLGRRH CPWENTLARMEMVLFFSSIASEVSFAFS HMN*FQI*SPRLGMTLQPPYLICAERR |
| 4468 | 12519 | A | 5372 | 135 | 273 | |
| 4469 | 12520 | A | 5373 | 1 | 344 | LNTLPEVPFTPLSCLPSLSLSS*LAPSPFICI CYAIVP/PPFLLPSDLADPSSHPGLPFLFP PHSPRHAPSAPPSKKKKKKKKKKKTTA PVQASLGTSSLYPLGGSETGPTWS |
| 4470 | 12521 | A | 5374 | 1 | 724 | GRRGRGRAGSRAGRRGGAQAAALVNR GGGPIRNYSDVAGGAAGGGRNRNPAP YSRPKQLPDKWQHDLFDSGFGGG/AAG VETGGKLLVSNLDFGIVSDADIQELFAE FGER*RRAAVHYDRSGRSLGTADVHFER KADALKAMKQYNGVPLDGRPMNIQL VTSQIDAQRRPAQSVNRGGMTRNRGA GGFGGWVDGTRKGTARGGARGRGRGA GRNSKQQLSAEELDAQLDAYNARMDDTS |
| 4471 | 12522 | A | 5375 | 37 | 331 | GLLCQASGPQAPGWAPLGRRGQGSNP LPVPPRPVPA*/APGHTCHAL/GKIPF*VPL PLQ*GPPETHLREPPPGPCPPS/PVPSPYQ GFLQPGGRAGGDRD |

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| 4472 | 12523 | A | 5376 | 1 | 385 | FFFFFFFETETCSVA*AGVQWRDL* LQPPPGFKRFLCLSRPSSWDYRCTSPYLAH F*FLVETGFHHVQGAGLELLTSSDPPISA SQSAGITGVSHCTWPKLTTSTLMNVFPL NIILLYLVILAK |
| 4473 | 12524 | A | 5377 | 21 | 352 | PTHPWPPTVLEATAPGSEYFFF*DAVLLS SRRLECSG/SISAHCDLHLPSSSDSPSSVP QVAWIIGVRHHVQLIFVFLVEMGRHVD QAGLK/A*PQVIHPPRPHKVLGLQV |
| 4474 | 12525 | A | 5378 | 2 | 545 | TCLGFFQMFFLGLSIFVCYILLKFDCVFIF SSNLGSLIFVCYILLKFDCVFIFSSQLPFFT FYMDYSNPLGLSMSSLRIS*KTF*MYG*V LYFFF*KRNSQCFFPNRDYFWIVCSSSV DLFCTLFFTSCHPQQPSCSPPPGNKGA PLPTVTLEALKMMMVFIFGLSSRJRGRS WKSP |
| 4475 | 12526 | A | 5379 | 545 | 1462 | GYFPCFIPVATS*QSIGVVNF*LFEYFVY IYIFEGFWGGLICLVSSVCLFQVYFSFA KIIIEPPGFKTILPPSTLVNNWELTSLHQ K/RPANFVIFGKRQGFHVGPGLSNGPHA IRPASASQSTGITGVSHCACALNFITEP |
| 4476 | 12527 | A | 538 | 163 | 372 | IRQRKAKLVVLAFAFNRRGLRKP/IFYAG VGKIVKKKYSGFFIELVTTGKNYLMCA LAVIDPRDSNIIRS |
| 4477 | 12528 | A | 5380 | 2 | 243 | GFKQFSCLSHPSSWDYRCAPPHPTNF*F LVEPGFHHVQGAGLELPTSGDLPALASQ SAGITGVSHHPWPMALNSKNVR |
| 4478 | 12529 | A | 5381 | 1 | 328 | SPETGSCSGAQAGVQWHDGLSLQP*LGL K*SSYLSLLSNWDYRCA/PPRLANFLFFV QAGSCHLAQAGLELLSSCHLPALVSQNA GITGVSHHARAGSCMEENTSLWLT |
| 4479 | 12530 | A | 5382 | 2568 | 3052 | RGTEGRRVKSSKAGFFCFVLCFVLRWS LTLAQAGVQRHDLSSLQPPPTFK*FSC LSLPSSWDYRRPPRSQ*F/SFVFLVETGF HQVGQAGLELLTSGDPPASASQSGITG VSHHAQPQLDLEPPVCGQORDMALLLE RLPETVTCFLFPSELRRAR |
| 4480 | 12531 | A | 5383 | 2 | 306 | FFEMESCSAAQAGVQWHNPSSLQPLPG FKQFSCSLSPSSWDYRRAPPHANFEFL VDARFYHVGQAGLELLTSSDLLASAS*S AGITGMSHHGWP*ATF |
| 4481 | 12532 | A | 5384 | 141 | 414 | IRITEGGAQASVVFKTPQV/WLGTVAHTC SPSTLRSRGGWIT*VQEFKTSQSNRNQRG CNLVWSLKLTSILLTFELDSIRQEEGKLV RRWGR |
| 4482 | 12533 | A | 5385 | 2 | 287 | GRVGNNKKFGGRISLC/QPGWSAVTQLQ LIVTLNSWAERFSQDLPS*DYRCTCLA NFLTFCKDECLAMLLRLVLNSWPQGIPL PQLKVLQV |
| 4483 | 12534 | A | 5386 | 663 | 1014 | ILKHYPSSQISSILQRKHTRQLSASLITNAK VFFQASRFNVSSHILALLQENIFYFNTKP VICKPG/CVIRITF*KL*IASQVRWLTPVIP ALWEAEAGRSRGQGIKTILANTVKPRLY |
| 4484 | 12535 | A | 5387 | 3 | 208 | EDVNRWRDIPSPWIGRVIRVRMSVL/PNP INNTYINTEFLILI*Y*YRNTSIPKISGRFF VLLRENEN |
| 4485 | 12536 | A | 5388 | 190 | 261 | ISIF/CFFKTDSSCVAQAGVQ**NLGSLQ/P CNLQPLPPGFK*FSCLSLLSNWDYRCAPP /HPNFCISRDGISP*LSILPTTFIKVARKI LI |

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| 4486 | 12537 | A | 5389 | 31 | 1431 | RETRSCWAHYHAESSKHQAKLKDSTRK ARRSIELIGPGSSQKGGDICSILHLSKLG LCYSKTGNMGGWEGGMQLRVSSNSM GKSSRERAAADLPQGSCHWELPGRINT RISLKPRHVWNLSSVLCQVVKVKS MFHMPITSAMQGDRLGICVTQFDPKLE RGLVCAPESLHTVHAALISVEKIPYFRGP LQTKAKFHITVGHETVMGRLMFFSPAPD NFDQEPILDSFNFSQEYLFQEQYLSKDLT PAVTDNDEADKKAGQATEGHCPRQW ALVEFEKPV/YLPSAVPGDWLQARCGHS PNTCRLAFHGQSCSTG*RTGT/NADSFLP RLKVYKLKHKHGLVERAMDDYSVIGRS LFKKETNIQLFVGLKVHLSTGELGIIDSAF GQSGKFKIHIPGGLSPESKKDPDTPPSKT GPGWPVGGQPGRRRSPSGANPHKMGW LTRPFKRYVFDTHKRMVQSP |
| 4487 | 12538 | A | 539 | 995 | 1192 | IILGNLTACSFYTSSLNAVWLIKSAMLQL YFIFFFGDRPSLCHPGWSAVVQSLLTAT STSWAQAE |
| 4488 | 12539 | A | 5390 | 1 | 421 | FFFW*GTESQLLPQCSGAITAHCSL*LPG SSEPPTSAS*VPETIGTY/RHAWLFFFN FFVETGSHYVAQAGFEPLGSNDPPFPQP KLLGITGMRHHSRPELLPLTVPMWSWESQ DGETEDFCAMETWKVNITCLAQTPRL |
| 4489 | 12540 | A | 5391 | 1105 | 1497 | LFRTSLLVIAFLPKKNFFF*HYA*SYNVH PNTARKIKPEFRAVRVSFLLSERMSNIFF FFDTEFHSVTRLECTG/T*SSTHCDPRLP GFEQILPASASQSSWDSACATHARLIFV FLVETGFLHVQAG |
| 4490 | 12541 | A | 5392 | 109 | 695 | LLLIPSAVTSYPPKDLPWGGMILSKPPLL GSMLANNCIVAGGCS*SSTLPS*LSSWRV GPQHLPRHARPPHQVQYIISQDGVQHL LPQEYVVVPEGHHIQGQKGRITHIQYEQ GAPFLQESQIYVVPSPGQQLVTQAQLE AAAHSAVTAVADAAMAQAPGPVWLQD EDKCPKHNSNKLQHPRASKYDVITPGR |
| 4491 | 12542 | A | 5393 | 1 | 405 | |
| 4492 | 12543 | A | 5394 | 203 | 458 | |
| 4493 | 12544 | A | 5395 | 2 | 1185 | LILNKKSRTRRSFRRHGSPSHGPFAPWRP SRLAEPGELG*REREGYNPPISGENLIG LSRARRPHNAIFVNFEEDEVPKQPLEAA AQITWRRVCTNPVDRKVEEELRKASPA LRLAPLFDIRPIWSRNAVKANITVHPNRF KAWLPFIAYMNTGPWRSWIRFGYDP RKNPDAKDL/YQVLDFAIRCGMKQGYA PSDLPVKAKRSTYNYSPLPITVKKTSQ VTMHDLEAWPWPRGRSGARKPASSKY KLKVSLLQTLRDSVYIFREGALPPYRQ FYQLCDLNVEELQKIHNRNDGAEDFLA QERGWGGCLPQGPDEF/RGDTMSPMIR ETIGSKRPALFSSSAKADGGKEQLTYES GEDEEDEVEEEEEEDFKPSDGSSENG NQNF |
| 4494 | 12545 | C | 5396 | 95 | 295 | MSTIKAPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXSSLRIJLFQNIYLYWDKIT FLYCEHTVGAQ* |
| 4495 | 12546 | C | 5397 | 262 | 390 | |
| 4496 | 12547 | C | 5398 | 118 | 132 | |
| 4497 | 12548 | A | 5399 | 109 | 559 | QFLHRLVHDSGEVWMKLVE**NTLLAK MVSISWPRDLPASASQSAGITGLIGALVL SVGIYAEVER/HEI*NP*KCLPGSSHHP PGRRHVHGLLHWCAGVPP*QPGKH |
| 4498 | 12549 | A | 540 | 77 | 199 | SKSRPIASNKIEAIKSLPAKKP/GPDGFAT EFYQTFKEEL |

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| 4499 | 12550 | A | 5400 | 1 | 362 | FFFFLRRSL/SSVPQAGVQ*HDLSSLQPP/ PPGFTPFSCSLPSSWDYRCPPPPAKFFL YF**RRGFTMLARMVVIS*PRDPPASASQ SAGITGVSHRARPPPPQFFIQLPLYNIHTL EGR |
| 4500 | 12551 | A | 5401 | 2 | 462 | NPPTSAS*VAGTTGACYHTRLILVCRDR VSPCCP/VLVFFFF*DRVAQAGVQWHG LGSTCQPSCPPGFKRFLLPSPALSPSS WEYRHPPPPRPAFFCIVETGFTVLAR MVIS*PRHLPALASQSAGITGLSHCARP VDSFLATSIY |
| 4501 | 12552 | A | 5402 | 3 | 352 | SSRPGSCRRGAVRAAIRYVRLRAVPSGG GEPPSGAPLQPSWK*AFARPGMLRCSMP SQAPSRSAAVLFEPLAEWMLHCA*QDEV RLGGH*GRRGPLLLDRSRA*RESPAEVRP ARE |
| 4502 | 12553 | A | 5403 | 3 | 286 | SVAQVGMHGHSLGSLQPLPGLK*SSHL NLPSSWDYRHAPPHLANFCIFFVETGFR HVSQAGLKLSSSNWPTLASQSVVITGV SHRAQPC*TF |
| 4503 | 12554 | A | 5404 | 73 | 542 | VLIFFFFLKLSD/DSVA*AGVQWCNLSSL QPPSPGFK*FSCSLSSWDYRCVPPSPA NFFIFLVETGFTVLARMVIS*PHDPPTL ASQSVGITGMSHCPWTDLIF**CKRDTLC IPMSLS**FKVPKGNLIWKLKGFGGLP LGIONAYFWIV |
| 4504 | 12555 | A | 5405 | 1 | 397 | EMESSSVTQA*VQWHDALLQPPPPRFN RFSCSLSSWDYRCPLSPANFCIFSRD/ MGFIVLARLVLS*PNDLPASASQSAGIT SVTHRIWSKIFFRVDNDHYIILFSSMELN VPTIVLCYHPQSSNMYS |
| 4505 | 12556 | A | 5406 | 72 | 243 | EPMTQVSMFSLRQPMKTTGMRIAMQE KVTQNTQSS*KIFRFPYSLIGVSLVISI |
| 4506 | 12557 | A | 5407 | 34 | 420 | MLYSHDPELS*QVLTALYAVPPFPVPV DFL*I*FPSALVSIGGSRL/PVLSHWFLDL RVFH*FEKAHL*KLCGNP/WLSALLSTF KVM*ERLVDQ*LSMAKTE*EPMTQVS MFSCGRVEEFRHHP |
| 4507 | 12558 | A | 5408 | 3 | 316 | FFNFNRQGLCHPSWSAVTQSRLTVASIF R/VQGSSHLSSLGSW/DARHVPPCLANF* FFCRD/RGLVMLPMSVSNWAQAILPPW LPSIGITGVSHHVWLASLFVF |
| 4508 | 12559 | A | 5409 | 905 | 1291 | RGADTCLGFQVSADLHHLFSFLFCSVAQ AGVQWRNLGSLQPPPGFKLFSCSLSS WDYRHAPP/RPG*FFVFLVETGFTRVGQ AGL*LLTSGDPPASASQTA/RGL*GMSH LASPIYLDYFK*NFNKP |
| 4509 | 12560 | A | 541 | 212 | 322 | |
| 4510 | 12561 | A | 5410 | 2 | 308 | FLRHNLAVTQPGAQWRLLSSLQPLPEL KPSSHFLPSSWEYRCEPPHPANF*FLVE TGFHHVAQAGLEFLASSDPPTSAFLNAG VTGVNHSAWLCFSYLL |
| 4511 | 12562 | A | 5411 | 3 | 368 | HRGESVWNICRWGTLR*GKIGKMTRAH CLEFIGALIVSITSPAPFEAPKWKNLDL *TLTHGRPVSVLLAKKCDHG/KDECRN SSLKMGQIYMEHSFVG*IETSAKENVNF DEASRCLDAK |
| 4512 | 12563 | A | 5412 | 73 | 380 | GQALQWCVSVMCSCIHSHPCV*VLWV CVCLCISMCMYSYACVLGYTKFGVCTE KNKQNCCTGNRSTQGLPLNRHTGSFRF WLDHFPLASPKGTLRSLSP |
| 4513 | 12564 | A | 5413 | 1 | 400 | NSEGAAWIQPPAGEPTWGQSGGTQAG AMP PGDYS*SQGHPFLH/RAPPLTRNR RIFLRRAPSPVLEDPRKPPSRGQQL*DA LHHVLVAQLREGMLGQPRPHPPKPIK *SQHA*QLPAGEPEVGPAGDR |

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| 4514 | 12565 | A | 5414 | 1 | 895 | LRRARPRGWAGREAGPHPH*LRCRSSSA ALRPAPFTRPGTGETGLDRTEGRDQTSV NSAT/RLPNTPSRSISAGSSLOQORGLPGS SPQQENRPGDKAEAPKGQE/RMPPGDYF VIPRTPLSPPAPPPLTRNRRIFLRRAPSPV LERPPEASKQRTATPLRRTAPCASGAAQ RGDVSGRKGVCCKAGEQG*PPNNPRLRR SQAHARKRRRGDKFGVRPLQYCAF*DF WRRLSWQNPPFKATLPLLR*PLPPPLQA GTAPSPSSSQAN*MITARVTVTGWRAG SGTGSKGP*EPGRASFPS |
| 4515 | 12566 | A | 5415 | 20 | 481 | PTDRPGEHSKTPSLQKCKK*KLACSGT CL*S*ILGRLRQKDHLSPGVRGYNEL*SC HCTPSWVAE*GPVSK*IIQSPPRKE*S/LY NEKNPSN*HIVDSGEWFSFVLGADRWG AGVLYQVRVRLSQMCNERGHKHCIPITI YLPYKPLCLPAL |
| 4516 | 12567 | A | 5416 | 236 | 820 | RRPQQAGKMKGSRIELGDVTPHNLFNCL ILCGVTSPNIKQLKRLNQVIFVSYNDKF YKDVLEVGETKLAYFNDAVGAVCCR VDHSQNQKRLYIMDTRDVWAPYRSLGI RELKC*IMCLKHLLKKMVLFDNIFLHVQI SNESAIIDFYRKFGFEIAPKKNYKRIEPA DAHVLQKNLKVPSQONADVQKTDN |
| 4517 | 12568 | A | 5417 | 15 | 209 | KASRKMQIETTLRYLSPMRLAKMQML INTSCW/RKSQETRTLIC*W*EGKMVQPL SKGIWPYLIQ |
| 4518 | 12569 | A | 5418 | 1 | 498 | VQTRQLVTSPSPMSSSD/EQSSSPQCTV PSKLLVDPLQHEFSKCGENDNNIP/TPSNS NTPLKHSASFISATGTTEESRSPQIKNGS VVSLQSPGSRSSSAGGTSAVEVKVEPETS SDEHPVQCQENSDEAKAPQTPSALLGQK SNTDGLQKPSNEGVIKATK |
| 4519 | 12570 | A | 5419 | 8 | 299 | |
| 4520 | 12571 | A | 542 | 1 | 518 | MAVARLAAVA AAVVPCRSWGWA AVPF GPHRGLSVLLARIPQAPRWLPDLPNLA YKKLKGKSPGIIFIPGYLSYMGTKALAI EEFCKSLGHACIRFDYSGVGSSDGNSEES TLGKWRKNVLSHDDLVDGPQILVGSSL GGWMLHAAIARPEKVVALIGVATRCR YLSDKV |
| 4521 | 12572 | A | 5420 | 1 | 3788 | MMRLEGAEPGQLQNIDEEVISSACRLV CEWAQKVLSQPFDTVLELARFLVKSHYI GTKSMAALTVM AAPAGMKGITQPSAF IPTAESNSFQPVKTLSPIDAKQQLQRKI QKKQEQKLQSPLPGESAAKKSESATSN GVTNLPNGNPSILSPQIGIVAAVPSPIP VQTRQLVTSPSPMS/CF*QSSSPQCTG GHSAAVCETGTDSPERSQSWSWGSF CPAPLPSDLTQTSEHQCTPIRSPTTVL |
| 4522 | 12573 | A | 5421 | 288 | 668 | VEKRQFLNSTADPECIRYPLTYFVLGQSL ALVTKAGVQWRNLSSLQPPPEFKRFSC LSLLSSWDERHAPPCPS*F/CVFFLVKTG FHRVSDGLDLLTSNDPPTSASQSAGITG VTLAPSLFVLIH |
| 4523 | 12574 | A | 5422 | 3 | 288 | STFFFFFK*NLARLSRLECHGTISAHCNFR LLGSSDSPALASQVA/GLRGTCCHHT*LIF VPTVETGFRHVQAGLELLA\WVICPP*P PKVLRQLA |
| 4524 | 12575 | A | 5423 | 1 | 781 | MVHITGLCADNLQYQAGARIISVPEEDN SKSLENIFGGIIEENFPSLARDLDIQIEAQ GTPGKCITKRSSPRHIVIRLFKVKTERIL RAVRQKHQVTYRGKPIRLTADFSEETLR ARRDWGHIFSFLKQNDYQPRILYAAKLS IIEGKIQSYSDKQMLREFTITNGKLLKG AVSLVVALNR*NKSWKHITHQNRSLK HKSHRTYKTKIPLHDEYNLRSALRPAS HTAYGSMLMILKSSLTLFKHGDEVVGRRAK |

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| 4525 | 12576 | A | 5424 | 2 | 392 | KTKIIQMANKHRKRHVQSQ**VRLMQKKI IMIHYYIPQWLKTSKSDMIKCCSGYGTTE IFTHYLWECKLLHLLWRMVWLLKFK TDTPHDPAIPLLGTYPAECCTCTPKAHT AALSIIVPSWEQPKYPQ |
| 4526 | 12577 | A | 5425 | 1 | 181 | |
| 4527 | 12578 | A | 5426 | 1 | 2162 | MALFVRLALALALALGPAATLAGPAKS PYQLVLQHSRLRGRQHGPVCAVQKVI GTNRKYFTNCKQWYQRKICGKSTALGT ADVKGVSLSVSDLGGEQMRKLRPR EMMKLAEDGPAALPLSNLYETLGVVGS TTTQLYTDRTEKLRPEME/GGPGSFTIFA PSNEAIWAPLPAEVAGTPLVSNVNIELL NALRYHMGVRRVLTDELKHGMLTSM YQNSNIQIHHPMIGIVTVNCARLLKADH HATNGVVHLIDKVISTITNNIQIIEIDTF ETLRLAIVAASGLNTMLEGNGQYTLLAP TNEAFEKIPSETLNRILGDPEALRDLLNN HIL/RSQAMCAESIVAGLSVETLEGTTLE VGCSGDMLTNGKAHSNKDILATNGVVIH VIDELLIPD\SAKTLFELAAESDVSTANDL FRQAGLGNHLSGSEARLTLLGPLNSVFA KDGNPID\ALTRDLLWNHINKDQLASK YL YHGQTLLETGGKKLRVYVYRNSLCIE NSCIAAHDKRGYGTFTMDRVLVTPP MGTVMDVLKGDNRFSMLVAAIQSAGLT ETLNREGVYTVFAPTNEAFRALPPRERS RLGD AKELANILKYHIGDEILVSGGIGA LVRLKSLQGDKLVS SA*KTNVVS VNKE PVAEPDIMATNGVHVHVNVLQPPAN RPQERIGIDLADFAVEIFKQAFSVFPGAS QRSVRLAPVYQKYL AERMKH |
| 4528 | 12579 | A | 5427 | 1 | 410 | FFFLKRRDLAVAQTVGVQGDHGSQLPQ IPGRRQSSDLSFLNS*DRHILSCSATFTS F*RSHSAAQAGLEILATSNPPA*ASQGPFI V*GVSHHTWQKATFCICLPANNILSCLNIY SFFYHKTNHNFMKTNHKQI |
| 4529 | 12580 | A | 5428 | 3 | 404 | RLFYNFTIEMRFSLVQGC/INSLG*SDL LVFASASAGITGVSYPHALASIVFVCVC V*WGSALVAQAGVQ*RNLSLQPLPPEF KQFSFLSLPSSWIYRHPPLSFYLPKLKS CGLCTGIWAWRLFIFIGS |
| 4530 | 12581 | A | 5429 | 2 | 240 | TRSAVV*SQLTAALTSLVKQLSQLSLPR SWDYTHVPPCLSIFYFL*R*GLPMLPGLV SNSWTQAIPLPQPKVLGLQA |
| 4531 | 12582 | A | 543 | 3 | 604 | VMSWAFTFIHSLTDSPRATSSPPSPIHE GDQDIIVLKLFLVGGKNSGAWGRNGR PQGRRRGARVFLRLNVGGCIYTARRESLC RFKDSMLASMFSGRFLKTDESACVID RDGRLFKYLLDYLHGEVQIPTDEQTRIAL QEEADYFGIPYPYSLDHLANEMETY/CF KALTDFCDSYGLVCNKPTVWVLHYLNT SGAS |
| 4532 | 12583 | A | 5430 | 3 | 468 | RWSFTLVAQAGVQRVILAHQPPPPGFK RFSCSLPSS/WDYRLAPRLANF*FLVE TGFLHVGQAGLELPTSGDPPASASQSARI IGVPLCPGISRIFVQQMALED RDSISLRL WFLSRHANLQCVTL SWACQLLPCGTWR ARETKANTLPAVP |
| 4533 | 12584 | B | 5431 | 151 | 344 | YENESALNLYETCKVRTVKAGTLEKLVE HLVPAFQGS DLSYVTIFLCTYRAFTTTQQ VLDLLFKS* |
| 4534 | 12585 | A | 5432 | 1 | 439 | PSASSQAGGFWSQSLFKQESSGFVRTS AESVLRQESLRGVLGVLELYWRGSEVC GSRQSLYGLSSGRGILQGPQEH*SP LCP SPPELKIPENANV FYAMNSTANYDFVLK KRTFTKGVKVKGH GASFTLPRMKQKGLK IAKGIF |

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| 4535 | 12586 | A | 5433 | 77 | 444 | GLGVPSELQEIRVLPLTVCPSSVPPQYEN ESALNLYETCKVRTVKAGTLEKLVEHLV PAFQGS DLSYVTIFLCTYRAFSASQQVLD LLFKR*A*ALHCTGCTRGPRPHPLAAG LGNAESPL |
| 4536 | 12587 | A | 5434 | 1 | 3190 | MVQRMWAEAAAGPAGGAEPFLPGSRRSR SVWDAVRLEVGVPDSCPVLHSTQLDP DLPRVEVGGGRGLLQKSASRVGSGGCR APSNSRDHGWGFAPLNTVPGPAVTCAA AAQVDLFLRHCPCLHRWPVPYFTQFPPR ARSASLAFTMQAVGLCSRQSVPYLGNRL HRCIPCTVARQALDVPAPGCRALSSQST QEIGEELINGVIYSISLRKVQLHPAGNKG QRWLGYESALNLYETCKVRTVKAGT LEK |
| 4537 | 12588 | A | 5435 | 1 | 435 | EKINKIRWLPQQNAAHFLGTNDKAIKL WKISERDKKAEGYNLKDDEGRRLDPFRI TALRVPIKPMMDLMVEASPRRIFANAHT YHINSISVNSDHETPNIVDIKPANMEELT EVITAAEFHHPHCNVFVYSSSKGTIRLCD MR |
| 4538 | 12589 | A | 5436 | 204 | 397 | VPILKPMGSYG*EASPRRIFANAHTYH NSISVNSDHETYL SADDLRINLWHLEIT DRSFNIV |
| 4539 | 12590 | A | 5437 | 1 | 1463 | PLRSWLRLPDSQADIISTVEFNYSGLL AT/GDKGGRVVIFQREQEVLQPRRPA P*SVSSFLSTSCREVWQGCEFSLPFRERIK /GRPHSRGEYNVYS/TAQSHGTGGFDYL KSLEIEEKINKIRWLPQQNAAHFLSTND KTIKLWKISERDKKAEGYNLKDDEGRRL DPFRITALRVPIKPMMDLMVEASPRRIFA NAHTYHINSISVNSDHETYL SAR*PGGIN LWHLGNHR*EAFNIVDIKPANMEELTE VITAAEFHHPHCNVFVYSSSKGTIRLCD MRSSALCDRHS/KSFFEEPDPK/SSRSFF SVEIISISDVKFISHSGRYMMTRGLPVR WKVWGPSTWEEAGPVGGPTRVHEYLAR TKLACSLAYENDCIFDKFECCWNGSDSA IMTGSYNFFRMFDRDTRRDVTLAEASR ESSKPRASLKPRKVCTGGKRRKDEISVD SLDFNKKILHTAWHPVGGCYLPWLATN WLYIFQDKIN |
| 4540 | 12591 | A | 5438 | 3 | 392 | FCACFIGSKTPASCRAQGRPPGEFSPGSP SGPAGGKGVLEKEPSEM/PP/PEAGERK LERKTVPGRGAEYGPPLRLSYPAVNS HPLPSSVNGGDSNNSSQLPESHCPFFSP KEGPRKGEVPLHATRA |
| 4541 | 12592 | A | 5439 | 1 | 297 | SLLGPPEPTTWT/PAPQDR*HGPC*GR*R KRRPSL*T*QWELASPP/REPMFVPKEM VAIQPLQEEASVGPTPELLSGSCRSPISGI SILGNCPSLAPLT |
| 4542 | 12593 | A | 544 | 3 | 533 | AEGDQDIIVLKFLKVLGGKNSGAWGRN GRPQGRRRGARVFLRLNVGGCIYTARRE SLCRFKDYNVASMFSGRFPLQTDSEGAC VIDRDGRLFKYLLHYPSWRSSEFPQMRD TRGRPTGKRADYFGIPYPYSLSDHLANE METYSLRSNIELKKALTD FCD SYGLVCN KPTVWVLHYP |
| 4543 | 12594 | A | 5440 | 3 | 11 | HELILSPGPTQGQTPDEAGVIIRVLKNVP DLAILNSKDALDPRQPGYQPPNPHGPSS PPAAPRPRGA*GNPQLENASRSDRNPSQ GLRTRIRRPETPCGPPSPAGSSPAPPPS DVPPAFHSSGPPEPTTWT/PAPQDR*HGP *GDKRGAPGVAGEDPDQP*GTS |

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| 4544 | 12595 | A | 5443 | 1 | 702 | MVAASAAIKFTNMSLAIAIAGEHVEFA LIPVTAVKYTYTVIPALVMTWCLSYIER WVDSITPAVTKNFLKPLMLIVLIAAPLAIL LIGPIGIWIGSAISALVYTIHGYLGWLSVA IMGALWPLL VMTGMHRVFTPTIIQTIAET GKEGMVMPSEIGANLSLGGSSLAVAWK TKNPELHLDTPHTESPTPHDSNSHRP/PT AGVYNRSKAKSTDKDNDQTRWGNWR WSQRKYCLPL |
| 4545 | 12596 | A | 5444 | 195 | 524 | RALTPRHLPCTSQVASCNLCCLFLADLD TLAHTESPTPHDSNSHRP/PTAGVYNRSK AKSTDKDNDQTRWGNWRWSQRKYCLP LIVLSFFQTKQNTGTGFRNFLSPFLMYV |
| 4546 | 12597 | A | 5445 | 2 | 884 | VPQFKPKLHQENGPGRLARCDHQQAQP TRETWLQDRDREFQSQTFLRSRV*LV LQLQESQHSRLERLREGQRLVEREQARMR AQQSLLGHWKHGRQSLPAVLLPGGPE VMELNRSESLCHENSFFINEALVQMSFN TFTKLNPVHQQDATYPTTQSHSDLVRS EHQVDLKVDPSPQSNVSHKLWTAAGSG HQILPFHESKDSCKNDLDTSHTESPTPH DSNSHRP/PTAGVYNRSKAKSTDKDNDQ TRWGNWRWSQRKYCLPLIVLSFFQTKQ NTGTGFRNFLSPFLMYV |
| 4547 | 12598 | A | 5446 | 269 | 483 | |
| 4548 | 12599 | C | 5447 | 5465 | 5719 | MRLGKTHSTAGAWKMGLLRQADSTRG EKRGKKAAIICVKSPPGYQVAVWKY HSSLGVFEFKKTCVSMGRHDTEKKMS WERP* |
| 4549 | 12600 | A | 5448 | 57 | 102 | |
| 4550 | 12601 | A | 5449 | 3 | 287 | RALYYFL*FALFGLT*M*LVS*KLQIIEYE KKQTLGQNDTGFCIDGTANTFRVMFKEP IEILPNVCYTACATLKVRVMHYVPDGL LNVAECVF |
| 4551 | 12602 | A | 545 | 1492 | 1672 | KQWHESHDPDYDRSPSQTGEGDEPCSWH RLFAQGDK*YEATACHRNLDWQKATDI SCNTNG |
| 4552 | 12603 | A | 5450 | 1 | 594 | |
| 4553 | 12604 | A | 5451 | 1 | 768 | SVEFPCRLSGAVVRWAEAEQCRQQLPV TFGNKQKVLGKALSLIRFPLMTIEEFAAG PAQSGILSDREVVNLFHFTVNPKEPRVEY IDRPRCCLRGKECCINRFQQVESRWSYS GTSDRIRFTANRRTSIVGLGLYGSVHGP TDY\QVNIQIIEYEKKQTLG\QNDTGFS CDGTANTFRVMFKEPIELPNVCYTACATL KGPDSHYGHKRI*RKVVHGGHLLASKD CFFLF*F/ALGINNGTSIEDGQIPEIFYT |
| 4554 | 12605 | A | 546 | 138 | 257 | IFLLYLKNKVQNK*EIKQHFLGKIMSRDN NTYLTWGTEN |
| 4555 | 12606 | A | 5460 | 69 | 418 | LKSKLSDYKINL/QKSVTFVYTNSEN*SEK/ QFKKEIQFTNSCKDN*KNYLGINVIKEVK /DLYN/ENY*ILIKNEKNPKK/WRAIPCSW FGRINIVNKFILPKVGYRSNAIPMKMPV TSRTRG |
| 4556 | 12607 | A | 5461 | 2 | 216 | YLFYLLPRLKCSGVITAHCSLYLPKSKY PPHSAS*VAGTTGPATMSS*YF*FFVETR FFLCSPGWS*GSSSDPSASASQIVKIGVS HCT\CPNRNFRNLAQSLHFTGEETVPRKK GDLPWVYRQTQG*IPGPHRCQVLA*PK DFLLSPHIYVSTSILWPPA*AQAEVQWC DHSSLQPLPPRFKISSPLSLSSWNHRSCH HVQLIFLIFCRDKVLPVFPRLVLRLEQ |
| 4557 | 12608 | A | 5462 | 59 | 403 | KRGFNFGAPDKREWGEGF*LPKPWLPG* NNFSGQTLRRSGD*RKTPHGGVNLVF*E KTGFSNLGRGLKPPPSGNTPAWPPKGV GITGGASSPPVFCFLGFCENTNLRAKKK FI |
| 4558 | 12609 | A | 5463 | 1 | 242 | |

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| 4559 | 12610 | A | 5464 | 15 | 276 | ASVTQAGVQWHNLGSLQPPPRFKQFSC LSLPSSWDYRRPPPCPTNLFLLVLARMV SIS*PHDPPASASRSAEITGVNHHARPGLF L |
| 4560 | 12611 | A | 5465 | 2 | 309 | EQKFNKQKGRRALRCRGGSLGLSCSK DVKVSSFFSVARLQCSGLLAHCNLHLP SDSPASAS*VVGTPGQQRHHAQLGFVFLV EMGFHHVPGMVFDLLTSG |
| 4561 | 12612 | A | 5466 | 1 | 1209 | GGIPALDKNVAELTVMDVYDILSLVGHE VERVIDQHGCIAIARLMPKVVRVLEILE VLVSRHHVAPELDELRLAFLRVRM DLIEKERKHQKELELVEDVWRGEAODL LSQIAQLQEENKQLMTNLSHKDVNFSEE EFQKHEGMSEERQVMKKLKEVVDKQ RDEIRAKDRELGLKNEDEALQQQOTRL MKINHDLRHRVTVEAQGKALIEQKVE LEADLQTKEQEMGSLRAELGKLRERLQ GEHSQNGEEEPETEPVGEESISDAEKVA MDLKDPNRPRTLQELRDVLHERNELKS KVFLLEELGLL*E*RNNGRGKPNTPPTH RPPEDGPPSRESGIKATCLASFFFEVKKR LGQTHRGNVHIQGVPLDKLGKHTAMT GYTEQRTGSPCSIC |
| 4562 | 12613 | A | 5467 | 1 | 388 | FKDPEAVRALTCTLLREDFGLSIDIPLERL IPTVPLRLNYIHWVEDLIGHQDSDKSTLR RGIDIGTGASCIYPLLGLATLNGWYFLATE VDDMCFNYAKKNVEQNNLSDLIKVVKV PQKTLLMDALKGSI*V*SMTFCMCNPPF FANQIGSQVE*YSRNP RP RPSSVNTGGI TEIMAEGGELEFVKRIHDSLQLKKRLRI DMAALLIGVCSEVSGRKDWIQQ LAPRW YSCMLGKKCSLAPLKEELRIQGVPKVTY TEFCQGR TMRWALAWSFYDDVTVPVHE GRLAVGGVTSDSQNKGSASPPSKRRKLE KPRKPITFVVLASVMKELSLKASPLRSET AEGIVVTTWIEKILTDLKVASINEFPVEK RKSAFS*RP*KTPGFI*GERKESV*DSDKS TLRRGIDIGTGASCIYPLLGLATLNGWYFL ATEVDDMCFNYAKKNVEQNNLSDLIKV VKVPQKTLLMDALKGSI |
| 4563 | 12614 | A | 5468 | 72 | 680 | LEEPRQSLEGHTEGERAALPGKAKVVE GRVADDGVPGQPAWPGAPHTAAFPV HALGSTRASQQGSLGDC*ACR*Q*KAP *VPKQGT*QERSSTK/PRAVPSGHWAGG SGCRCSE*RAALG*TTEPQQSGELPGPPW PLEGAHPLSAETGSCVPPRAFSGQKQ PRGPG*AAEGPHGDFPQTGDRHCPPSSTE PSGMTGR |
| 4564 | 12615 | A | 5469 | 259 | 373 | |
| 4565 | 12616 | A | 547 | 5 | 960 | PTFSRAVATMFSRAGVAGLSAWTLQPO WIQVRNMATLKDITRLKSIKNIQKITKS MKMVAAAKYARAERELKPARIYGLGSL ALYEKADIKGPEDKKKHLIGVSSDRGL CGAIHSSIAKQMKSEVATLTAAGKEVML VGIGDKIRGILYRTHSDQFLVAFKEVGRK PPTFGDASVIALELLNSGYEFDEGSIIFNK FRSVISYKTEEKPIFSLNTVASC*QHGV YDDIDADVAAKITQEYNLANIYYSLKE STTSEQSAIRMTAMDNASKNASSEMIDKL TLTFNRTRQAVITKELIEISGAASSVKKE NSAS |
| 4566 | 12617 | A | 5470 | 1 | 336 | |

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| 4567 | 12618 | A | 5471 | 1 | 1396 | GAHAPHPNVMPASMGSAVNDALKRDK DAIYGHPLFLLALVFEKCELATCTPREP GVAGGDVCSDFSFNEDIAVFAKQVRAE KPLFSSNPELDNLMQAIQVLRFHLLLELE KGHELCDNFCHRYISCLKGKMPIDLVID ERDGSSKSDHEELSGSSTNLADHNPSSW RDHDDATSTHSAGTPGPSSGGHASQSGD NSSEQGDGLDNSVASPGTGDDDDPDKD KKRQKKRGILPIVFPNIMRAWLQHLTH PYPSEEQNIQLAHDGTGLTIFQVNNWFN ARIGIVQPMIDQSNRAGFLLDPSVSQGAA YSPEGQPMGSFVLDGQQHMGVIRPAGTY EWDGA*IWAWMGNGTTC*PSSC*RHSQ SKGEVCRAWPGDYVSQGGPMGMSMAQ PSYTPPQMTPHPTQLRHGTPNAFHILPSL PHHPGLD*LHGGTPYPTWD*LC*AQSPT MLNSVDPNVGGQVMDIHAQ |
| 4568 | 12619 | A | 5472 | 3 | 862 | TMRPDIDNSQAAHQPPGRLPNSRKLKKT RRQMCCVQTKKRIARLPCCRNTPPTAR SHPGRDCAKPN*SLRSPGGDCH*QGNT TWRMPMAR*LSGDSESGRSPVRTIICHQP SRSQSPVDRLQQLPASQSTQLPCSSSPQ ETTQSRPMPPEARLIVNKNAGETLLQR SARLGYEGSVLYCLENKICDVNHRDNA GYCALHEACARGWLKFVRHLLLEYGAD VNCSAQDGTPLHDAVENDHLEIVRLLL SYGADPTLATYSGRTIMKMTHESELMEKF LTDLFK |
| 4569 | 12620 | A | 5473 | 1 | 444 | KLLRWLRQENCLNLGGGSCSELKSHHC TPPWMIEGDSI*KKQNKTKTRKRKPQGS HS/TLSGGPDWV*QNCVSVQVLPISHFPL LQDILPPLPYLGANGQAGEQATDGH*/R TTTESHRASVGCRIPLWLCQRPLALALSFF LCEMRTP |
| 4570 | 12621 | A | 5474 | 2 | 330 | EMSFALVAQAGVQRHNLGSLPLPPGFK *FSCLSLPSSWDYRYAPPTPANFAFLVE TGCLHVGQAGLKLPSGNLPTSASESAG IIGVSHCAQPGTATHSNTVLSGLFC |
| 4571 | 12622 | A | 5475 | 2 | 363 | ELDTLCDLYEP*PSPSIIFINTRRK/VDWLT EKMHardFTVSAMHGDMQKERVIM REFRSGSSRVLITTDLARIGRGGFRGRKG VAINMVTEEDKRTLRLDIETFYNTSIEEMP LNVADLI |
| 4572 | 12623 | A | 5476 | 112 | 434 | ARGIDVQQVSLVINYLPTNRENYIHR*A *IWNTPLPLHTWPSLGLKLLIFLPLVFQ IGRGGFRGRKGVAINMVTEEDKRTLRLDI ETFYNTSIEEMPLNVADLI |
| 4573 | 12624 | A | 5477 | 3 | 724 | NSNVEREEWKLDLTLCDLYETLTITQAVIF INTRRKVDWLTEKMHardFTVSAMHGD MDQKERVIMREFRSGSSRVLITTDLL/A E*RELIKAEGRIQGDLSKGTSPVLRKV AAWNIIWHA*GLWGTGMLISSAFLGCPH GCLSVFPPG*SVLRAHAEELSFLTHARGI DVQQVSLVINYLPTNRENYIHRIGRG RFRKGVAINMVTEEDKRTLRLDIETFYNTSIEEMPLNVADLI |

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| 4574 | 12625 | A | 5478 | 1 | 1274 | MSASQDSRSDNGPDGMEPEGVIESNW NEIVDSFDDMNLSESLLRGIYAYGFEKPS AIQQRAILPCIKGYDVIAQAQSGTGKTAT FAISILQQIELDLKATQALVLAPTRELAQ QIQKVVMALGDYMGASCHACIGGTNVR AEVQKLQMEAPHNIVGTPGRVFDMLYR K/YTLSPKYIKMFVLDEADEMLSRGFKG QIYDISKRLNSTTKVLLSATMPFDVL EVTKKFMRGPPFRILVKKEELTLEGIRQF YINVEPEEFNLDTLCDLYENLDHHPRQ VIFHQPPGGKVDW/LSPEKMHARDFTVA SAMHWRFWTQKERRT*L*REFRSGS*PE F*ITPLTLPAQRAFDVASRVSF*SFKLMTL PPPTRGKLLIHRUGSRVDRFGRKGVPINM LTE/EKTKRNLEDIETVYNTSNEEMPLNV A |
| 4575 | 12626 | C | 5479 | 114 | 302 | MKEEILKKTAE LYKRAMXNKXKQKHHS WVXKAPSRPFIKWETRLGLKTAHSPNVF LQQGQR** |
| 4576 | 12627 | A | 548 | 1326 | 1780 | YLSKLPYFELESIAAARSRPTAQRHPRER KLKPARIYGLGSLALYEKADIKGPEDKK KHLIGVSSDRGLCGAIHSSIAKQMKSEV ATLTAAGKEVMLVGIGDKIRGILYRTHS DQFLVAFKEVGRKPPTFGDASVIALELL NSGYEFDEG |
| 4577 | 12628 | A | 5480 | 1 | 2043 | |
| 4578 | 12629 | A | 5481 | 153 | 332 | QTFVLAEGKH*ENE/PVFKLNVSPLEW REGAFPPKSDVSASFISIALLYNSAASFSS PPS |
| 4579 | 12630 | A | 5482 | 2 | 904 | HILLVNLKHLQLCTRNRNIFKLFHFRKK SFMGHQRAIKKGNLYGFALLRRRALQ VEELTLGKDTDPNARTNELGGLYYLQN NLETADQVLKRFL*MRERVLGPDHPDC AQALWNGAGSYAMKKNQYDKPEDLYK RALDIGRRALAPDHPFLAYTVKHLAILY KKMGKLDKAVPLYELAVEIRQKSFGPK HPSVATALVNLAVLYSQMKKHVEALPL YERALKIYEDSLGRMHPRVGETLKNLAV LSYEGGDFEKAELYKRAEIKEAETSL LGGKAPSRHSSSGDTFSLKNQLHFS |
| 4580 | 12631 | A | 5483 | 2 | 331 | PGQHGETLPLKIQKLAGQGGTSL*SEPL RRLRQENCLNLGGRGCSETRSCHCTLV WVTGRDSISKQKTAVDQAEERVSELEDR LFENTQSEKTEKRIKISTLRGFRK |
| 4581 | 12632 | A | 5484 | 26 | 117 | AKGQVALGRPGARMQGGSKVVGVLAG PGSRSEAGTVPSYPAAQTRPHPPQPLIF RSPGVVPNGHQPPNSTASSKQCNLRC WGLPTVARHPKSGQRPO/PRPTR*PGPSP QGPTPGRKNPERP*LVQQ*PCWAREPV |
| 4582 | 12633 | A | 5485 | 111 | 270 | |
| 4583 | 12634 | A | 5486 | 240 | 406 | |
| 4584 | 12635 | A | 5487 | 128 | 657 | ESESYWAICSRKRSPVLSSYGHHIYLKIR CPVDSISVGRRGFLTIFEDVSGFGAWHR RWCVLSGDCISYWAYPDDEKRKNPIGRI NLANCTSRQIEPANREFCARRNTFELITV RPQREDDRETLSQCRDTLCVTKNWLS ADTKEERDLWMQKLNQVLVDIRLWQPD ACYEPIGKP |

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| 4585 | 12636 | A | 5488 | 1076 | 3513 | IKALSSSAEDASLVNASISSSVKATSPVKST TTSITDAKSCEGQNPPELLPKTPISPLKTGV SKPIVKSTLSQTVPSKGELSREICLQSQSK DKSTTPGGTGIKPFLERFGERCQEHSKES PARSTPHRTPIITPNTKAIQERLFKQDTSS STTHLAQQLKQERQKELACLRGRFDKG NIWSAEKGGNSKSKQLETKQETHCQSTP LKKHQGVSKTQSLPVTEKVTENQIPAKN SSTEPKEVIREIEMSVDDDDINSSKVINDL FSDVLEEGELDMESQ/AGDGSSISR/TA AKNRKMH*ISPQCLYLHHWHKQLV*V* CPHLDWN*KTPAEVMKVQNQENSKELV S/RAESGDSLSEDRDLLYRSQRFKETE RPSIKQVIVRKEDVTSKLDEKNNAFPCQ VNIKQKMQELNNEINMQQTVIYQASQAL NCCVDEEHGKGSLEEAEERLLLIATGK RTLLIDELNKLKNEGPRKN*G*S/APSEF IAIPKDQFTLSEIRLP*KADFVCSTVQKPD AANYYYLILKSRSENMMVATPLASTSNS LNGDALFTTTFTLQDVSNDFEINIEVYS LVQKKDPSGLDKKKKTSKSKSNHSSV MASPGGLSAVRTSNFALVGSYTLSSSV GNTKFVLDKVPFLSSLEGHIYKIKCQVN SSVEERGFLGCPGGRLQPKRQTIFEDVS GFGAWHRRWCVLSGNCISYWTYPDDEK RKNPIGRINLANCTSRQIEPANREFCARR NTFELITVRPQREDDRETIVTNAGTHSV FTKNWLSADTKEERDLWMQKLNQVLC DIRLWQPDACYKPIGKP |
| 4586 | 12637 | C | 5489 | 135 | 206 | MFIFAFGKSIFKITTTFQSTIVG* |
| 4587 | 12638 | A | 549 | 20 | 403 | KVQGPASAHASGEGSLTIIPVTRSPLAT MNHIVQTFSPVNSGQPPNYEMLKEEQEG AMLGAPHNPAPPMSTVIHIRETSVPDH VVWSLFTLFMNTGCLGLITFVYSVKA RDRKMGRRTTRPGAQG |
| 4588 | 12639 | A | 5490 | 67 | 388 | DAVFA/GAMPTMASVKLSTLHPVNHPH YEDADLRPGCSMLEIWDVEDPSNAANPP LRSILLEADARPKMPVFQNSVYRVLKVN* EGNYPLHYGTMPCKNNHPLAYLH |
| 4589 | 12640 | A | 5491 | 3 | 107 | SIKSLTHPIVNHQHYEDADLRARTKIV YSTYSRTSAKEVRDKLELHVNYVLEE AWCVVRTKFILQDGPVLAQAEK*COM VTQIYKKYSNALEMPGCSMLEIWDVED PSNAANPPLCSVLEADARPYFTTVFQNS VYKVLKVN*EDADLRARTKIVYSTYSR |
| 4590 | 12641 | A | 5492 | 3 | 289 | YYLSPPEMGAIFEDPAHVVVYIIFMLGS CAFFSKTWIEVSGSSAKDVAKLKEQQ MVMRGRDTSMTVHELNRPKVKLRRWK GEGRHFTKRILFY |
| 4591 | 12642 | A | 5493 | 2 | 652 | RVDLPIKSARYRGQYSSYPKLFYTSNPII LQSALVSNLYVISQMLSVRFSGNFLVNL LGQWADVSGGGPARSYVGGLCYYLSP PEMGAIFEDPVHVVVYIIFMFGSCAFFS KTWIEVSGSSAKDVS*TA*KEQQMVMR GHRDTSMTFELNRYIPTAAAFGGLCIGA LSVLADFLGAIGSGTGILLAVTHIYQYFEI FVKEQAEVGGMGALFF |
| 4592 | 12643 | A | 5494 | 58 | 596 | KFIFRDGGSLCCPSWT*TLGLQSSHMSL PSDWDSRVRATKPNFPSS*HSFSALYM HLPRSPLNFIQPCRFYKGPAGLSRGRE* HGL*SDFSVANLWQLGFLWQALTDYRA ELPGMDPIISTHLAKLYDNLEQNLIRVIE PFSRVQVRTLWGLHFWPGILTVATSLPH LSRMGTHF |

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| 4593 | 12644 | A | 5495 | 2 | 951 | PRVPRVRPRVRSSRPRSRDPSRRARLR WQLRWKPRWCPRPKTPGVWKRPRTRP RSSAGGSTGFPSSPILRRSPSTRRRSSRKA SPTATRATGTPPRQAQRKTARAAGRRA SPGIATAGTRSMISMRPGRKPSNPSWEG RTNEETSSLSRLKPVSPGTITCPLRTPGSL LKDSKIPISIKHLTNLPSSHPVVHQPSRS EMPRTKIPVSKVLVRRVSNRGLAGTTIR ATACHDSAQKVVRSSRPRWMGPMRNT TFPWETTKVSFAFPKESLL/WTPVPRPA PERGPRRSLCPE*GPDNTRKRDATRGFLL SR |
| 4594 | 12645 | A | 5496 | 1 | 279 | VQWHDLG*PQPPPGFKRFSCLTPP/RSS CDHRCPPPTD*FLCFLVETGFHYVGQA GLELLTSGDPPTLASQSAGIAGVSHHARP NFLIFFFN |
| 4595 | 12646 | A | 5497 | 2 | 291 | FLVARVAGSGDGLTLFPRLECTSVITAP ASISWAQGDLPASASQVAQTAGACHHS WPVFTSCVEMGFPCVP*AGLELLGSSPPA PQPPKMFRLQA |
| 4596 | 12647 | A | 5498 | 2 | 345 | SHSVAQIGVQWRDLGSLQSPPGFKRFS CLSLPSS*DYRHAPVHPANFFLVEMWL PRVSQDGLDLLTSIDLSSASQSTGITGM SHRARPNFCIFSRDRVSPCWVWSQTPD LR |
| 4597 | 12648 | A | 5499 | 2 | 311 | QVLENPHFPRG*APPPSW*YPSGFYKSNR PRACFNPRSLAPRGPHQGFFPPGPLAFP PPFLGPPYGSRRFPSEHFQKVQPLNQPPF LSLKNPP*RFFFFF |
| 4598 | 12649 | A | 55 | 730 | 950 | SFLKDIGLFKIIYFFFFFETGVSFCHPRLE CSGETMAHC\SLTSLGPDPTSAS*QAG ITGVHHHARLIFF |
| 4599 | 12650 | A | 550 | 2 | 431 | DAWAMNHTVQTFSPVNSGQPPNYEM LKEEHRVGCAGAAPTTLFPPTSTLIHNRQ RDLPCPTHVWSLFTLFMNPCCLGFO *EFAYSVKSMRDMVGDVTGAQAYAS TAKCLNIWALILGILMTILLIVPVLIFQA YG |
| 4600 | 12651 | A | 5500 | 1 | 2500 | MEDAWGIRKETGRVKEEAKEVTGWGN NWRNVEKSSMSRKVKAARPFGFKLPM SDIPPKCTIKDLLPKEKSSTEAVFHTVVL ERHESPDIEDFSFKEPQKNVHDFECWR DDTGNYKGVLMAQKEGKRDQRDRDIE NKLMMNNQLGVSFHSHLPELQLFQEGEK MYECNQVEKSTNNGSSVSPLOQIPSSVQ THRSKKYHELNHFSLTQRRKANSCGKP YKCNCEGKAFTQNSNLTSRRHSGEKP YKCNCEGKTFTVRSNLTIHQVIHTGEKPY KCNCEGKVFRHNSYLATHRRHTGEKPY KCNCEGKAFRGHSNLTHQLHTGEKPF KCNCEGKLFTQNSHLISHWRIHTGEKPY KCNCEGKAFSVRSSLAIHQTIHTGEKPYK CNCEGKVFRYNSYLGRHRRVHTGEKPY KCNCEGKAFSMHSNLATHQVIHTGTGKPF KCNES\QVFTQNSQLANHRRHTGEKP YKCNCEGKAFSVRSSLTTHQAIHSGEKP YKCNCEGKSFTQKSHLRSHRGIHSGEKPY KCNCEGKVFAQTSQARHWRVHTGEKP YKCNDCGRAFSRSSLTFHQAIHTGEKP YKCNCEGKVFRHNSYLATHRRHTGEKP YKCNCEGKAFSMHSNLTHKVIHTGEKP YKCNQCGKVFIQNSHLANHQRHTGEK PYRCNCEGKAFSVRSSLTTHQAIHTGKK PYRCNCEGKVFTQNAHLANHRRHTGD KPYRCTECGKAFRRQGVTPGPSLENGT ILAYSSLKFVGSSDTHISLLRSQDDRQVL PHLANPNFREGLLPAFLLLCSDSHFLQFC SQFAPRKTQSGSGSVNNIQANIIAK |

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| 4601 | 12652 | A | 5501 | 1 | 2508 | MPHQLGPNLVPDIPPKCTIKDLLPKEKSS TEAVFHTVVLERHESPDIEDFSFKEPQKN VHDFECQWRDDTGNYKGVLMQAQKEGK RDQRDRDIENKLMNNQLGVSFHSHPLE LQLFQGEKMYECNQVEKSTNNGSSVS PLQQIPSSVQTHRSKKYHELNHFSLLTQR RKANSCGKPYKCNECGKAFTQNSNLTS HRRHSGEKPYKCSECGKTFTVRSNLTH QVIHTGEKPYKCHECGKVFRHNSYLATH RRIHTGEKPYKCNECGKAFRGHSNLTTTH QLIHTGEKPFKCNECGKLTQNSHLISHW RIHTGEKPYKCNECGKAFSVRSSLAIHQ IHTGEKPYKCNECGKVFRYNSYLGRHRR VHTGEKPYKCNECGKAFSMHSNLATHQ VIHTGTKPFKCNECSKVFTQNSQLANHR RIHTGEKPYKCNECGKAFSVRSSLTTHQ AIHSGEKPYKCIECGKSFTQKSHLRSHRG IHSGEKPYKCNECGKVFAQTSQARHW RVHTGEKPYKCNDCGRAFSRSSLTFHQ AIHTGEKPYKCHECGKVFRHNSYLATHR RIHTGEKPYKCNECGKAFSMHSNLTTTHK VIHTGEKPYKCNCQCGKVFTQNSHLANH QRTHTGEKPYRCNECGKAFSVRSSLTTH QAIHTGKPYKCNECGKVFTQNAHLAN HRRHHTGEKPYRCIECGKAFRVRSSLTT HMAIHTGEKRYKCNECGKVFRQSSNLA SHHRMHTGEKPYKECGEVIRYNSLLSH QLIHS*QNPYKSDSGQSLMS*SINRYER P*ARD/YHVNICGRGSIQASQVTRHQDFI SLMKRNKCNMHPEAITQ*PMVSEDS |
| 4602 | 12653 | A | 5502 | 3 | 361 | PKKNYFPLHLKGPKTKGVFFYSSSSSSQK GVSLCNPRWNAVGPFPGFSTPPSLVK*F LCPNPWS*CDFRPPSPRPGYFCFFKNKA LLARVVFNS*PQVIPLFQPPKMVGFOGLT PLAG |
| 4603 | 12654 | A | 5503 | 32 | 392 | FLFLSFPLSFKMTLNDAMRNKARLSITG STGENRRVMTPEFPKAVHAVPFT*SPGH GNGMSSVTESLGGLIRTLALSALPQWFSC VFIVQSGERHPSILEDFSFQPKNSLNMWS SILKL |
| 4604 | 12655 | B | 5504 | 473 | 524 | MGEAKKTGEQVRVLPRTX* |
| 4605 | 12656 | A | 5505 | 1 | 627 | LVSSFFFFFFCRDRVSPCCLGWSPTWSPG LKRSARLGLPQCWDSRRELPRPAYLLFL LSWGSPSPSAWQEGG/WCKKKRGTEHPE VPSIPSTCPSPTVQQ*S/GEKQVQETGRQ S/LGEAKKTGVQWHDQGSQLP*SGLK*S SYLSFLSS*DHRCAPTTD*FL*R*DPTML PRLVLNSWAQ/CDHPALASQSTGIIGLSH RAWACDQNSHFF |
| 4606 | 12657 | A | 5506 | 3 | 649 | RVSSVMSTSLEEIFNCIFDAHVPLWGKA YPSQKPLAAWTRDLAMRVEQFELWASR ARPPVIFWLSGFTFTGFLTAVLQSSARQ NNVSDLSLWEIFVSTVE*QAT*VYPPKD GCWVRGLYLEGAGW/DPEELLGGRQS PCKLVWLMPTIHFRAESRKKSPKGMYS CPLYYYPNAGSSDRASFVIGIDLRSGA MTPDHWIKRGTALLMSLDS |
| 4607 | 12658 | B | 5507 | 167 | 377 | XKLIQFGLMKNLIRRLQKYPVRVTREEQ SHPARLYTGCHSYDEICCKTGMSYHELD ERLENDPNIICWK* |

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| 4608 | 12659 | A | 5508 | 2 | 1247 | TPLREERGATGLGPVIAMGSGCRICIFFS EFHPTLGPKITQVPEDFISRELFDTVQV YIITKPELQNKLIIT/VLESSFVSMEESKQK LVPIMTILLEELNASGRCTLPIDESNTIHL KVIEQRDPDPVAQEYDVPVFTKDKEDFF NSQWDLTTQQLPYIDGFRHIQKISAEAD VELNLVRIAQNLLYYGVVTLVSILQYSN VYCPTPKVQDLVDDKSLQEACLSYVTK QGHKRASLRDVFQLYCSLSPGTTVRDLI GRHPQQLQHVDERSEENLLGHLGVT*GK LDPLCLSGALDHGALPIQAGFLEMMGYR DKIEGRLOERVGLPERRPGQGVTPSSDP HPRKLIQFGLMKNLIRRLQKYPVRVTRE EQSHPARLYTGCHSYDEICCKTGMSYHE LDERLENDPNIICWK |
| 4609 | 12660 | A | 5509 | 1 | 512 | CTLPIDESNTIH*KVIEQRQTPRVAQEYD VLVFTKDKEDFFNSQWDLTTQQLPYID GFRHIRKISAEADVELNLVRIAQNLLYY GVVTLVSILQYSNVYCPTPKVQDLVDDK SLQEACLSYVTKQGHKRASLRDVFQYD EICCKTGMSYHELDERLENDPNIICWK |
| 4610 | 12661 | A | 551 | 137 | 838 | SSGICALIWPWPALHLTNARKRKLRLK RNYWRKGESLRTIPVTRSLVTMNHIV QTFSPVNSGQAPNYEMLKEEQEVAML GAPQKPCLECPPVIHURSETSVDPHVIV WSLFNTLAFMNTC/CRLGFIAFAYSSEVS GTRKMVGEVTRAQGLLPPPKCLNIWA LILGWFMNQFLINHPPPSVGSSRPSDRSG RHHLRPRELCPVEPVSVQKNSIFHSLALP PEARKEFCP |
| 4611 | 12662 | A | 5510 | 1 | 474 | HTIHLKVIEQRDPDPVAQEYDVPVFTKD KEDFFNSQWDLTTQQLPYIDGFRHIEKIS AEADVELNLVRIAQNLLYYGVVTLVSIL RKLIQFGLMKNLIRRLQKYPVRVTREEQ SHPARLYTGCHSYDEMCKTGMSYHE LDERLENDPNIICWK |
| 4612 | 12663 | A | 5511 | 199 | 562 | KESPGPGRHPVPLIPHP*ES*IPVRAL*KN LIQATYRKYPVRVTREEAHPARLYTG CHSYDEICLQDRWRQAGSQGGFRAGCA RPRPLTSPPPHPGMSYHELDERLENDP NIICWK |
| 4613 | 12664 | A | 5512 | 1 | 1224 | EFGTRPLREERGATGLGPVIAMGSGCRIC CIEFSEFHTLGPKITQVPEDFISRELFDT VQVYIITKPELQNKLIITVAMEKKLIGCP VCIEHKKYSRNALLFNLGFVCDAAKTC ALEPIVKKLAGYLTLELESSFVSMEESK QKLVPMITILLEELNASGRCTLPIDESNTI HLKVIEQRDPDPVAQEYDVPVFTKDKED FFNSQWDLTTQQLPYIDGFRHIQKISAE ADVELNWRVRIAQNLLYYGVVTLVSILQ YSNVYCPTPKVQDLVDDKSLQEACLS YVPKQGHKRASLRDVFQLYCSLSPGTT VRDLIGRPPSSCQHVDEKRLAQGLM KNLIRRLQKYPVRVTREEAHPARLY TGCHSYDEICCKTGMSYHELDERLEND PNIICWK |
| 4614 | 12665 | A | 5513 | 2 | 313 | FETESYSVAQAGVQWWDLGLSQPPPGF KRFSCSLSSWDYRPPPRLANF*FLVE TGFHHVQAGLDLLT/S/GDPLASASQSA GITGLSHCAWQTTYITFNHK |
| 4615 | 12666 | A | 5514 | 731 | 1156 | SVLGLISDTSNTFLSFFFFFEMESHSLAQA PLQWHYLGSLQAPPPCKLRLPGSRHSPA SASRVAGTTGARHHARLAFGFLVEAGC HRVSQDSLDDLTS*STCLKP/AQSAGITRR EPPTPLGFFFLKMESCSVGPRLGVQSW |
| 4616 | 12667 | A | 5515 | 3 | 365 | LLNSRPVDDFFFFFLLSHSL/DSVVQAGV QWHNLGSRLLQSPPPGSMPPFCSLLSS WDYRHPPPYLANFFFFCIFSRD/MGFTML ARMVSIS*PCDLPALGSQAGITGVSHHA |

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| | | | | | | WPAYFYFQ |
| 4617 | 12668 | A | 5516 | 400 | 619 | MPEQICPLETSQS*INNLPKKFFMSI*CP GFERSYFFF*CC |
| 4618 | 12669 | A | 5517 | 274 | 693 | KYQILLYNGDVMACNFMGDEWVFD LNQ/KGKVEIPGPIEPAGEEWGAGMPG SGQLAAWLWAHRGQVWRNSQP*GLAG SCEQGCSCRLMSFLVGQMEVQRRPW VKYGDSGEQIAGFVKEFSHIAFLTIKVG TGAER |
| 4619 | 12670 | A | 5518 | 3 | 766 | NRLWSSLQTHCCSQNKCNFYDNKDLEC VTNLQEVARI/VGNSGLNIYNLYAPCAG GVPSHFRYEKDTVVVQDLGNIFTRLPLK RMWHQALLRSGDKVRMDPPCTNTTAAS TYALTNPYVRKALNIPEQLPQWDMCNFL VNLQYRVFLPSQNSRYLKLSSQKYQIL LYNGDVMACNFMGDEWVFDLSLNQK MEVQRRPWVKYGDSGEQIAGFVKEF SHIAFLTIKAGHWMVPTDKPLAAFTMFS RFLNKQPY |
| 4620 | 12671 | A | 5519 | 2 | 279 | FLRDVILL/C/HPGQSVVV*S*LTVSPT ELPGSSDPSSAFNCWEYRCVTPCQLMF*FT LLSIGIGSTLPRPVLNSSPQVILAPWP PKVRLQE |
| 4621 | 12672 | A | 552 | 1 | 528 | |
| 4622 | 12673 | A | 5520 | 2 | 1045 | CPSRPCRRRPPPPRGPKPRASYGGPAP/ GDKKKRPPQ/GPRGSSPAPGPPPPQEA A GPARPRPGQDAAAGPSGRVPPQALPSV R GPQPRAPRPGRQAPATAQRGPPMRPRR GRGPPPRAPP/PGAGPC/PLRRCALLP ESH PRGRPGHPEASSGEAAAGAAPQALPL TL GRTQAPTRPVSPG*GRGPAEGRPRQR/ PP THPPPPA/GPPRASARRPAAARRPAGSP A QPAARGPAADAQGVAAQRAAQVRRRG VRGGARGGGRGP/RGPRGRP/PGSSGR QR PLSGPSPAQAGPRGAQPDSPDGHGPP PAL ASRQPGPFSFTPVVSTPDACLPHSGL LL ASPSIHAVRGELSN |
| 4623 | 12674 | A | 5521 | 84 | 202 | |
| 4624 | 12675 | A | 5522 | 3 | 576 | ILGFPFFVRWGSHTVAQAGVQWCDHGS LQPRSPGVK*SSHLSLLGSWNHRHAT TT PG*FCFFSRIRSHCVAQAGL*LLTSN HPP ALASQTVGITGVSHWTPNTGFSVLTA TNKNLKFFHYAISKCLVRAKLSSRL LKIE ERNKALSAPVVSVSIFDRVLRLLGYS AS DWQPEFVETA VSNFVIYGIFRGQ |
| 4625 | 12676 | A | 5523 | 177 | 904 | ESHLQNDTAAHPLLNGTECGVSPPLTS RQGVVRRRTQSSTSRCT/SPVIPKQTF PQP VLHMSAGVALDSPAAPPWPQPPQGF AHT*DRKEEGDPIGIWAPEGKSC TPKPP PSLPRTSPGWKRALQKGDTCGPSTAS TPHPLILGPSQAPPKPKPP/PSGVP ACAP S/YPALPAPSLTEKEQARAPGGQD GAG HTVGGGGAAGRREGQNKTFSGFFFS FF FLPFTLWVVLFLSFL |
| 4626 | 12677 | A | 5524 | 1 | 173 | FLGPSKFPPPGFPPFPFPPPRERGN QRSS PPSSSS/P/PSQKKTGVPPG*PGG FPPPP |
| 4627 | 12678 | A | 5525 | 1 | 390 | LILNTRPAFIFDLLHNLDPKEQAYAD LV SAYTLNSMFWLYLATQGVNPTDHPV KH ELDTT/RACMNRSSSPTDKKAGLLY RG AASKFVKNALWEPKSKNA*KVGNK GKS PTSLFGFDVHIFKKNMLPPP |

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| 4628 | 12679 | A | 5526 | 1 | 1548 | MPERDSEPFNSNPLAPDGHVDVDDPHSFHQ SKLTNEDFRKLLMTPRAAPTSAPPSKSR HHEMPREYNEDPAARRRKKKSYAK LRQQEIERERELAKEYRGRAKERRDGVN KDYEETELINTTANYRAVGPTTKADKSA AEKRRQLIQESKFLGGDMEHTHLVKGLD FALLQKVRAEIASKEKEEEEELMEKPQKE TKKDEDPENKIEFKTRLGRNVYRVLFGN/ KAYKRNELFLPGRMAYVKVDCPTMEA QTILTTNDIVISKLTQLLSYLRQGTRNKK LKKKDKGKLEEKPAEADRSIFEDIGDY TPSTIKTPWDKERERYRERERDQ/RDRDR DRERERERDQERERDRERERDRER/GPG SAKELIKSINEKFAGSAGWEGTESLKIAE DKKQLRDFFGMSNSYAECYPATMDDM AVDSDEEVDYSKMDQGNKKRTLRSWD FDTQEDYSEYMNNKEALPKAAFQYGIK MSEGRKTRRFKETNDKAALDCQWKISAI IEKRKKMEADGVEVKRPKY |
| 4629 | 12680 | A | 5527 | 1 | 3162 | |
| 4630 | 12681 | A | 5528 | 2433 | 2540 | |
| 4631 | 12682 | A | 5529 | 1 | 1739 | MPERDSEPFNSNPLAPDGHVDVDDPHSFHQ SKLTNEDFRKLLMTPRAAPTSAPPSKSR HHEMPREYNEDPAARRRKKKSYAK LRQQEIERERELAKEYRGRAKERRDGVN KDYEETELINTTANYRAVGPTTKADKSA AEKRRQLIQESKFLGGDMEHTHLVKGLD FALLQKVRAEIASKEKEEEEELMEKPQKE TKKDEDPENKIEFKTRLGRNVYRVLFGN/ KAYKRNELFLPGRMAYVKVDCPTMEA QTILTTNDIVISKLTQLLSYLRQGTRNKK LKKKDKGKLEEKPAEADMKYVS*PLA SDQREGVCTFLVSGILGRC*HENLEKWS GGVKVYV*IWPASDLHFPSIFEDIGDYVP STTKTPRDKERERYRERERDRERDRDR RERERERDR*HERERDREREEKKRHSY FEKPKVILLGPWTFDKGPGSTKELIK/SFI EKFAGSAGWEATESLKKPEDKKQLGD FLGMSNSYSECYPATMDDMAVD\SDEE VDYSKMDQGNQEGGP*ARWDL*FPQE EYKRVFVTTKEALPRVAFQYGIKMSÆ GRKTTRRFKEPQ*PKQSLIRQWKKI |
| 4632 | 12683 | A | 553 | 1 | 1682 | MDNLSDTLKKLKITAVDKTEDSLEGCLD CLLQALAQNNNTETSEKIQASGILQLFASL LTPQSSCKAKVANIIAEVAKNEFMRIPCV DAGLISPLVQLLNSKDQEVLLQTGRALG NICYDSHSLQAQLNMGVIPTLVKLLGIH CQNAALTEMCLVAFGNLAELESSKEQFA STNIAEELVKLFKKQIEHDKREMIFEVLA PLAENDAIKLQLVEAGLVECLEIVQOK VDSÆKEGGITELKTGSDLMVVLLLGDES MQKLFEGGKGSVFQRVLSWIPSNHQL QLAGALAIANFARNDANCINHMVDNGIV EKLMDLLGRHVEDGNVTVQHAALSALR NLAIPVINKAKMLSAGVTEAVLKFLKSE MPPVQFKLLGTLRMLIDAQAEAAEPIGE RMLKLVÆRLVGVWCEAKDHAGVMGÆEQ NRLLSALIRHHSKSDVIKTIVQSGGIKHL VTMATSEHVIMQNEALVALALIAALELG TAEKDLES AKLVQILHRLADERSAPEIK YNSMVLICALMGSECLHKEVQDLAFLD VVSKLRSHENKSVRQQASLTEQRLTVES |
| 4633 | 12684 | A | 5530 | 93 | 546 | YNCRPTLGVSGCAGLDAQVVCQDCAFE LGKKP/PSGGEQYPSSSAIKQGPKEPYAD FIARLQESLKKVIADLAAQDIVLWLLAFD NANPECQAALRPIRGKAHLVDYTKVCD GIRDKLHKATLLAQAMAGLRMGKGNTPT FPGACFNCGKHGH |
| 4634 | 12685 | A | 5531 | 1 | 541 | |

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| 4635 | 12686 | A | 5532 | 365 | 661 | |
| 4636 | 12687 | A | 5533 | 3 | 74 | RMGPRTGP*VFPETGFPPLSNLE |
| 4637 | 12688 | A | 5534 | 83 | 262 | CTVTPPPQDTGQSKS*STRVSSSLVPRSPT VAPVTLRPGFEPP*WTPLAKTSSVLTQW C |
| 4638 | 12689 | A | 5535 | 636 | 698 | |
| 4639 | 12690 | A | 5536 | 125 | 340 | |
| 4640 | 12691 | A | 5537 | 81 | 1007 | QPKAEHAALNLRKTFQHASHTPPFSAQQ *NPHRPHQPWL*HALVQHCSCSDMQRPS ASGP*/PPGTFSRWSSCKMPVPPPAQVPK SLCGVLSSSC*PGRRSPPGAEPSPRACRP CRQDSG/PAQAGGPCRQDSG/PDPAGGPR DKI*ASQPLPAGERAIAPAGGPCRQDRGQ PRLASSAGGHCRQLRG/PTPAGGPCRL/P QRAAPAGGPCRQDSEQLRLAGPAGRLA GRHGRRSPGPAEPSPRACRQESG/PAQAG GPCRQHSG/PDPAGGPRGQSLPAGPAR RRAGNPGRQPLQTGQRAAEAGEPAFAT AVSGRD |
| 4641 | 12692 | A | 5538 | 1 | 766 | |
| 4642 | 12693 | A | 5539 | 74 | 1178 | |
| 4643 | 12694 | A | 554 | 3 | 910 | GRPPRVPPWLRERRRLEGGHRAAPPAPY DLRLAPPVPHPRGATWQIILSDTLKLLKI TAVDKTEDSLEGCLDCLLQALAQNNNT ANKCKKSKQVAILQLFASLLTPQSSCKA KVANIAEVAKNEFMRIPCVDAGLISPL VQLLNSKDQKVLLQTGRALGNICYDSHE GRSAVDQEGGAQIVIDHLRSLCSITDPAI NEKLLTVFCGMLMNYSNENDSLQAOLI NMGVIPTLVKLLGMHQCNAALTEMCL VAFGNLAELDAIKLQLV EAGLVECLLEI VQKQVDSKEDDITELKTGSDLMV |
| 4644 | 12695 | A | 5540 | 1 | 857 | MGQVWGLVHFTLELFQTDDEEEQEYNK VTEEVTEHVYLP*PDVHLNQPSHQPPK AGLQLY |
| 4645 | 12696 | A | 5541 | 518 | 578 | |
| 4646 | 12697 | A | 5542 | 750 | 797 | |
| 4647 | 12698 | A | 5543 | 2073 | 2844 | IVRSLSRQAQKIRSGCPCQSW*RRGRPVG SPSQSTEGPGQVRLRT*PLPFHHPGEGP GAGRRSRSSLERPTSQPHRSQSGRCPAAP ATPLPSPGPQA\PLGAPFERG/PRSRSA/QG APGTGVRRFFSMAQFPFPCSTSQPLKPCSP QELKMRLRPKGAPDSSAPGRTAGTPPCL RCWAGSVEPLRRVRGPRRCGRGPAAAA TQWARPLCRARRGTLGGIA*PRSVAAARG SAPAPAAPGAARPGPMGPPAAVAIAAG RP |
| 4648 | 12699 | A | 5544 | 3 | 611 | SLPPRASRLPPGPSFSGWSPGDNRKLPNT PPPPRAGPRPPSRAPPA*TPGPSSAGSWP* PPGTGSAPRGPAAPSAPGARRPGRPGCPA PAGRPRVPTAGAGACSAASRPGTRPRCT RPGAPRSRRRGCGPGGA*PGARRPPRP RPPATRAPRSRSPRGAAPPPTPTRTARGA AARELRVQRGP/APLHAPQQHTPAIIVP YKM |
| 4649 | 12700 | A | 5545 | 3 | 42 | |
| 4650 | 12701 | A | 5546 | 1 | 160 | SMQQTLLSYF*KLP*PPQPSATMTQISQ QPSTSRQDPPPTK/RL*LVEGSNNH |
| 4651 | 12702 | A | 5547 | 298 | 421 | LHPHILPIDKLLHQ*KVVSVSSEYRQNEV PLYSISSNLVHS |
| 4652 | 12703 | C | 5548 | 598 | 762 | MNSMIQICQDRAEIHSSYCNLKIHQRLQN LLISFLQSLKLLKNVNLFSINKNLK* |
| 4653 | 12704 | C | 5549 | 138 | 296 | MNLEVTVARDYLSPLADLAQRRGNIQ EIQTRQDNKVVGIFVPLAEIMVGTI* |

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| 4654 | 12705 | A | 555 | 1062 | 1421 | DRVSLCC/PRLECSGMISAHCNLPSPGFK QFSCLSLPNGWAYRSVPPCANFCVF/SV ETGFHHVQGAGLELLTSGDLPALASEKC WDYRREHTARGPVTKPSYFQVLFRLHP IFINHLNT |
| 4655 | 12706 | A | 5550 | 2 | 1575 | AMLGTRVERCLRVLGDGAVAEFDASAGV EAQTLTVWRQADKHNPICFLNKMMDKT GAINFKYAVESIREKLKAKPLLLQLPIGE AKTFKGVVDVVMKEKLLWELQFK*WE KTLRRKAPLGK*MIPEFAGRETT*RKEC L*LEQVADLDDEFADLVLEEFCEFNFDLLP AEKLQTAIHRVTLAQTAVPVLCSALKN KGIQPLLDVMTMYLPSPEERNYEFLOWY KDDLALAFKVLHDKQRGPLVFMRIYS GTIKPQLAIHNINGNCTDRTQIALSVNNH EVHIYKKNRQCCKAHELKEHNGHITDI DWAPKHDHIVTCGADHNAYVWSQKDG VWKPTLMILRINRTATFVKWSALENKFA VGSEARLISVCYFESENDWWVSKHIKKL IRSTVLSLDWHPNNVLLAAGSCDFKHRV FSSYIKEVDEKLASMPWDSKMLFGQLM SESGGGGTGGWVHGLDIPKQSIQRNMSA MECFCNTDKRATTEGNSMALKMLRQNS ITQVSIYEVDEKDCRKYCTTGIDGEP |
| 4656 | 12707 | A | 5551 | 1137 | 1288 | RTLNLKAMASRVLRIILTR*CLDVSIKI PL*ENLGESIMVDSLMLVKVP |
| 4657 | 12708 | A | 5552 | 1 | 1851 | MALKKADKQVLEPLMNLEVTVARDYLS PVLADLAQRRGNIQEIQTRQDNKVIGF VPLAEIMVADLDDEFADLVLEEFSENF LLPAEKLQTAIHKSDTKLRQQLPVLCS ALKNKGIQPLLDVMTMYLPSPEE/L*PM EFLQWYKDDLALAFKVLHDKQRGPTG FYAPFNSRPL*KPQLAHSIILMETATERIS RLLLPFADQHVEIPSLTAGNIALTVGLKH TATGDTIVSSKSSALQLVEPNGREKRS TDKTMKAERLLLAGSGRFQEPVFFCTIG TPITV*GSQIWEHAFEMSFSVRIPVLKVR LDPDSGQTVLCGMGELHIEIHDRIKREY GLETYLGPLQVAYRETIILNSVRATDTLD RTLGDKRHLVTVEVEARPIETSSVMPVIE FEYAESINEGLLKVSQEAIEGHSACLQ GPLLGSPIQDVGNLYIP*QIHPWAPSTT YDFCLCLKMPCKKALERKADKQVLEPL MNLEVTVARDYLSPLADLAQRRGNIQ EIQTRQDNKVIGFVPLAEIMGYSTVLRT LTSGSATFALELSTYQAHESRSKYTAQP EKWFDLNLVLFGRGNSGRHPRLLHFSV RNNFYCLYLLGRNKGTVSGTFRGT |
| 4658 | 12709 | A | 5553 | 2 | 499 | RCQKAKFTPVNRRHHCRKCGFVVCGPC SEKRFLPSQSSKPVRIKDFCYDLSAGD MATCQPARSDSYSQSLKSPNDMSDDD DDDDM/TVTKDTFGSI*SGEAL*EINFGG NARL*ALSLDCSVMNLPEKLGTYVPQYI P*KEGAPAFCHSSHSTGIGFCKYIR |
| 4659 | 12710 | A | 5554 | 147 | 315 | LIPQPWGQHLPLPPNISNYD*RPQKFLGL PHPCSFGGRALTPHWSTGLRLTPSAQ |
| 4660 | 12711 | B | 5555 | 105 | 508 | XPGTREVEELNALQEELAPFGLVILGFPC NQFGKQEPGENSEILPTLKYVRPGGGFV PNFQLFEKGDVNGEKEQKFYTLKNSCP PTSELLGTSDRLFWEQESSRHPLELWKF LVGQMDTHHALHHRPRQRR* |
| 4661 | 12712 | C | 5556 | 4 | 165 | MCLSGNVYHLCACSCVVPQCCTTSLQF STPMIIVHLHLNPKEKPALGPVILL* |
| 4662 | 12713 | A | 5557 | 1 | 1803 | |

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|------|-------|---|------|------|------|---|
| 4663 | 12714 | A | 5558 | 2013 | 2024 | KVAGSAGHLRRTVARDQAAAQRDPECA PTPSLARLLQASCLLSLLLAGFVSQSRGQ EKSKMDCHGGISGTIYEGALTIDGEEYI PFKQYAGKYVLFVNVAISY*GLTGHVH LN*TALQEELAPFGLVILGFPCNQFGK QEPGENFRRSFPNPSRYGPTKVGGFCSL NFPALLRKGDVNGEKEQKFYTLKNSCP PTSEALLGTSDRLFWEPMKVHDIRWNFE KFLVGPDGIPIMRWHRRTTVSNVKMDIL SYMRRQAALGG*RVGCPFFSKILYFPSR VYSLGGGWSILFPPQNKGSFPKFPSPRFL GPP |
| 4664 | 12715 | C | 5559 | 2 | 226 | MLLPLPSPSPSTALPGLGEMGRPPPPY MLSVAPQTFCFISHSSPSHRVSFSAPCS VLPPPSQKFLHRTSF* |
| 4665 | 12716 | A | 556 | 213 | 513 | GGKSLARRVPKGRMDGLLNPRESSKFIA ENSRDVFIDSGGARRVAELLLAKAAGPE LRVEGWKALHELNPRADAAVNWVF VTDTLNFSFWSEQDEHKW |
| 4666 | 12717 | A | 5560 | 2 | 1308 | ALSLLALPPASPP/AGRGRFAGPGPAPLP WHQGLPLTRPGPEG/PLPQGRPLSPPLQP TPAQPLLLPAFPLLPAPGPRRVGFACWC P*SPGLSPPGLPSPDFQTLPCGISFLPEMR KLESWSPAGEPSPPPAPPATRVSSRMQLP DPLTLLPPAGPKATFNSYGV/PPPAPE/PS QGRVRGHPEPTGPLLHSSQGQEAAPLPP GPCCYGDТАF/PRTEGPPSLPPTTRARLSS PPPRFPADVVCVLSVSLVLCPTSLLVVPM */PHPCCTGSLSSWLPLLMLLPLPSPS PSTALPGLGEMGRPPPPYMLSVAPQTF CFISHSSPSHRVSFSAYPCSVLPPP*APA WAQDPILPARVSPPGRVPFPPC/PPPSHPT PGSEAPHS*PSVFLRWLKGATGPPAQPSA PPKPGNLGPHKPLWKLFCASHSFPSPFC TELPF |
| 4667 | 12718 | A | 5561 | 3 | 259 | FLFWVFQIPAPFPEYVTDLCICTPTSASP GYLLA\GRDKAQR\WERLRVVFQRALR DGA*AGEAGGSTPNTVTMEMQCPGNA S |
| 4668 | 12719 | A | 5562 | 2 | 329 | AGVQWRNLCSLQAPPPGPRSFRLSLPSS QVAGTYRRPPPPSPANFLYV**RRGFTTV NQDGLDLLTSGS\PASASQSAGISGVSHR AQPSFTFFRLACHVFVRHCHLPT |
| 4669 | 12720 | A | 5563 | 3634 | 4389 | LIQFLLHSIGLYSYTTICLIFILLMEYWL FPVFSYYYYYFFFLRRSLALSPGWSAVV QSRLTATSASQVQTILLQPPE*LGLQVC ATTPS*FLYF**RRDFTMLARMVLIS*PR DLPTLASQSAGITGVSHRAWSFLVLF *TESHSVAQAGVQWHDLSLQAPLRF K*FSCLSLPSSWDYRRPPLRPANFFVFLV ETGFCHVGQAGLELLTSSDLPALASQSV GITSVSHHTRPGMSFFITSHKL |
| 4670 | 12721 | A | 5564 | 1 | 369 | LQPQP\PGLNQSSLLSLLSSWDYRHMPPY PANF*YFPETRFCHVAQTGLELLSSSDPP YSASQSAGITGVTHRA*PRFTLCTGLIRG QHGEKGLAQGHNVRASSSIQGSVVTWG LRGLFFPHH |
| 4671 | 12722 | A | 5565 | 161 | 231 | |

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| 4672 | 12723 | A | 5566 | 1 | 1401 | MQIFDYNSEITDPGIQEEAAGLEGTRKP WNISMLLTTRNISLCQWFSKCGPEPDTST SWGTPQKEHCHLVNKVGVDLSLRMRGY MHGHIQPLNLFQESQLMPQTLFFHNFQN CFFEELHKWRCPDYYENNVRKMQLPFS SKLLGSTLTSEEKQERRQQQLRRLQELN ARRREEKLQLDQERLDRLLYVQELLEDE QMDQFHKALIELNMDSPPELQSYIQKLSI AVGAG*AENPPSGSQPR/EWDVV/TTASQ RPLTWEQLEPSLEDVESMNDFDPLFSEE/ D/TLEWRSRSP/RVQPVFNLAAYHQLFVG TERIRAPEIIFQPSLIGEEQAGIAETLQYL DRYPKDIQEMLVQNVFLTGGNTMYPG MKSARMKELVAG*DP SRLSFKVNLASNP CAGM/DWYGGLVNWALNHLDDNEVWI TRKEYEEKGGEYLKEHCASNIYVPRLP MSCLPLLRCPRHPSQGSAAAGGGGAG |
| 4673 | 12724 | A | 5567 | 2 | 131 | |
| 4674 | 12725 | C | 5568 | 170 | 394 | MKTNGYQGRVQWLTDLVLNLKSRPVQS SRPSLGNMVKPPSIQKLGKAWVACTCCP SYSGAGAGGWHEPRSLRLQ* |
| 4675 | 12726 | A | 5569 | 2 | 583 | DRKGLESSPEPPSDCRPPGMDLLAISVP LLAPSPQPVQSWPSG*CGRQAPCVLES GHSAGAGVSSWDGPPVPCKCPHPGLSQ AHPGKTFGPKNLHMVPSGGAQAPGPHK ANQQSWPSCPPVPRSRPTFSHIAENPME RKSFAQGSAGGNWQRKVSNPHPWELQV FESPSRPCVKNGRAAGLVTGGFREG |
| 4676 | 12727 | A | 557 | 584 | 827 | FLFYLFIFETGSHSVTRLECGDTMARC SLNFFGSSDPPASASWVAGTAGVLYHT WLSFAFFRRDGVSRVARAGLQLLAW |
| 4677 | 12728 | A | 5570 | 3 | 312 | FFLNROQLALLKLEYSGMIDHCKPQIS GAQVILPVASWVARPTGVYHHA*LIF KWGREVETESCYVAQAGLELLASSDPPT STSQRAWITGLSHCAWPA |
| 4678 | 12729 | A | 5571 | 1 | 121 | IFHVLKNCQTRSYLALMSFKNEGEIKMF SNIQKLKEFITDRSK/LQEMLKNAL*AERI YY |
| 4679 | 12730 | A | 5572 | 2 | 228 | FETGSHSIFWAGVQWYNHSSLQRLPGL R*FSLSLPSSWDHRCPTPRPCNFSIFSRD GFSSC*SGWSQTLGLK |
| 4680 | 12731 | A | 5573 | 1 | 1896 | MVSQGCRRSREMRDAHAGWDSPTALHM ARGLGRRVFSAPRHTEGGTDPGNSHLS NQKMEKLTEKCKQLRQGGLCVRVSDR TVRSVQETTATITLKGSLGTYCRGTRN LLTAEGFMPHASVCIQSKSGKVARNTVQ GFTAHGKAVLEAAVSAAGPAGTWGCLR IKWPRSVSWLLKPERAATLVGHGCRKS GCPPGLGGSAM/PPRHQSAAPAGRGR PCWGPEPTSGSLSNQQLPGVALHAPPLP SAPLLGPPLSRTVDTGPGGSGREVEATT CGRRLKDKDSEHAGAGSRHHQSQVTGS LGEERAVRAESPGEGPAEFLRRIQGAVQ TRAVTAGSSVEKINTKLETCDCADEEE VLGGDNVETEERSVCVPEPVKMTLFEKR VFADIIRCLARWAPAAATNRDLVNTLPG HGPPCSLVAFL/APPSRPYP*PAARCWW ASDFPERGKRLPAHSSFPVAPPVQ SQSGPLPCTPRHPLFPAPAFGICRGPR APGG/SKAVATQRPWWLYAPGTAPGGL PW*/AVPGHNKSIPPQVSNLTETPLNAP QSSWAALGSKRLGQGC SHGFFAFSFTAD VCTNDDTLNANSLTEVLATEIKHDINLA NEGLAWDRGWQDYQGDMLSL |

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| 4681 | 12732 | A | 5574 | 1 | 475 | FWKSPYSVQPRTEARAQGNKQKEFRET APGSSSKADTKSEHLWALLPSRRWGGG QTQHPPLAREPQFLACGPMKDIRLADWS TPLLSNPS*KLP*ICQSCPLEQEGKKA*D ARGVPSFPELQPPSGLTAQQGQTHRPHPD LRMTCGRTWHHFLAKTLH |
| 4682 | 12733 | A | 5575 | 2 | 468 | SRGILADPPRPGGQPDFLQP*PTRVAALS GLSNQDIDLGLMRRQPQVPAGPEAET AASRTALPCAVNPWTVLRATLPDLDCIQ TEACGMKPSAVSKFLVPRQYVPRLPFKV AVMAVVSTLRTVLSLTLTHSPPCRSL QPFVSFSIFWFGDK |
| 4683 | 12734 | B | 5576 | 90 | 1686 | XWWEPSFPQQRDSLKVTLQRAAFNP VAPTHSFKDQHPMPSPFCHLSGPVPSSRT TLATGRAAPHSSPLKSLVQGYAPWQTS MSCDYQPPRQEHKETSRRNSEKQLQAP AQRPTPKANTSGRSLQEDLLPEAQPL SVPVCHPCPLLHAARLAVSAAAAIRGLE VAEAAALVCAQKLLAACSSHSLLITVWSRG KVKETGLPSTVQAVSELLQVLLCKQKAG GCTPDQGPHTSKVLTEASSLPRISMCLL QPGPFSNIPGLTATLTPAATAATPGPLL PCTKHGNPLGHGLTCHYPLAPLPLPPAP HVRFAALSCLERSAGCCLCTPSCRITTVG GSVGCASELNHRACFSLPLMLGFQAPI ATHQWLFVSRNDKNTLDTPRSAGCDGA HRPRQEPAPDGPIVLLCLEMPAPGSYPG GAPVSGHRQVHPQWQVQHLGQSGGIR TGLGANCGKSHDSAYKKGGDVCFPGEM VPVVHQLKGVQHPNKCGRHWGTLVQQ KQPWTGSRGPTADQLHPKNSSLTLVFP R* |
| 4684 | 12735 | A | 5577 | 171 | 1631 | GLPQAGADSDPRTTRPFLLLGGLPLPSPR PYP*PAARCWWASDFPERGKRLRAHSS FPVPA/PPMRPRTVPVRAAPHPSPFTSV PSTGIRHLPAEGW*TGQ*RNTPNKSRRR LSPLVTPGSCRSSPTQSPGPSGITVEMPA RRWCAGATGPATSP/SSLKVKETGLPST VQAVSELLQVLLCKQKAGGCTPDQGP TSKVLTEAS/SSAPHLQNVLAAARSISDN IPLGTATLTPAATAATP/EASPLHQAWQ PS/TAMASPAITPWPHYPCQLRMSGLLP CPA*NAPQAAVSVPPAE*RLAALWVH VLRN*TTGPASHCH*CSASKPPSPPTNGY SVSAMTRTPWILPDLAVMVLTPGPKSQ PQM/RPIVLLCLEMPAPGSYPGGAPVS/ AA*AGTPPAVAGAASRAVGGHPRPGC KLRQIP*FCIQEGWGRVFSRGNPCRASD SQRGPAPKQVQGS LGDTGATEAALDWE SGPHCRPAPP |
| 4685 | 12736 | A | 5578 | 718 | 2209 | IPSACFLVLLPSWWLVVAAHGSPLGRVA LDQAFQWTRVRGCSACGKGCAPAG/PQ AQRGSGRSWAWDAGP*RSVWGPLG*TQ PAAAL*P*VSPFVAGKGLAPTLVGTAI QSILOGLILSWNPGGEPAG*RNDLGAGG RACCPDEDDQIRGGAVLAEVT*QCSCSP MPDAAHHRHRVRVGVSGAAVCPQWEL GGHGGNARPDAGRGVLRSCRGTRNLLT AEGFMPHASVCIQSKSG/TSGTQHCPGV HCTWQSCPLPSAPLLGPILLSRTVDTGEE GHPVDASWTPSTPREPGRWAHCLPQRK P/PLGPAREASVPPAHS GTVAGEAPPVIS HFR/SPAPAFGICRGPAGATEALPAPRA DAPVKA AV/PAHTGAAS/EPARHVRPFPT ATAPFTFPSAVHKSGFSTSLQTLVIFCC VLMVAIPMGVRWHLTVVLWNLAVISR VPISV CALDSFISVPCPLRCWCWWNRV SPKLASPGCSECDLGGQMRVMVSSHFSV E |

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| 4686 | 12737 | A | 5579 | 2 | 354 | LPSSWDYRRPLIFVFLVETGFNMLARM VSIS*PLDPPDLASRDEIIGVSHRAWLIL S**KGERKSTNVSHKEGLG*WSRATVLQ VYSVGFWEVFPQGCPSQSYFHNNTNM LFAF |
| 4687 | 12738 | A | 558 | 442 | 626 | VEEGGSEAGWALRIKCVSPKLV/LQL LHFPQIFNGSFVKLNKASVNTLRIVEPYIT WST |
| 4688 | 12739 | A | 5580 | 1 | 1263 | MAEEQGRERDSVPKPSVFLHPDLGVGG AERLVLDAAALQARGCSVKIWTAHYD PGHCFAESRELPVRCAGDWLPRGLGWG GRGAAVCAYVRMVFLALYVFLADEEF DVVVCDQVSACIPVFLARRRKKILFYC HFADLLTKRDSFLKRLYRAPIDWIEEYT TGMADCILVNSQFTA AVFKETFKSLSHID PDVLYPSLNVTSFDSSCS*KAGMT*SPRG KNSWLLSINRYAREGKIWTLTGTGKALV QLRGRLTSQDWERVHLIVAGGYDERVL ENVEHYQELKKMVQQSDLGQYVTFRLS FSDKQKISLLHSCTCVLYTPSNEHFIVP LEAMYMOCPIAGNSGGPLESIDHSVTG FLCEPDPVHFSEAIEKFIREPSLKATMGL AGRARVKEKFSPEAFTEQLYRYVTKLLV |
| 4689 | 12740 | A | 5581 | 200 | 705 | LSQTL/TVLYPSLNVTSFDSVVPKLLDDL VPKGGKFLLLSINRYERKKNLTLALEAL VQLRGRLTSQDWERVHLIVAGGYDERV LENVEHYQELKKMVQQSDLGQYVTFRL SFSKQKISLL/RQLARVCFYTPRQ*GTL GIVPLGRPCYMAVPQFICCLIRVGPFGSSI |
| 4690 | 12741 | A | 5582 | 1 | 259 | ERGSRSIARLEC/SG/AISAHCNFRPPGSSD SSPSACRVAGITGRHHPQLFFVFLVEM GFHHVA*DGLKLL/NFMIHLPQPPKVLGL QV |
| 4691 | 12742 | A | 5583 | 94 | 395 | PIIITYFEFLNGYIISQKIKFSHHQLQKIDFL P*TWHLFLIEQR*NILMEGNQFSVTDDVK ILFSGKLYSHSKIQSMML*LVTRE*CYMF NCNICLLSFSSLSVIINDLQNP |
| 4692 | 12743 | A | 5584 | 3 | 270 | FFEAGSHSGCPGWSESGAIIAHCSLDLPG SSNPTSAS*IAGTRSMHHHAHLIFVFLVE TGSFYVVQPSLKLARVQAILPPRPKVLG LQA |
| 4693 | 12744 | A | 5585 | 13 | 775 | YSVRGLVPAERRTPYPGSIVAPADGMVY ALEGMGPDAPQAQVRVYEPRRDCWLS LPSMPTPCYGASTFLHGNKIYVLGGRQG KLPVTAFAFDLEARTWTRHPSLPSRRA FAGCAMAEGSVFSLGGLQPGAPQLIYS RPHFVNTVEMFDLEHGSWT/IIAPQPAHE G*EGQTLWLGPLGATLWPLGALETSHVL WALLESFSLARRRWEALPAMPTARCS SLQAGPRLFVIGGVAQGPSQAVEALCLR DGV |
| 4694 | 12745 | A | 5586 | 1 | 936 | |
| 4695 | 12746 | A | 5587 | 1 | 1023 | |
| 4696 | 12747 | A | 5588 | 3 | 345 | LNLLMYFRDNVSFCHPGWSTVM*S*LA AASNSWVT*SSCFS/LPSSWD*S*LPPCP ANFFFF/CQ*RQNLIMSSRLVSNLSAQPV MLLPQPLKALGLYRVSHHASVKVFNLI NM |
| 4697 | 12748 | A | 5589 | 1 | 430 | GDGVLLCRPG*STVALSQFTAISASWVK RSSCLNLPSSWDYRCAPPCAKFCIFSRD GGFTMLARLVNS*PQMIHPPWPPKVP LPACVWYFSMACNFLTPTSFLLRFCQ PKMEKAALCQGSPTVKSCSQMFTFNF F |
| 4698 | 12749 | A | 559 | 3 | 398 | |

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| 4699 | 12750 | A | 5590 | 3 | 389 | GVSPCWPGWS*TPDLK*STRLGPPRCWD YRLLEVDPC TGHSLYL*KDPPVLP LPAEG CDYQKGKEYALSSCCDKSYLLPDYRTKFL CCHPERGTWKLGT VGGCYAPIQSFGIAD EQAWLQHGS GAVYLC |
| 4700 | 12751 | A | 5591 | 3 | 53 | |
| 4701 | 12752 | A | 5592 | 363 | 777 | DMRPQLCSVDNHREQRAEFINIYQHQQF FLRQSLTSVAQAGVQWCSLSSLQPLPTG FKPFSCLSLLSSWDYRHMPPSLANFFCIF SRDRGFTMLARLVSS*PQ/CDPPALASQ NAGITGMSHHA WPTPTFSYLLNTQD |
| 4702 | 12753 | A | 5593 | 3 | 85 | FFFFFLMLHNNVYLVHLFTSYKHFIIV LYKQQKFITYVY/TFICLLVFQFQIILLES FPFLKIILL*SL |
| 4703 | 12754 | A | 5594 | 1 | 281 | FFFAPETESYSVARLECSGTILVHCTLCL PGSSDSPASASQVAGTTGACHHTWLILVI LVEIGFHHV GQAGLG/IS*LQVIRPPWAP KVLGIIG |
| 4704 | 12755 | A | 5595 | 2 | 369 | FFLRWCFA LVAQAGVQWQDLGSLQPLP PGFKRFSCLSLPSS*DYRCPPTRLANF/SV FLVEMGFHHVSQAGLELLTSGDLTTLAS QSAGTTGVSSRAWPDLYLFSYLIEKTSPF KFSIPFHLEI |
| 4705 | 12756 | A | 5596 | 432 | 1490 | KKGCGKPGELCGCMPSSWKNAYCPTAQ QTAQEYLSSPCGSAAPCLP/DRASSSSRS VEASSLDSAPGTS AAGSPSPRPFGEYH HPGPGANNEPTPPAESIVVPSWP*GCHSS VAVEKLSLAPGTPT/SDLPLDSSMNRKA PIPVFGLSASSLLPLKDARASETSSR*TH Q*FFGKDVH*TQNSLAQSLQHSSGPQLL WGKTGNSQSSFPQAG*HSRHKEGCWRE PSHKPLEPHSLSQHHGTASSARIPEVPPP HSLGHSPACAWRSSSPRPPRLAALPGC RRRRGAGSSHKAPDRSTARPGRCRRR GRRGARRGCGGSGRGPSSGPRSESAP PAGAHTRLQPLRSHSLH |
| 4706 | 12757 | A | 5597 | 1 | 2163 | MARMSFVIAACQLVLGLLMTSLTESSIQ NSECPQLCVCEIRPWFTPQSTYREATTVD CNDLRLTRIPSNLSSDTQVLLQSNNAIK TVDELQQLFNLTEDFSQNNFTNIKEVGL ANLTQLTTLHLEENQITEMTDYCLQDLS NLQELYINHNQISTISAHAFAGLKNLLRL HLNSNKLKVIDSRWFDSTPNLEILMIGEN PVIGILDMNFKPLANLRLSLVLAGMYLTDI PGNALVGLDSLESLSFYDNKLVKVPQLA LQKVPNLKFLDLNKNPIHKIQEGDFKNM LRLKELGINNMGELVSVDRYALDNLPEL TKLEATNPKLSYIHLAFRSVPALLES LM LNNNALNAIYQKTVESLPNLREISHSNP LRCD CVIHWINSNKTNI RFMEPLSMFCA MPPEYKGHVKEVLIQDSSEQCLPMISH DSFPNRLNVDIGTTVFLDCRAMAEPEPEI YWVTPIGNKITVETLS DKYKLSSEGTL EI SNIQIEDSGRYTCVAQNVQGADTRVATI KVNGTLLDGTQVLKIYVKQTESHSILVS WKVNSNVMTSNLKWSSATMKIDNPHIT YTARVPVDVHEYNLTHLQPSTDYEVCLT VSNHQQTQKSCVNVTTKNAFAVDISD QETSTALAAVMGSMFAVISPASVAVSFP KRFRRKNYHHFIKKVLWQKTSIPLNE LVPPLI*PLGKVDSEKDKGSADTKPTQ VDTSRSYYMW |

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| 4707 | 12758 | A | 5598 | 50 | 824 | SLLKPYVVRIFTKEKSYKCKECKGFHKS CSRH*NHKKIHTGEKHYKCECGKVFNH C*QLIAQKKIHAEKNSDFKECGKAFNNY YELTHQRFCAK*KQCKCNDTHYIYLWK DVTK*KP*STQGVMIHYICTWKDFKNI SLRVHKSFYTEEKHYKYKDCCNTFTYVT DFVVHRRYTER*PSNSCSNFIPF*IIYIGK KPYNCNEYEKNCLKSTP*KTLV*GRARW LTLIIPAPWEAKAGGSRGQEIETTMKPCL Y |
| 4708 | 12759 | A | 5599 | 1 | 2043 | |
| 4709 | 12760 | A | 56 | 939 | 1603 | GHSANWWLGPEENPALPTPELVSPPRGC RQSSRPSLRRHKEEKAK*KSPQPTILRPPP APPTGSLQAPKGGARPPSRPPPPRPAA PNPRLPPPPSPPE/PGRSSCPAPPTTRTTPR VQSQTHRPPPSAYEKKDAARAPTATGR APRRPGLRPKSWMPEQEKEPPTDRSIDR TPVPSPYQTREGGRAVPRASSI*GPDSPAT RQDGSSGPHRSYRPGCVAR |
| 4710 | 12761 | A | 560 | 1 | 960 | IMATSATSPHAPGFPAGEGRGYYVEKKK RFCRMVVAAGKRFCGEHAGAMEEEDA RKRIKPLDPKHTVYEDQLAKHLKCNCS REKPKPDFYIQDINAGLRGETEIQEL/CL NSTLTDHIMSHPALHDALSDPINGDSAT KHLKQASNLGNIENLKLGPRLCFVEF GAGKGLSHWVDIALKDAEKVHFILVE KVTTRFKVDGKHKRKNVFERLQIDIQH LCLNKIPVLRKLPVVGIGKHLGCMAT DLALRCLVETYAASFEERNEEPLAKRIK NDKTEKEIYTLAKEGNEKNVPEKWNPV AGIVIALLCCHRCW |
| 4711 | 12762 | A | 5600 | 18 | 403 | FCIFSGDGVSPCWPGWSRIPDLR*SACLS LPSSWDYRRPPPSANFF*FLVKTGFHH VGQAGLELLTSGDPPASASLSAGITGVSH CTRPMYAFLKQLNFHIDKSDYRLYRKL YLKATTMVFRYAFL |
| 4712 | 12763 | A | 5601 | 2 | 497 | ETESHVSTQAGVQWCDLGSLOPPPPRLK RFSCLSLPSGWDYRHVPPHLANVCIF**I WCFTMFARLVFNSRRTPSDLITSAS*SAG ITGVSHRARCIFYFYFFVAEMVRMSCF VTQVGLFVALSDLPWPVKVLGLQA* ANSAWPVFCNSFFHSHLNAFPN |
| 4713 | 12764 | A | 5602 | 3 | 303 | LSCFPQATFFFFIF*DRVLLCPGRSTVVQ SQLTAALTSRAQGSSCLSLPTKWDYRHV PPYSAFFLFDKSLALLPRLVLNSWAQ AILPPQPPKVLRLLA |
| 4714 | 12765 | A | 5603 | 122 | 525 | QFFFFEIGSLVAQVGAQWRISTSPLOPW SPGFK*FSHLSLPESWEHRPMPQGLDNFC IFVETGFRHVAQASIKLLGSSDLPALASQ SAGMTSMHHAWPIVKNFVCIYYVPDIV LSMLSVKSIHINHVRGLQ |
| 4715 | 12766 | A | 5604 | 1 | 198 | LTGRL/SKCEVVSWRFDVQLKDLKRWQ NHLLLSQLACIVLTSAGIMDHKEMR*K HTGGKSLGFFF |
| 4716 | 12767 | A | 5605 | 156 | 1047 | VPAGEARVQWHDLSLQPPPPGSSDSP ASSSRVAGITGIKTNTICKKCAQNVQLYG TPKPCQYCNIIAFIGNKCQRCTNSEKKY GPPYSCEQCKQCAFDRKDDRKVDGK LLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSQKTLSTS SIQNEIPKKKSKFESITNGDSFSPDLALD SPGTDHFVIIAQLKEEVATLKKMLHQKD QMLEKEKKITELKADFQYQESQMRK MNQMEKTHKEVTEQLQAKNRELLKQA AALSKSKKSEKSGAITSP |

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| 4717 | 12768 | A | 5606 | 156 | 960 | VPAGEARVQWHDLSLQPPPPGSSDSP ASSSRVAGITGIKTNTICKKCAQNVQLYG TPKPCQYCNIIAAFIGNKCQRCTNSEKKY GPPYSCEQCKQQCAFRKDDRKVDGK LLCWLCTLSYKRVLQKTKEQRKHLSSSS RAGHQEKEQYSRLSGGGHYNSFSPDLAL DSPGTDHFVIAQLKEEVATLKKMLHOK DQMLEKEKKITELKADFQYQESQMRK MNQMEKTHKEVTEQLQAKNRELLKQA AALSKSKKSEKSGAITS |
| 4718 | 12769 | A | 5607 | 1 | 354 | ETEFPSCCQAGVQ*HDLGSRQPLPAGSS DSPASASRVAGITGMHH*SRDVLIRILEL EEGLELCPHFVSRNLPKTGQILTLMLSLA PVKLAPQPKLSWMELTRHSRLWAALSG GGQV |
| 4719 | 12770 | A | 5608 | 3 | 403 | YIFSRDRVLPFCFGWSQTPGLKQ SARLCL PKCWDYRREPPQLAED/SYFQFRASLKM TL*GIVSMV/PLLQKLLWMCKAQGNQAE EGTGVALPEREASSWSCLLQLPFPVDEP CSSFKRRESEKEPSPNGFPNLNI |
| 4720 | 12771 | A | 5609 | 340 | 1015 | VGSVEEFQGQERSVILISTVRSSQSFVQL DLDFNLGFLKNPKRFNVAVTRAKALLII VGNPLLLGHDPDWKV*APPPHSPS*WP QPLPRAGGSFLSACL SLS*SSDVSIPTASL LYL*VK*HPEVEQVQLRWDRVA*PPVS AGHSSVPHRFLAEFCENG GYTGCFFPAK LDLQQGQNLQGLWSKLSPTSGAPHSH GLTSPREREGERGPVFCKWEPEWRNEL |
| 4721 | 12772 | A | 561 | 111 | 349 | SLDSDSGCKAYVGD EYLPGLDLHAQP SLLKEHEEEKMFTLKG NR LPAADVKN IIF FVRPRLELMDIIAENVLSEDRRG |
| 4722 | 12773 | B | 5610 | 769 | 809 | GFPIIFHGMGKDEREGNSPSFFNPEEAA TVTSYLKLLLAPSSKKGKARLIPRSVGI SPYRKQGA SEDLEIKDFEGGFSKKNSK AQERSVILISTVAKRPRALLQLDLDF* |
| 4723 | 12774 | A | 5611 | 99 | 341 | SELGTVAHTCNLILPSSGDYRRPSPHLAN F*FLVEMGFHHVQSGVELSSGSDSLAL ASQSPGITGVSHRAQVPPPPFFF |
| 4724 | 12775 | A | 5612 | 1 | 1795 | MRQSHQLPLVGLLLFSFIPSQLCEICEVSE ENYIRLKP LLNTMIQSNYNRGTS AVNVV LSLKLVGIIQITLMQKMIQIKYNVKSRL SDVSSGELALILALGVCRNAEENLIYDY HLIDKLENKFQAEIENMEAHNGTPTLNY YQLSLDVLALCLFNGNYSTAEVNVHFTP ENKNYYFGSQFSVDTGAMAVLALTCVK KSLINGQIKADEGSLKNISYTKSLVEKIL SEKKENGLIGNTFSTGEAMQPSGVLPLN GCSTTTLAVACSTGHRKASRALENRCR SPA AKVTKNKRLSNCQTGQRKLRRCDN RMQCGVLDRIEQKEDISGTTSEIQIKWG VELHSVSRWRLGKVAMEMVQCQKAGY PERGDGVGAVAEGPNIKVAGGLRELETR KTALPENESSQEHAFITITLQHLVQGLAH SGYSVLSKCLLNENRAMQKHGT VWTQQ IQSSAAEKSEKTMSWDRLGRGTAHSWQ ACPVSLLKKQAVEGAHQEEQCKRRDEM R PGESDLVTMASGRDALLCGRCCQQA KT EELTITVPRLGEQREAPLPCSTPPGSTPPA AKVPRPSAAPDGPSS*SPGARRQVARPRR GQAPENK |
| 4725 | 12776 | A | 5613 | 12 | 367 | LGGASEATGASAAQPPPPPPAPRAPNPAP GPAPAQR*SALDPPLPGRAPRSFLKGPRP ATARPPG/WRLQSPLP*PESPPDTRGVRG EAPAPADPAAGPRKSKSDCLAAVIRCLC RAPR |
| 4726 | 12777 | C | 5614 | 231 | 302 | MNSFLVFFPLYVQMYMLRLNFCA* |

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| 4727 | 12778 | A | 5615 | 194 | 737 | EGGVCLSWCGWFGPVCDDYTPPLPEPR DGCLC/PLPKMPPAPPMLPIQQSFQPFQE RPGSPVPETASPPAGN*ISHLSEGPPNTQ WSPGFKPWGVCHL*/CGHVGVPLKPAP CPLE/CCPSGCVDSGAFFQKHSPSGSGPE TAAGPSHLNDNWQRLGFYELLSGIFCRA PNKCICYVSIFVLK |
| 4728 | 12779 | A | 5616 | 2 | 360 | PRVRDPRVRPRVRRRIYKPLRTRDELQ FLDKMDDPDY/WPAVDFFSGDVMHPVT NRPADKRSFIPSLVEKEKVSARMGHAIRM GWIQPRRPRDPTPSFYDLWAQEDPNAVL GRHKMHVPA |
| 4729 | 12780 | A | 5617 | 1 | 2072 | DSGSDSSEDDDEGDEEGEDGALDDEGHS GIKKTTEEQVQASTPCPRTEMASARIGDE YAEDSSDEEDIRNTVGNVPLEWYDDFPH VGYDLGRRRIYKPLRTRDELQFLDKM DDPDYWRTVQDPMTGRDLRLTDEQVAL VRRQLSQFGDVGFNPYEPVAVDFFSGDV MIHPVTNRPADKRSFIPSLVEKEKVSARM VHAIKMGWIQPRRPRDPTPSFYDLWAQE DPNAVLGRHKMHVPAPKLALPGHAESY NPPPEYLLSEERLAWEQQEPSEKLSF LPRKFPSLRAVPAYGRFIQERFERCLDLY LCPRQRKMRVNVDPEDLIPKLPRPRDLQ PFPTCQALVYRGHSDLRCLSVSPGGQW LVSGSDDGSLRLWEVATARCVRTVPVG GVVKSVAWNPSPAVCLVAAVEDSVLL LNPALGDLVAGSTDQLLSAFVPEEPPL QPARWLEASEEERQVGLRLRICHGKPV QVTWHGRGDYWPLVLA PRGHTGVLIH QLSRRRSQSPFPCTHV*VHRVAFSPARPF LVLGPQRSVRLYHLALRQELTKKMPA NCKWVCQPGGCNPAGDNVICGSYDSK LVWFDLSTKPYRMLRNH/HRRALLA VAFHPRYPLFASGSDDGRVIVCHGMVY NDLLQNPLLVPVKVLKGVHVLTRDLGVL DVIFHTQPVWVFSSGADGTVRLFT |
| 4730 | 12781 | A | 5618 | 1 | 214 | QDSALLQL*IIYPVYNLSPAGQGRDLF SCLLRHRLKLTSEGVRTQSAQAFKGP NAQTQWIYGHDPN |
| 4731 | 12782 | B | 5619 | 58 | 280 | IHCAISKIDIEKDIQAVMEETAILSTENKS EFLLDYFEEDPNSAMDKERRKSLLKPK LLRLQRDIEKASKDKEX* |
| 4732 | 12783 | A | 562 | 223 | 747 | CIGKVYVWLGGVGWLQKSWGTPLFSPH PPGRPRSFAGHSPPOGILGVGLGENRI LVIIFNLIYCTYLGQGLGEVEGEGSPLS APPTPFLRRFVCVAGPHPLPIPHCCLDVVL FFYRSFPSPSPFSPPHPLLPFVSCSFLG FCTTQLVYTYTQPAKRKPNGKHFKKK KK |
| 4733 | 12784 | A | 5620 | 2 | 785 | HFNMRLDPLDCPYNKVYKNLKEFSQNG ENFCKQVTSVLQQRANLEISYAKGLQKL ASKLSKALQNRKSCVSSAWAWASEGM KSTADLHQKLGKAIIELEAIKPTYQVLNV QEKKRKSLDNEVEKTANLVISNWNQIK AKKKLMVSTQET*STFPSL*ESS/ARQSM TEKEKRKLLNKLTKSTEKLEKEDENYYQ KNMAGYSTRLKWENTLENCYQSIL/ESW RRKEFNFYAITLNQYSQHISLFGQTLTTC HTADSLCHQQD |
| 4734 | 12785 | B | 5621 | 13 | 543 | MFLAPIAVSVRRFFXVKASVYAYTMFFS TFYHACDQGEAVLCILSYDTLQYCDFL GSGAAIWVITLCMARLKTVLKYAYRCG HRRQCYPTLWQRWAFYLLPGVFMASVG IAIYTSMMTSDNYYYTHSIWHILLAGSA ALLPPPDQPAEPWACSQKFPCHYQICK NDREELYAVT* |

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| 4735 | 12786 | A | 5622 | 1 | 1798 | MLCFYAGSCRHFRSGAPPVINPLGTSFPD DTAVQPSFQVGVPLSTTPRSNASVNVSH PAPGDWVFVAAHLPPSSQKIELKGLAPTC AYVFQPELLVTRVVEISIMEPDVPLPQTL LSHPSYLKVFPDYTRELLLELRDCVSN GSLGCPVRLTVGPVTLPSNFQKVLCTG APWPCRLLLPSPPWDRWLQVTAESLVGP LGTVAFAVAALTAACRPSVTVOPLLQS SONQSFNASSGLSPSPDHQDLGRSGRV DRSPFCLTNYPVTREDMDVVSVHFQPLD RVSVRVCSDTPSVMRLRLKPGMDSGGS LTISLRANKTEMRNETVVVACVNACLAL PLALILSLNCTTAFFQGYPLSLA\GSRRRA NLIPYPETDNWYLSLQLMCPENAEDCE QAVGPRWEDHLCTWGALF*TDCGPYQG C\SLRRHSYLYASCCKAGWRGWSCDT NSTAQTV AQQAATLLLTLSNLMF/LGP PSPSSVRRFFLVEASVYAYTMFFSTGCG VGGQDRAHGASPFQFYHACDQPGEA VLC ILSYDTLQYCDLFGSGAAIWVTLCMAR LKTVLKYVLFLLGTLVIAMSLQLEPQGH VEHLGGPASLPS |
| 4736 | 12787 | A | 5623 | 121 | 291 | AFCFPKYELTINFKNFQLGVVTHACNPSI LGGRGGRT*AQEANLANMAKPCLLNK |
| 4737 | 12788 | A | 5624 | 571 | 690 | CQQGSFLQAYGPAQHAISMRFKAKY PDYEVTWANDGY |
| 4738 | 12789 | A | 5625 | 130 | 943 | |
| 4739 | 12790 | A | 5626 | 45 | 473 | GIPGRRNMAVADLALIPDVDDSHGVFK YVLPSPGLPAPGIRPAESKEIVRGYKW A\GHADIYDKSVGATCRKQGLRTVSV WTAGPHLPTKSPGQERFT*YG*FHGPMV LPKNANFNLRKSKAKYPRLTEVTLGLNR PAT |
| 4740 | 12791 | A | 5627 | 3 | 348 | TLRLTHLHTDTHQ/HSYSYTHTEIHTPHT PHTETQTH*YTYALQ/PLRSHLIFLRQSRP QNGNAPLCEFSHPSPDVLQTLHLTSVV VKIPSTSLLMCRSSGGAQCRESLDQHEG VGP |
| 4741 | 12792 | A | 5628 | 3 | 331 | FFEMESPSV/SQAGV*GPNLGSLOPPPPQ FKQFFCLSLPSSWDYRRTPPCPANFWIF* KDGVSPSWP*WSQSLDLGLFKFYFFKET LILCTQSSTTTTTKRTTRSSHR |
| 4742 | 12793 | A | 5629 | 3 | 336 | SHSVAQAGVQWHNLGSLQPPPPAFK*FS CLSLPSN*YRRPPPPHADF*FLVETGFS HVGRAGLKLLTSSEPPACASQSAGITSVS PPCRAHTFELIPLCPFLFWPLFCP |
| 4743 | 12794 | C | 563 | 238 | 267 | MQINSQMER* |
| 4744 | 12795 | A | 5630 | 1 | 267 | EMESCSVTRLECSGAILAHCNLCLLGSS DSPASAS*VAGITGMCHYTRPTFLFLVE MGFCHVGQAGLELLTQVIRPPRPKVLG LQA |
| 4745 | 12796 | A | 5631 | 3 | 521 | FSFFFFPAFKMSNRGRGGSLLAGRKFPDF PLGPSGRLL*SNWCLTNTRSPKTYIHLF *RGNQGDRLDQTSPLLGVDMMVAHS/ VKKGKPELRKKIVHPSSGSFRQPKVHY* EKMVGVLFFEG*LQGVIVEPFKGRDGK VSCHLPGTQLGKGSFADFVAPGICIMP WQPLH |
| 4746 | 12797 | A | 5632 | 3 | 216 | DRSHSVTQAGV/Q/WCDLSSLPPPPGLK *FLCLSLSSWDY\GAPPHQTNFYIFIRDG VSPYCPGWP*TPSLG |
| 4747 | 12798 | A | 5633 | 1 | 412 | IIRSKNI*YLEINPTKHTKTFSKTLTK\EMK EDLN*WQENPCSWIGSVSIVKMSVLSKL IHTEIQCNRNKYPQIGLLLP LLLFLLDR LVLKFTWKGTGPRMAKAILRKS/SEDLT LTYINTYYKATVIKLVGAKPD |

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| 4748 | 12799 | A | 5634 | 276 | 2588 | NKHFSFQTPKKSHQKSLSFSKTTPRRISH TPQTPLYTTPERLQKSPAKMTPTKQAAFK ESLKDSSSPGHDSPLDSKITPQKRHTQAG EGTSLETKTPTPKRQGTQPPGFLPNCT WPHSVNSSPESPSCPAPPTSSTAQPRREC LTPIRDPLRTPPRAAAFMGTQPNQTHQQ PHVLAARAEPAQKLKDKAIKTPKRP NSTVTSSPPVTPKKLFTSPLCDVSKKSPF RKSKIECPSPGELDQKEPQMSPSVAASLS CPVPSTPPELSQRATLDTVPPPPPSKVGK RCRKTSDP/MKEAS/SECQLDASATPGVG TADSPAAPTDSDRDDQKGLSLSPQSPERR GYPGPGLRSDWHASSPLLITSDTEHVTL SEAEHHGIGDLKSNVLSVEEGEGLRTAD AEKSSLSHPGIPSPSPCGPSPLMPSRDV HCTTDGRQCQASQDLNLPASAWHSTD SASPQTYEVELEMQASGLPKLRKKIDPS SSLEAEP LSKEESSLGEESFLPALSMPRAS RSLSKPEPTYVSPPCPRLSHSTPGKVTGGK PTSARVPVPPPT/SPSSTPSFFQTDGVPWTP SPKHSKGKTTDIIKVTGPGGRGRWAVAPA PLPGGARSVQPSWEPVTA*VRGQGRP* TQHPQDAHLGGF*ARGSVAPRPVASQE /ACLPRKPLPGDSL*VPGRESCWPRK KLTVEPKGSVT*EKIQKLVVRKRGLOVG VHGSYPPRETKRCLFPAPPHLPAVPCGAP SPASALQALTQSPLLFOGKTPSSQSKDPR |
| 4749 | 12800 | A | 5635 | 29 | 268 | ILINHFFLESCSVAQAAVQWHNLSLQPP PPGFK*FSYLSFLSS*DYKHAPPRPANFCI FSRDAVSPMLASWSQTPDLK |
| 4750 | 12801 | A | 5636 | 2 | 118 | |
| 4751 | 12802 | A | 5637 | 1 | 262 | ETDLALSARLECSGVTILHRKLRPLGSR HSPASASQVGGTTGARTTPG*FFVFLVET GFHRVSQDGLDLL/NLVIHPPWPKVLGL QA |
| 4752 | 12803 | A | 5638 | 3 | 309 | IDTFFFFFFFFFFFETESLSVTRLECSGAIL AHYKLRPLGSRHSPASASRVAGTTGARH HARLIF/VYFLVEMGFHHVSQDGLDLTS *SGPPRPKSLGLQA |
| 4753 | 12804 | B | 5639 | 49 | 754 | MAGAAPRLPWSRPHGSCGWWMQPLQ GPGRRAVAAAWEVATPVFMPVGTQAT MKASRPNSWTLWVAASAWELPSGSK AGGTAAPFDGVAAGVSVRGDGGGLRFRS PYDGNETLLSPENPCRSRMRWAPGVVT GALLQVNPLAGPVHAAHQRPDKQNLFA IQVGWQTQISGPPALKRFGSAWHSRAFLT HCCTVTTRPRCTTSRPQHRLPAELMSAV RTSIVEKRFPDSCGTSWAPX* |
| 4754 | 12805 | A | 564 | 549 | 848 | LFFPHSQSTKVFSSTYEQIMCVVFLFFCF FVFPETGSHSVTRLGCSGVIMAHCSFNL PGPSPSTASQVAGTTGVCHHAQLIFKF FVEPGQHTIETPSL |
| 4755 | 12806 | A | 5640 | 3 | 906 | TVKMAGAATQASLESAPRIMRLVAECRSR SRARAGELWLPHTVATPVFMPVGTQA TMKGITFAEFLDALGCRICLGNTYHLGLR PGPELIQKANGLHGFMNWNPHLLTDSG GFQMVSLVSLSEVTEEGVFRSPYDGN TLLSPEKSVQIQNALGSDIIMQLDDVVSS TVTGPVVEEAMYRSIRWLDRCIAAHQRP DKQNLFAHQGGDLADLRATCLEEMTKR DVPGFAIGGLSGGESKQFWRMVALSTS RLPKDKPRYLMGVGYVVDREARALPVG SGFLGTPYPAWGGGIWKGRTQV |

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| 4756 | 12807 | A | 5641 | 379 | 677 | EGLRP/ELQNLFAIQGGDLADLRATWP* RDDQARNVPGFAIRGALSGE*EQSREF/C AGWLAAEHTLG*PKDKPRYLMGVGYAT DLVVCVALGCDMFDCVFTRTARFGSA LVPTGELQLRKKVFEKDFGPIRPGCTFP HVPKAPARAFLHATAAQ*QHGPCRTILT VHNIAIYQLMSAVRTSIVEKRFPDFVR DFMGPMYGDPTLCPTWATDALASVGIT LG |
| 4757 | 12808 | A | 5642 | 2 | 335 | AGVQWPDLSLQPLPPGFKRFFHLGLPSS WDY/RVHEAPRPANFLKFLVEMAFCHV GQAGLELLGSSDTPVLAQSGITGESHLA WPVFNF*NGSFNVFSLRVINEHLALHL |
| 4758 | 12809 | A | 5643 | 56 | 571 | YYQNPPKKKLAASCSLSPVLQVLKSLKG EVLPLGETQHYFPLNRELRLLTQHFLLL MPLSQ/QTSKAGTHIARLIDPDYQGRTKF KIRNGKKILNGRRKEIAWNVGFSIT/PCLL WKVIGILEQSNMAIYWYIHPRMKV*ASP PGKEQRPFEVTPEGQRNMEWLEERNG RCLP |
| 4759 | 12810 | A | 5644 | 2 | 1085 | |
| 4760 | 12811 | A | 5645 | 387 | 533 | RWSDYVERYMNSDITTSPELREHLA/QKP VFLPQGE*AMSICQVHTVHD |
| 4761 | 12812 | A | 5646 | 1 | 169 | VFLVETGFRLLARLALNS*PCDPPASAS QSVGITGESHCARP GTILMKHRGQLCT |
| 4762 | 12813 | A | 5647 | 2 | 369 | FLRWSFTLVAQAGIQWCGVSSLQPLPPG FKQFFCLSLPSSWDYRCPPPCPTNF*LLV EMGFHHVQAGLELLTSGDLPASASQSA GITGISHRARPGTLFF*AVNGGNGQVFLF LRVLNGL |
| 4763 | 12814 | A | 5648 | 1 | 340 | FRPQSC*CPPADSRLFPATPEAVLSLLVK ASPPPELPRSPPEKPTGLSGGALG*QRFSR AARNRGDPLTRKNSKITSLLSFLQELTKA LEQKPDDAHILSSKSLSSHSSWELL |
| 4764 | 12815 | A | 5649 | 2 | 660 | RPPAPAPGPQGPWPQGPYP*AESPPARS RTPHASQLPRCGPRPTADPSSAPSRRLRP TSRSRHCFAAGS/PGTPPQPPSADVRRV PPFSPLSSRW*PFPQSC*RPPADSRVRSR PPLRPSFRFL*KPARPQSSSVASREAKGPL VERQVDSVLAGPRETASSFATRPCATLP GKVTANCKPPQKTSGQLLVRGLSRVA AYSSPFFGAPEIGEEMPI |
| 4765 | 12816 | A | 565 | 178 | 375 | ANFIAGVWSQSRFHALALHIIQQGSKKV P*ANFIAGVWSQSRFHALALHIIQQGSKK VPIVSKLENDTAARHELFIAEWRKQCSE KKAQAKGWRQW |
| 4766 | 12817 | C | 5650 | 19 | 153 | MKMTSNFLLFSSGIFSSTFIHLDVPLEL QTQNTVMGCLMRIHP* |
| 4767 | 12818 | A | 5651 | 2 | 306 | ETKSCSVA*AGVQRRNHGSM*RQPPGSS NPPISASRVFG/ITGICRTHLIFLFFVETG SHYVAQGSS*TPEAQVIRLHQPPKL/VFF YIFQLFLCFLVCY |
| 4768 | 12819 | A | 5652 | 2 | 760 | FFFFWSENDGHLDTGARFAPDRRHTGV GRTKDTQVGYRCHTAPARARGGWGED GCLAS*PGVRVKSRWSVPGAPGRGGQC HNPSGFPT*PGGRHRKQPRPGARVLQAG GQQQAFPLAGWHLSPGYWLSTPWAC KGLGVVLSVTPLPPSPWVG*GLGSR/Q AVEGRAAQGRYLSFCPGTQW*WPPSAPI PTGT*SEVAHTKGVPGPEPPAARGLRT LTLAVGGLPGSRLVQHPKRYRALQALT SCFCSA |
| 4769 | 12820 | A | 5653 | 1 | 834 | |

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| 4770 | 12821 | A | 5654 | 674 | 1268 | PRDLPASASQSAGITGVSHRLRFYFDHQ DVAPECGAYFFHELAKERKGV**NTL LAKMVSIS*PRDLPASASQSAGITGVSHR LRFYFDHQDVAPECGAYFFHELAKERK KGVRLKMQNQRRGPAVFQDILKPGQ DEWGTKLEAMEAAMAPGKNLNQSLD LHALGSAPTDPHLCDFLSHFRDEEVTF MPRKSADLHAAGEAASLGGVSLNVMK GASLHALCLRLNSFGPGVATLCGERVV HKNNRASALRKCFWP |
| 4771 | 12822 | A | 5655 | 2 | 612 | RYDFFFFFFFVFTESRSG*LQSQAGVQ LRDLGSLQAPPPRFTPFSCPASPSWDYR RPPRPANFFLYFYS/MRRGFTVLARMVS IS*PRHLPALASQAGUTGLSHCTRIFFF* WMESPSVTQAGIQWHDLGSLQPMPPQF R*FSWLSLPSSWDYRRPPRPADFCFTR DGVSPC*PGWSRSPDLVIHPPWPKVLG LQA |
| 4772 | 12823 | A | 5656 | 140 | 261 | RAEPHLANHILFF*DRVSLCRPGWTAM A*TWLTVASTSRAQAVLPSPASPS*DY RHVSPHPLIFVFSFLIMLSRMVSNWAQ GILLPWSPKVLELQA |
| 4773 | 12824 | A | 5657 | 79 | 358 | AGVKWGDGSL/QPPPPRFKRFSLSLPS SWGVRHAPP*PG*FSVFLVKTGFLHVGO AGLELLTSGDLPVSASQSAGITGMSHCA WPTKALISK |
| 4774 | 12825 | A | 5658 | 2 | 350 | SQVDR*QSEPSIRICREDHMERLQAFDA NSRKQEAWEKKAKELEEWYARQDEQ LQKTKANNRVADEAFYKQPFADVIGYV EEAFVNDIDESSPGTEWERVARLCDFNP KSLD |
| 4775 | 12826 | A | 5659 | 3 | 752 | HRCGVGGSVGFCLTVGVRAVQLPAMAE LDPPGAPAGAPGGPALGNGVAGAGEED PAAAFLAQESEIAGIENDEAFAILDGGGA PGPQPHGEPPGGPDAVDGVMNGEYYQE SNGPTDSYAAISQVDRLOQSEPSIRKWRE EQMERLEALDANSRKQEAWEKKAINE LEEWYARQDEQLQNTKANNRVADEAF YKQPFADVIGYVYVAKLIPFSTSDSYFC LELMLLLCHKLLCFLNYFKLALWGLPKN |
| 4776 | 12827 | A | 566 | 656 | 874 | |
| 4777 | 12828 | A | 5660 | 1 | 348 | NSLGEANALGNQ/QPITQNVCPRLAMQ APGMAPSPSFIMNTLEVRKAFLKRFPWM SAPIQVGLVGFCLVFATPLCCALFPQKS SMSVTSLEAELQA*DPKRAHPVELRRVY FNKGL |
| 4778 | 12829 | A | 5661 | 3 | 430 | LRQSL/DSVAQAGVHWRDLGSR*APPPG FTPSSCLSLPSSWDYWHPPRRPAVFLYF* ERRGFTVLARMVSI*RRDPPASAPQSAG IIGM/SHRARPOILFFIHIFSTVSAGINES*V CFYCIILEVPSKEGILES*CISEAAH |
| 4779 | 12830 | A | 5662 | 3 | 756 | GAISAHNRNRLFLGSSDSPASASQEHWGT ETLAH*RSQLTATSASWVQVILLPQPPKN TGAQKHWPTEGEAKEHCVSDDSESTLK AGGQHRIKQGGNSSSGAREPAPNILNSR RSWWTLVAKAAAVTVIIRVILMAAILRG TLAKEVNWWVLDLTDKNEAADPRAR HKDSPSPHQTEPSWLHSVDPTPGPQVE LPASPTMCAGTSQPLVSRWDWSPWSRK RHIIAPSSHNKYAGESFPGIYDAIFDIEN KANSRLAWKEVKKHISIAAFTIQAAAGT LKEVL |

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| 4780 | 12831 | A | 5663 | 2 | 773 | LANFCIFSRDGVSP*WSGWSRTPDLR*ST RVGLPKC*DYRREPPHPPGLLPVFSSHFA FGLFQRRRLVFCFFAFLRQSLALVTQA GVQ\WHDLGLSQPPPGFK*FSCLSLLSG WNYRCVPPRQANFCIF/M*RRDFTMLAR LVSNS*PQ/CDPPTSASQSAGITGVSH/H/A RLAFVS/CYTHTHHTHTLA*IPFPSVFP NSLSPPLQOGFCPHHCTELTSYLIKITNPV HVIRPNGHSALCILVQVSAPLHWSLPL E |
| 4781 | 12832 | A | 5664 | 2 | 415 | LDPGSLAGFTSYIQFMYDEFVEEYEPTK ADSYRKK/VAQDGEEVQIYIINTAGQEDY TAKDNYFHCVFSITEMESFAATVDFKEQ /ILRVKKDENIPFLLVGNKSDLEDKQVSI EEAKNRAD*WNVYVETSPKT*AN |
| 4782 | 12833 | B | 5665 | 151 | 1312 | MMGGRLLTGGIPGEAAVWGCSRSTAP SVFPPPPAAAAAAAVSSGNLRLHPGQV PRVVLRSREGGLAPRRGCPKSGGSESTR VPRAGPRGESTGDRDPAPPPGPPSSSHF SPLRIERKADKPPENSGESSHDVASREQP LVLLAEHFRWAILLACHSMPTVGRKQV NNEIKTEIKKFETSENKDTTYQNLWDT AKISFFPDFSYNFFMPISVLDAGGGSETA KHHHQDVHEIQPHIEPQISLGSFEHPFGS CTIKEGTYRKRVLVDGEEVQIGILETAGQ EDYAAIRDNYFRSREGFLCVFSITEMESF AATADFREQILRVKEDENVFLLVGNKS DLEDKRPVSVEAKNRADQWNVNYVE TSAKTQLMLTRHKPGTSSQSX* |
| 4783 | 12834 | A | 5666 | 3 | 955 | LLLLLLLLLLLLQPPRLPRHPSDSSDRSR RGAFQATRTEYPPGGATQPRLPEPSGR TGSRCFFLILWRKLRLHKMAANKPKGQ NSLALHKVIMGGSGGVGKSALTQFMY DEFVEDYEPTKADSYRKKVVLVDGEEVQI DILDTAGQEDYAAIRDNYFRSGEGFLCV FSITEMESFAATADFREQILRVKEDENV FLLVGNKSDLEDKQVSVVEAKNRAEQ WNVNYVETSAKTRANVD/KEWPFLKTR WWNTCKYISSHCPAPVSRKTAHWAE VFFDLMRERARKMEDSKEKNGKKRK SLAKRIRERCCIL |
| 4784 | 12835 | A | 5667 | 1 | 635 | MAANKPKGQNSLALHKVIMVGSGGVG KSALTQFMYDEFVED*EPTKADSSRK RVVLVDGEEVQIGYPLDTAGQEDYAAI RDNYFRSGEGFLCVFSITEMESFAATAE FREQILRVKEDENVFLLVGNKSDLEDK R/QVFSRKRQKNRAEQWNVNYVETSAK TRANVDKVFDDLMREIRARKMEDIYYL NGTKNTKRLAERIREGGCIL |
| 4785 | 12836 | A | 5668 | 2 | 178 | WGFTMLARLVLS*SQVIHPPWLPKVLG LQALGSGSLHRSFFISVKGSSGFTAPSR L |
| 4786 | 12837 | A | 5669 | 208 | 339 | RGQRLPVSRKWLLGTEEAVALR*STRLS LPKCWDYRHEPPCAH |
| 4787 | 12838 | A | 567 | 718 | 971 | |
| 4788 | 12839 | A | 5670 | 73 | 269 | DKIFFFFF*DRVSLCRPGWSSVARSRLTA TSASQFKQFSCLSRPSSWDYRHVPPRPA NFCIFSRDR/SFTMLVRLVLNS*PQVIHLP RPPKVLGLQA |
| 4789 | 12840 | A | 5671 | 1 | 586 | KKPYECKEKGKAFSSGSNFTQHQRHTG EKPYECKEKGNAFSQSSQLIKHQRIHTGE KPYECKEKGAFRSGSDLTRHQRIHTGE KPYECKICGKAYSQSSQLISHHRIHTSEK PYEYRECGKNFNYPQLIQHQNLYW**N RIYEMCREAFNYGSKQNLSC**FL*IE/C/ SKHFICGLQLIQPGKNNVGEILYE |

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| 4790 | 12841 | A | 5672 | 2 | 355 | LFLSFLFFSFFFFFETGPHSVAQAVVQWL NHGSLQPQLSGFKQSFRLLRLLSG*DYRC TPLRLASF*FFVEMGCHYVAQAGLQLL DSGDLPASASQRAGITDVSPCIWPPMSC YVKRT |
| 4791 | 12842 | A | 5673 | 921 | 1086 | TQPWYRHGGGGPKTLRQRSWSPCQAYH VPHACPSHHKNLSSRPWCPNATNML LSLKALQPPTLLSPLP*QVCROGKNPPKQ RCRGP GATHHIPVHLWHSGWPLLHTLPA RISAVQPSFPFPKETLGQAELONRWVPL GPGKQVLRERPLSHQREKREAQLTPRLL ARRPQAGEAAARRQKGTAEGERG**D GPSKPSLVRARVRKRAGPKQGPSASA*P GPSTPNPPTTQGSHPREQAPAPTPMSS EEPVLVSQQTARP/RPSPGTGMGVGVLK PFVSVPGALAKLTMCMPMHVLHITKCPA AQGHGVHRMPQTCC |
| 4792 | 12843 | A | 5674 | 2 | 70 | |
| 4793 | 12844 | A | 5675 | 2 | 118 | |
| 4794 | 12845 | A | 5676 | 446 | 756 | ISFFLSFFLSFFFFFEAESRSFTQIGVCSGTI SAHCKLCLPGSHSPASAS*VAGTTGAR HHTRLIFLYF**KTGFHRFSRDGLDLL/NL VIRPPRPKVLGLQA |
| 4795 | 12846 | A | 5677 | 2 | 276 | LRWSFSLVVQAGVQWCDLGSLOPPPSGF K*LSCSLPSSWDYRSAPPCPANFVFLVE TGFLHVGQAICLELLTSSDLSTSASQSAG ITRREQ |
| 4796 | 12847 | A | 5678 | 60 | 235 | VRVLQIYHSLRLPGSHHPPRGDRLOGRG FLTACQPC*STYC*TFPPGVLGNTGRDLL L |
| 4797 | 12848 | A | 5679 | 1 | 2059 | MSSQEVTFEORPEGDEGGAVELSRQQTQ QERRRQLGQTQLMYKWAKPKICSEDL GAVKLPAAGVKTHCPPCNPFGFKTNNST CQPCPYGSYSNGSDCTRCAGTEPAVG EYKWWNTLPTNMG/TRPFSVGSTSSSTR/C MTGWEVAGDHIYTAAGASDNDFMILT VVPGRFPQSVPMADTENKEVARITFVFE TLCNVNCELYFMVGVNSRTNTPVETWK GSKGRQAYTYIIEENTTTSTYCAFORRTF HEASRKYTNDAAEIYSIICHPCY*MPWAS YAGPCAQKASEEGSSCTSPAGYIDRD SGTCHSCPNTILKAHQPYGVQACVPCG PGTKNNKIHSCLYNDCTFSRNTPTRTFN YNFSALANTVTLAGGPSFTSKGLKYFHH FTLSLCOGQGRKMSVCTDNVTDLRPEG ESGFSKSITAYVCQAVIIPPEVTGYKAGV SSQPVSLADRLIGVTTDMTLDGITSPAEL FHLES LGIPDIVFFYRSNDVTQSCSSGRST TIRVRCSPQKTVPGSLLLPGTCSGDGCDG CNFHLWESAAACPLCSVADYHAIIVSSC VAGIQKTTYVWREPKLCSGGISLPEQRV TICKTIDFWLKVGISAGTCTAILLTVLTC YFWKKNQKLEYKYSKLV MNATLKD CD LPAADTCAIMEGEDVEDDLILTSKKSLLG EDQIYLOEDS |
| 4798 | 12849 | A | 568 | 480 | 683 | |
| 4799 | 12850 | A | 5680 | 1 | 1098 | |
| 4800 | 12851 | A | 5681 | 143 | 571 | |
| 4801 | 12852 | A | 5682 | 3 | 355 | FEIGSCSITQAGVQRHDLCSPLPPPGFK QSPRPSLPSS*DHRCAPPCPASFCIF**RQ GFHHVQAGLELLTSGDPPALASQSAGI TGVSHQAWPPFGFLDRTLSIVSQKTNTN RP |
| 4802 | 12853 | A | 5683 | 1 | 2472 | RYDLALWPRLECSGAITARC NLKLLGSS NSPTSTSCI/C*GYRLIFFKFFVDTGSCYV AQAGFKLPASSDPPPPKMLR/YRPGHHA R/LCLTVNRTNVP |

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| 4803 | 12854 | A | 5684 | 5 | 298 | TGSRVAQAGVQ*H/DYQGSLOPPPPRP M*SSHLSLPRNWDYSHTAPHPAKLFFFL DTGSHYVAQAGLKLGGSSDPSTSASQSA GITGMSHRIQPHISF |
| 4804 | 12855 | A | 5685 | 9 | 320 | FIYLF/RDGVLLCCPGQSAVAFRLTLVTS T/FL*SPDGELLTL*STRLGLLKWWDYKG EPPRPVFLFCFLNV**RCSLAMLRLVLN S*AQAIFLPQPSKVLGLQG |
| 4805 | 12856 | A | 5686 | 2 | 438 | FFFFSRLENFEFYNKPFCTNPGPRGPPR VGPPFAPRRGAFSLPQGGPF*SLLFSRPN P/SGPLVRPGLPPTGALPCSVR*VDRSLP YMVSPGPPGGLRGAGPGPVHPRGPEAP PRARGRGREGGPAESVTRFPWQLRGH FQP |
| 4806 | 12857 | A | 5687 | 243 | 377 | |
| 4807 | 12858 | A | 5688 | 1 | 867 | |
| 4808 | 12859 | A | 5689 | 1 | 874 | TVLAFADGCGVLAHGRSRSYGRGRRP YSREPLWSRGPFTMSDEEARQSGGSS QAGAVTVSDVQELMRRKEVEIEAQKAN YDVLESQKGIGMNEPLVDCEGYPRSDV DLYQVRTARHNIICLQNDHKAVMKQVE EVALHQLHARDMEKQARDMAEAEHKEA MSRKLQSESQGPRAFAKVNISISPGSP ASIAGLQVDDAEIVGVSGSVNTQNFQSLH NIGSVVQHS/EGGPGTHHPTFCLYFDYS RDLI*KPLNVTVIRRGKEKHQLRLVPTRW AGKGLLGCNIIPLQR |
| 4809 | 12860 | A | 569 | 811 | 1481 | GNGILLMVHHHCDAGTVIMRADRFIPGE DQKNRVLVNTVLVRISRAVDGKHLASAGI RHTVFRICHNACTQHRGLFRGFNVFGEF LRFAYILIVKENADQCAGFVGIIELGEID RVMQALPDVEQAVTHACVINQAAATGG DARQLVGYLVQSQGFNINGNRHLTTIN PVGFPAADK*GFPLMLPRVSGRNQHRIS/R VYLPCTATLLRPGNGPPSSVRPRR |
| 4810 | 12861 | A | 5690 | 30 | 512 | TPVRDMAEAEHKEAMSRLQSESQGGP RAFAKMNSIEPRLPQPSIAGLQVDEIVE FGSVN/TPQDFQSLQNNGNVQVHSEK PPECDO*SARGEKHQLKLVKNAAGPGK GALLGCNIIPSAKDELSPRGNSKQEKHPS PCPRTWVLGDFTCPSSPLKA |
| 4811 | 12862 | A | 5691 | 945 | 1358 | KKQNFIYTVHGFSCCLGRGKGQDRDQW ESRDGRFLSRSLTFPQFAIIRLVGQKEFS MLPKSFTLQILPRGSLSLPDPQEQLSK*S MPHRAVQSPSRHALGNPKTAREGSAPRS PLTGRPRPPVAAG*CRACRGAPQVARPP QGDQHRGFRGAHSDWRVWRGWASPSL LPRSSSSSGIANQASVPVESPGRS/RPAL GGRSGSSPCRRP/PPKPPWRGAIGS*SGT WRRWLAGWRTRRPAPGCARPAPRPGPP SWPSRPQTGLAAGLSGAPSVPSRRCTP RRSRPPLPARWTPPGAPACRRRPWS*SP GSTTAA |
| 4812 | 12863 | A | 5692 | 3 | 316 | FFFFFLRQSL/DSVAQAGAQHNPGLQA PPRFTFPFSRLSLPSSWDHRRPPPCPTNFS AFPVETGFTVLARMVISIS*PCDLLTSASQ SAGTTGTSHRARPIIFK |
| 4813 | 12864 | A | 5693 | 2 | 769 | LAIYKHAGGVFSFILLQTLNTYGPQDQ KGSVLAYWRLPGLCIIYLVKQSAKDDFS YYDINRQSVSKLAQNVEQLPPDEIKELRQ TITMPAGVDKSSDQKYVQAGRRLGKVI QQSRLNCFPLVSYIIETCLFILWRHLEY L/LHCOMPTD/SQKSLFASR/TLF*KQKDCQ GFPSPOETQS*DF*KVGLAYSEANHGF*T QLSGLMPINGFLENHYPKRNFLDIEGL/YI SKVRFFGYSFIALVRRIRGLLRISRN |

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| 4814 | 12865 | A | 5694 | 189 | 424 | TLPISIYQSSPSGFHNYQFLASGVGATLPI TPHPTS/ELPYRVSPSPSPRPPS*FSRTF QPP/V/PGPAH*PPDEIVEPG |
| 4815 | 12866 | A | 5695 | 243 | 1660 | AEPDTSPI*TPGQSGSS*GNTS/EPWTVTP PGLKMQQRVLCCTL*PP/RRLPVCRPAA G*TRLDRA*ESGHPGPAVPREATGVPGA LPAQASVRSIWPALATCVATTVQTST/DA EVARQG/ICPAPHPAYPPA*PALCCPARA DPRGRVLQ**ADAVPGPPAI*AVHRAVS HPGGAQC PHPNPPAPQARVPRETCLPAL QLAAPVLRGAGATAASAPTEEEEEACLE EEEEEDSDEEDQSRGKDSEAWVPDSEE RLILREEFTSRMHQRFLDGKDGDFDYST VDDNPDFDNLDIVARDEEERYFDEEEPE DAPSPELDGD*WPPPPPPAPSPSPTRQLI PGLLSDPFSRGTS/AAVPHNPHTPPSHWV *SHLRQPPPLFLGFPSLPPCLLPLSLV SVWASFCLFLSFCLSPYPRSLFPVLWLAV SPFLPLSLCLRLCLHRRAQGESPLAGGQ LAGPFVAGSQFGSGADP |
| 4816 | 12867 | A | 5696 | 7 | 558 | GWLDLGLTKVC*NAEVPTCEWVRLMC MSVCASK/CGGGCGCLC/MASGHCECLG MCWSL*ACVFLSKNECLCVSLGTCQCL CLCVPVSHHLCIRVAHAASLCAMVCQC LCVDGWPMSPDRQGRPGWLDPAHLPSG SLALWVRVTEAFGLKTGCSGSALRVA GGLPSLLPFRLVKRTPGGQGAV |
| 4817 | 12868 | A | 5697 | 272 | 1146 | GFLGLEPLSSSPQVAWATVPLWAQLQ GGLAGSCLGQILAPGPSEARDWWASLA GP*ERVEGADRPWRFHLSSTEALVLAAG R/SKARASDPGRSSTLSLLHVLAKVEKRR VNLPRVLSMPPVAGTACHAYDREVHLR CELSPGYYLAVPSTFLKDAPGEFLLRVFS TGRVLSAIRAVAKNTTPGAALPAGEWG TGPIPG/CSWKFGIQTAGGHKNFASYPTN P/CVPLFGSPKGPGRVCVRITLHQHCRAIS DTEFHPIGFHIFQVPEGGRSQDAPPLLLQ DPLLSCVPHRVTPRR |
| 4818 | 12869 | A | 5698 | 281 | 535 | |
| 4819 | 12870 | A | 5699 | 1 | 1014 | |
| 4820 | 12871 | A | 57 | 1 | 1513 | |
| 4821 | 12872 | A | 570 | 961 | 1627 | LHPPAVAVIQNVRSRGRFHSPTLVVIPG NPRHSRTITLIKLLHGIIIVIGRVKFRHPG CGQAKFIFFTLRQNKPNVVSSTGRPKG VMVGQTAIVNRLLWMQNHYPITGEDV VAQKTPCSFDVSVWEFFWPFIAKLV MAEPEAHRDPLAMQQFFAEYGVTTTHF VPSMLAAFVASLTPQTARQSCATLKQVF VADLCREWQQLTGAPLHNGLCVFLMR |
| 4822 | 12873 | A | 5700 | 155 | 2916 | QQKAAGVLPKFGYGVFPWQRAGQQFQ TDKAKGLTFLGGKAVHLS*/HLEREQPPR FAQPGTYASRWKALEEMEKQREQVDR NIREAKEKLEAEMEAREHEQLMLMRQ DPGLALVSCMQGQSMRSRSPKKVFKHL YELNLTKLQSLGSRSLRWKDSPFWGEE AGGKRPLVSLALHRSPSLLLLFVPKHPS KGRPDCTVQSPKPTKSQLLDLRECISI HVGQAGVQIGNACWELYCLEHQIPDG QMPSD |

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| 4823 | 12874 | A | 5701 | 37 | 1542 | PREPTPPA/PPRLQRTTRTRRCGFTIDIKSF LKPGEKTYTQRCRLFVGNLPTDITEEDF KRLFERYGEPSEVFNRDRGFGFIRLAEQ NPWAEIAKAE LGRAPFLKSRPLRICFRL HMGAAFDCSRNLFSLLFFQLSCLEQAFS QFGSVEKAGVVVDDRGVPTGKIGFVEF ASKNLPATKRLWKRCDDGAFLLTTTPR PSPLWKPMEQFDDDEDGLAQRLLMHKTQ QYHKEREQPPRFCTWGHCLKFEYQSR WKA LDEMEEKQREQVDRNIREAKEKL EAEMEAARHEHQLMLMRQDLMRQEE LRRLEELRNQKLQKRKQIQLRHEEHRR REEDMIRHQKQEGLRQEQEGFKPNYM ENREQEMRMGDMGPRGAINMGDAFSPA PAGNQGPPPMGMNMNNRATIPGPPMG PGPAHGTRRSRKYGNSQ*QIMEQCTND RFPQGPPSQMGSPMGSRTF*NPLKHPM SGVGPVSGGPGGFRGSPGGNFEGPNN RRRY |
| 4824 | 12875 | A | 5702 | 81 | 334 | HNVHC*VPCGEVGSVIHCWWNGDNLI* PS*KVSWKYESRAFKTSRPLDPTPLLLGI QSK*/YNKGHKDLDIRILITALFVVTKKL |
| 4825 | 12876 | A | 5703 | 3 | 448 | WGPEP*/PTRPTLDEGPGCGCGCSPSLP MGPPRGRGPPTSMSLLCRWPGVPLGSP GCPPRARVKLFPHPGDVSTSPWAGHG AHQDP*GPVSGSESP/PPAGHWAPPASTS SPKIQAGL*PEGMRTAQPPSAVAGSPQG SFRHKEGWG |
| 4826 | 12877 | A | 5704 | 1 | 206 | GSL*SPSPRFKRFSCSLSSWDYKHVPP HLANFCIF*RDWVSPCWLGWSRTPDH LSWPPKVLGLPS |
| 4827 | 12878 | A | 5705 | 32 | 401 | AFDPKLPWNFRLCQVNRGISEWAGMS EMGMSDIQLSVGKLVAR/CWLQAE L*G* QFTKQER/CPSLTRSRWHGQPREGQAE PFLCAPPEGAPIGFLR*HHLRVQLAMAWI KFKMLGQSPLYI |
| 4828 | 12879 | A | 5706 | 252 | 415 | PFCRPPRADSVTKQER/CPSLTWIRWHGQ PQGGQAERPFLRAPPEGASTGFLRQHH |
| 4829 | 12880 | A | 5707 | 2 | 164 | FFLYLFLFLRWSL/DSVIQAGVQWHDN CSLQPLPPGFK*FSDCSTVLQGRQSETG LKYFFITV*EMESCSVIQAGVQWHDNLF PATASWVQVILRLLHCTPAWATE |
| 4830 | 12881 | A | 5708 | 1334 | 1706 | VRPHEGARAGPGGRGRGDPGLGARALP QPRVAVAGAACQPPSRLRHAGHRGPMV HAVGGSTFLGFRQ*LSSHSTRCQPSRD SVWGLQPHISLLHCPSRGSP*GPHPCHRL LPGHPGISHLL |
| 4831 | 12882 | A | 5709 | 57 | 376 | KRGSLSGCPRPRVQW/RKTALQLOPSKL PGLK*TFP/CLSLK*TGHTCAPLCPNFF VFLTYLIEMGLTMLPRLVSYFWPQVFP SLASQSTGITGVSHHALAWWSMQ |
| 4832 | 12883 | A | 571 | 803 | 1403 | FNRRILKINGLTREQTSGVQQQIRQALSA LPLPVNRLEEFDCREAWRKQAWLKD IESARLQHNQAYTEAMLTEYADFFRQVE SSPLNPAQARAVVNGEHSLLVLAGAGSG KTSVLVARAGWLLARGEASPEQILLGL VAKPLKRWTSGFANGYIPKTLPHARFMR /*ALHIIQQGSKKVPVSKLENDTACRHEL FIA |
| 4833 | 12884 | A | 5710 | 9 | 264 | PCPPNTIN/CPLGLRLPC/PPHLCPSLCLGK VGGP*KVPQTPSLGETELEQKKPPVPMMA SGWTGGRNGGWEKSLRGKERRVFSQEG FP |

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| 4834 | 12885 | A | 5711 | 124 | 770 | QYFPTATHGNVKSLLSGKASLKRHRV CCSCLFYIVQKQPKLNKTLFRQSYICDQT TFRKSKGIINIKFIFFFEMESRSVAQAGM QWRNLGSLQ/PPPPGFMPPLSCLSLSSWD YKRPPPCPANFFVLVETGFTVLARMVSI S*PCDLASTSQSAGITDVSHHAWHIKFK PEVTWRERGEEHVDRHIFRLDIRFTDT HFIKKELMRSDTL |
| 4835 | 12886 | A | 5712 | 2 | 232 | CLSLSS*YYGRMSRPANF*FLVETGFH HIGEAGLELLTLGDPPASASQGAGITGVS QRGQSLFAFLMSSTSFCK |
| 4836 | 12887 | A | 5713 | 1 | 242 | QAGVQWHDLGSLQPPPLGKQFSCSLP SSWDYRRVPPRLANFC/DFLVETEFHHV GQADLELRTSGNLPTSASQSAGITGVSH HA*PKVLGLQV |
| 4837 | 12888 | A | 5714 | 1 | 133 | ERLRYFRVEHLDQRLKAAENKFSY\CLM TWLKCWFCEKFKFLNRNAYIMIAIY GTNFTCSARNAFFLLMRNIIRVAVLDKV TDFLLGKLLIVGSGVLAFFFTHRIRI VQDTAPPLNYYWVPILTVIVGSYLIAHGF FSVYGMCDTLFLCFLEDLERNDGSAER PYFMSSTLKKLLNKTNKKAES*RLRYF RVEHLDQRLKAAENKFSYVPHDLAQMR LLVPGEVHQIP |
| 4838 | 12889 | B | 5715 | 166 | 969 | MGSACIKVTKYFLFLNLIFFILGAVILGF GVWILADKSSFISVLQTSSSSLRMGAYVF IGVGAVTMLMGFLGCIGAVNEVRCLLGL YFAFLLLILIAQVTAGALFYFNMGKLKQ EMGGIVTELIRDYNSREDSLQDAWDYV QAQVCCGWVSFYNNWDNAELMNRPE VTYPCSEVKGEEDNSLSVRKGFCEAPG NRTQSGNHPEDWPVYQEGCMEKVQAW LQENLGIILGVGVGAJIELLGMVLSICLC RHVHSEDYSKVPKY* |
| 4839 | 12890 | C | 5716 | 300 | 347 | MIHLPRPPKVLGLQA* |
| 4840 | 12891 | A | 5717 | 316 | 797 | APALPQPTGLAASSHMVQVPLWICLKLS HSKSRNPQLFF*VFQFLRRSL/SSVPQAG VQ*HDLSSLQPP/PPGFTPFSCSLPSSWD YRCPPRPAPKFFLYF**RRGFTMLARMV SIS*PRDPPASASQSAGITGVSHRARPPP QFFIQLPLYNIHTLEGR |
| 4841 | 12892 | A | 5718 | 2 | 519 | WHPQSDVQAEVQWRDLGLLQSSPPAGF TLFSCSLSSWDYRRPPRPG*FLYF**R RGFTVLARMVIS*LHDPPALASQSAGIT GVSHRTRPGADL*PRVQKPRASLGG*NH MCNMKSLPTGQTRLNKGRRLGHFDPHW RWKETPGL*CFHGNFCGALKAGRAHLD GQGR |
| 4842 | 12893 | A | 5719 | 1 | 663 | |
| 4843 | 12894 | A | 572 | 3 | 1642 | |
| 4844 | 12895 | A | 5720 | 1 | 1561 | MATSTGRWLLRLALFGFLWEASGGLD SGASRDDDLLPYPRARARLPRDCTRVR AGNREHESWPPPATPGAGGLAVRTFVS HFRDRAVAGHLTRAPELRTFSVLEPGG PGGCAARRRATVEETARAADCRAQNG GFFRMNSGECLGNVVSDERRVSSSGGLQ NAQFGIRRDGTLVTGYLSEEVLDTENPF VQLSGVVWLIRNGSIYINESQATECDET QETGSFSKFVNVISARTAIGHDRKGQLV LFHADGHTEQRGINLWEMAEFLKQDV VNAJNLDDGGGSATFVLNGTLASYPSDH CQDNMWRCPQVSTVVCVHEPRCQPPD CHGHGTCVDGHCQCTGHFWRGPGCDE LDCGPS*LAAQHGLCNGSTGLSAVDAG WTGSNCSEECPLGWHGPGCQRPCKCEH HPCDPKGTGNCVSRVKQCLQPPEATLR AGELSFTRTAWLALTALAFLLISIAA NLSLLSRAERNRRLHGDYAYHPLQEM |

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| | | | | | | NGEPLAAEKEQPGGAHNPFKD |
| 4845 | 12896 | A | 5721 | 1119 | 2008 | ALHPPAQGELFCDYFKDPSWSEGPQSPP LTRLAPHPQTQCTELSGGRRGS AVLEEC VPTPASAHLAASPAEAGTAGVWR*RHH F/HSTGLLGPR*LSMSLLMS*CKAGRCPP GEDCPRPLPGCSLSPLERKLCFSSA*GPA SFLGGLTAKASGCSLSLRP/HSHIQGHGL WEKL*VPARRAGGGVCFKSAPHLQSL** KPSSKASKREG*Q*TLPSATIGELPFK*HA PKHLCNAQGFLCKIH*HHK/QTANAIA* GGPGSLEGLRRPGSPSSLGVGSGKTEV NSQNCRHLGREGVS |
| 4846 | 12897 | A | 5722 | 3 | 444 | FFFFLRLQSL/NSVI*AGVQ/QPLPPEFKRL SCLSLPSSWDYRCAPAHSAFNCIFSKD/M GFTMLTRLVSNWQQ/CELPTLASQSGIT GVSHHTQPIYHFIFVETEFHHVAQAGVK /PPSLK*SSRLSLPKQWNYSHEPLYALF NETFFFK |
| 4847 | 12898 | A | 5723 | 1 | 6738 | |
| 4848 | 12899 | B | 5724 | 107 | 467 | MRLHETLKQCQDLKTEKSQMDRKNQL SEENGDL SFKLREFASHLQQLQDALNEL TEEHSKATQEWLEKQAQLEKELSAALQ DKKCLEEKNEILQGKLSQLEEHLSQLQD NPPQEKGEALX* |
| 4849 | 12900 | A | 5725 | 149 | 577 | GLLSTRPISCRHTL*GPLQSSWEYMDVP WDLRASEGNGKLLYSARDCTLQIHSVF QKLDVEEPDSANSSFYSTRSAPASQASLR ATSSTQSLARLGSPDYGNSALLSLPGYRP TNRSSARRSQAGVSSGAPPGE GTTGTYY |
| 4850 | 12901 | B | 5726 | 24 | 219 | MPRSSRTKSCRSSCGAWSSCMKENKELR AEAERLGHELQQA GLKTKEAEQTCRHL TAQVRS LGGTX* |
| 4851 | 12902 | A | 5727 | 272 | 683 | |
| 4852 | 12903 | A | 5728 | 1 | 406 | |
| 4853 | 12904 | A | 5729 | 211 | 5508 | IWCLFPLSVHMG LIYSQKCLEEKNEILQG KLSQLEEHLSQLQDNPPQEKGEVLGDVL QLETLKQEAATLAANN TQLQARVEMLE TERGQQEAKLLAERGHFEEKQQLSSLIT DLQSSISNLSQAKEELEQASQAHGARLT AQVASLTSELTTLNATIQQQDQELAGLK QQAQEKQAQLAQTQQEQASQRLRHQ VEQLSSSLKQKEQQLKEVAEKQEA TRQD HAQQLATAAEEREASLRERDAALKQLE ALEK |

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| 4854 | 12905 | A | 573 | 114 | 5270 | SARSASFRPGRPAARRPKCSHPLVPDGV PECKCVHPASTNFPRTSTAARHSHHN DGSTSTMGRWQI/VGYLVQSGLPLDT SALQAQLRETLPPHVMPEVLLQLPL NANGKLDKALPLPELKAQAPGRAPKA GSETIIAAAFSSLLGCDVQDADADFFALG GHSLLAMKLAAQLSRQVARQVTPGQV MVAHVAKLATIIDAEDSTRRMGFETIL PLREGNGPTLFCFHPASGFAWQFSVLSR YLDP |
| 4855 | 12906 | A | 5730 | 111 | 407 | NLLRTMIFWFGFEDRVWLCCPVLATSV LTATS/TFPGFKQFSCSLSSWDYRCIPP HPGNLWYF**RQFTMLARLDSNSGPQA IHPPQPPKVLGLHV |
| 4856 | 12907 | A | 5731 | 3 | 613 | GLRALRRGQGLPGL*CCSRPQSPRAQG HPSMGGPMQVRTPPRGMASVGPQSYGG GMRPPNSLAGPGLPAMNMGPGVRGPW ASPSGNSIPYSSSSPGSYTGPPGGGGPPGT PIMPSPGDSTNSSENMYTIMNPIQGAGR ANFPLGPGPEGMAAAMSAMEPHHVNGS LGSGDMDGLPKSSPGAVAGLSNAPGTPR DDGEMAA |
| 4857 | 12908 | B | 5732 | 134 | 471 | MYAKGGKGSAPVSDSQAREKLALVYVE YLLHIGAQKSAQTFLSEIRWEKNIMPSPG DSTNSSENMYTIMNPIQGAGRANFPLG PGPEGMAAAMSAMEPHHVNGSLGSGD MDG* |
| 4858 | 12909 | B | 5733 | 223 | 692 | MEPSPRAQGHPSMGGXMQRVTPPRGMA SVGPQSYGGGMRPPNSLAGPGLPAMN MGPGVRGPWASPSGNSIPYSSSSPGSYTG PPGGGGPPGTIPIMPSPGDSTNSSENMYTI MNPIQGAGRANFPLGPGPEGMAAAMS AMEPHHVNGSLGSGDMDG* |
| 4859 | 12910 | B | 5734 | 228 | 292 | XLARDDHERVMGRQPRASLRA* |
| 4860 | 12911 | A | 5735 | 1 | 1753 | MYAKGGKGSAPVSDSQARENLSAFQAA TELTSLDRLALVYVEYLLHIGAQKSAQT FLSEIRWEKNITLGEPPGFLHSWWYGL GCCGVFWDLYCAAPDRREACEHSGEAK AFQDYETPERPAHRHGNAGRAGSSSGMI DVGGSSDPQILRPTTPVCSLTNASSLSHG AGHLQRGGGTPQSAAAAPSPVMGSMAP GDTMAAGSMAAGFFQGPPGSQSPHNP NAPMMGPHGQPFMSPRFPGGPRPTLRD GSQPPAGPPWVPSPPSGAMEPSPRAQG HPEHGRPNARGVTPPRG/MGPAWGPRA YGGGMRPPNSLTRPRACLPMNMGPRK FVGPWAQPPVEYSIPYSSSSPGSYTGPP GGGGPPGTIPIMPSPGDSTNSSENMYTIM NPIQGADRANFPLGPGPEGMAAAYGA GMEPHHVNGSLGSGDMDGLPREFFQAP VAGLSNAPGTPRDDGEMAAAGTFHAPS SQSENYSPGMTMSRVNWAAAPGALCG PRLPRRCLRAKGLKVTPSGTLDLAN QGLPMLGGPTRKTLTILKTQGPREFFS VWTLPAICILVPERKALWGGPSSPGRQG GGAH |
| 4861 | 12912 | B | 5736 | 315 | 458 | NGPSRTQQPSLTDVLYCPEAIVSLVGLR RLAACQEHKRAPEVYVFT* |
| 4862 | 12913 | A | 5737 | 202 | 402 | |
| 4863 | 12914 | A | 5738 | 1 | 3156 | |

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| 4864 | 12915 | A | 5739 | 1 | 1470 | MAPEENAGTKLLQSFERRFLAARTLRS FPWQVGGGASGEACGACGSPGADGMG LPAETPGAPATEGSHSALPTHSIACFNVP VNAPLRFSLPSTRSLEAKLRDSSDSELL RDILQKHEAVHTELLDELYEALAETLMA KESTQGHWSYLLPRYPSCDVKVTPRKA RSHSPSTAIHSGTTGLVTWDAARYLAE WAIKNLAAFTNRTVLELGSAGLTGLSI CKM/WPPDIIHLHDCHSRVLEQLRGNVL LNGLSLEADITANLDSPRVTVAQLDWDV ATVHQLSAFQPDVVITADVLYCPEAIVSL VGVLRLAACWEHQWAVEVYMAFTVR NPETCQLFTTELAPSTCEGVLSLSLTDK NTRTHRGQETPELPQIAARPPGFSFTVH PSPPLPPDFAPAPPEHSPSWQPCAKMHPQ QPLPAHRDMDDPVVHVGVQPVNYRANK QASTRRHTGFHDRVPHNLAQEAGQAWG SGLSSQHFRRLRQED |
| 4865 | 12916 | A | 574 | 1 | 2967 | |
| 4866 | 12917 | A | 5740 | 2 | 413 | |
| 4867 | 12918 | A | 5741 | 3 | 231 | |
| 4868 | 12919 | A | 5742 | 83 | 1503 | SWNTPYNHWATKQ/LSSHYSRGGAKYE GEAVKQSLVESYTHPNSNETERSANIDT VMNWFTKEDFDFVTLCYREPNDVGHFR RPEAENRKLMIQIDRTIRPWDDHREET QCQDPLSNYIKFMDLVKFDIVGYGGFG MPLPKLGQEEALYQALKNAYPHLHIYK KEGFPEHFHLAKHDRVLPVIMYANFGYS INGISLLYFYTHLCDKYFNHFFHEPLSL WRAQTTPSLSHRYISLVRHMDATNLDS EAQLPGSPYPDSAPGPANLDSTQDLPQR RLSWPYPRPRPPNAHGPALQAPRTLLL TLPPGPAPSLPPRTALGPPPLQSRPGFRPV SRQRCGPAHFMAPEENAGTELLQSFER RFLAARTLRSFPWQGGGGRAERPAGLA GVQGGQTGWVSVLKPPALLPREFLGSPRS GPRDPVPVPGA WPKSLAPLLPRELAAED EGVSTALGGQTRARCGVQFTIITTF |
| 4869 | 12920 | A | 5743 | 266 | 477 | DFSLSRPHGA*KQN*ETHQILSCC/GDILH KTVK/HSCVCEAPAVRQICPVLRLRTHQK ARGCPHRAFGRAV |
| 4870 | 12921 | A | 5744 | 148 | 592 | SHVALGQLGWLTRAVRSSWRWELCVSS TGSGLPAPFSLKQPKSCRCW*EEVKTGSC VGISHWQTST/VFPQAVFHLPPVLLPRSL ACLSCPRGCAQIR/CQ*TPPYLPFIILTYS FGMLSSTVLIRHILETNKKEKSLAAEGV RHLQVS |
| 4871 | 12922 | A | 5745 | 164 | 667 | ERGTYICQITTSLYRAQQIQLNIQASPKV RLSLANEALLPTLICDIAGYYPLDVVVM WTREELGGSPSPSLWSSFSKPQAKALAG TYSISSSLTAEPG/RLQVPLYTCQVTHISL EEPLGASTPGCPTRAENSLGSHLCQQSLP SCTDVPWGFDRDQAPNRTWAASG |
| 4872 | 12923 | A | 5746 | 1 | 790 | VEELSKKLADSDQASKVQQQKLKVGQL GEVWWPLDKGGKLFSLWGRGGLVYK WFLLIYKISYATGIVGYMAVMFTLFLGN LLFKIKPEDAMDFGISLLFYGLYGVLER DFAEMCADYMASTIGFYSESGMPTKHL DSVCAVCGQIFVDVSEE/EDH*EHRC/CFHEFCIRGWCIVGKKQTCPYCKEKVDL KRMFSNPYPLLGSLGVCCKKVLASVT CIWVLLGPSLLPPTRTCTMNNKKIMKV MMRIKRMMDTMTAS |

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| 4873 | 12924 | A | 5747 | 1 | 1005 | FRGRAVKMAAVVEVEVVGGAAGEREL DEVDMSDLSPEEQWRVEHARMHAKHR GHEAMHAEMVLILIALTLVVAQLLLQW KQRHPRSVMVTLFQMWVPLYFTVKL HWWRFVLVWILFSAVTAFTFRATRKPL VQTTPLRVYKWFLLIYKISYATGIVGYM AVMFTLFGNLNLLFKIKPEDAMDFGISLLF YGLYYGVLERDFAEMCADYMASTIGFY SESGMPTKHLSDSVCVCGQQIFVDVSE EGDHETTYRLSCNHVSHEFCIRGWCIVG KKQTCPCYCKEVDLKRMFSPNWERPHV MYGQLLDWLRYLVAWQPVIIGVVQGIN YILGLE |
| 4874 | 12925 | B | 5748 | 99 | 236 | XTTSTSTVTVTAPGPAATGSPVKKHRP LLPKETAPAVQRVVWNSSX* |
| 4875 | 12926 | A | 5749 | 1 | 783 | |
| 4876 | 12927 | A | 575 | 1882 | 3402 | LDASFWIPPKATQGMTWIFTFPPSSPSYNS S/CYAGWLKGSAPLQLSQPHHTAYIIFTS GSTGRPKGVMVGQTAIVNRLWMQNH YPLTGEDVVAQKTPCSFDVSQFFAEYGV TTTHFVPSMLAAAFVASLTPQTARQSCAT LKQVFCSGEALPADLCRVWQLTGAPL HNLYGPTEAAVDVSWYPAFGEELAQVR GSSVPIGYPGYLGRPDLTASRFIADPFA PGERMYRTGDVARWLDNGAVEYLGRS DDQLKIRGQRIELGEIDRVMQALPDVEQ AVTHACVINQAAATGGDARQLVGYLVS QSGPLDTSALQAQLRETLPPHMPVVL LQLPQLPLSAKAGCPAAQVPRVAQVRV CAVLEDLGDIRESEGERKQEADAVLGTQ DTPRVTSQPNGLLLKIEPQENVKIEGQHQ GLVWLCVAASPVLVRVTREKEEKKKEE GNNMRFTSLVLSVLVNIVRALEKKVLDI MFNNCRTGVQAITLSHRRALAIAlAR YIKSALYDG |
| 4877 | 12928 | A | 5750 | 1 | 1626 | |
| 4878 | 12929 | A | 5751 | 1 | 542 | CGWNTGYCD/YPCQQAHWPEHIKSTQS ATALQQGADVEVNTEPLNKSSQSSSST QSAPSETASASKEKETSAEKSKESGSTL DLSGSRETPSSILLGNSQGSVSKRCDKAT LLCPNHHRPPAAPQLPRPEVPFPEL*NSR LSPPVFKKKGIRRVPIPTSTSTKSLLPKE SRLDTFWD |
| 4879 | 12930 | A | 5752 | 1779 | 3628 | MEISEDVYTAVGHSDESDSEKSDSSDSEF ISDDEQKSKDEPEDTEDKEGCQMDKEPS AVKKKPKPTNPVEIKEELKSTSPASEKAD PGAVKDKASPEPEKDFSGKAKPSPHPIK DKLKGKDETDSPVHGLDSDSENELVI DLGEDHSGREGGRKNKKEPKESPKQDV VGKTPPSTTVGSHSPETPVLTRSSAQT AAGATATTSTSTVTVTAPAPAATGSPV KKQRKLIPKE/TAPA/VQVRVELIK*SF KRPPKSGTCRRCSVSSSSSSKTSSSHQS SQGTRYQTRQAVKAVQKKEITQSPSTSTI TLVTSTQSSPLVTSSGSMSTLVSSVNADL PIATASADVAADIAKYTSKLMDAIGT MTEIYNDLSKNTTGSTIAEIRRLRJEIEKL QWLHQELSEMKNLELTMAEMRQSW EQERDRLIAEVKKQLELEKQQAQVDETKK KQWCANCKKEAIFYCCWNTSYCDYPCQ QAHWPEHMKSTQSATAPOQEADAENV TETLNKSSQSSSSTQSAPSETASASKEK ETSAEKSKESGSTLDLGSRETPSSILLGS NQGSDHSRNSKSSWSSSDEKRGSTRSDH NTSTSTKSLLPKESRLDTFWD |

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| 4880 | 12931 | A | 5753 | 2 | 1711 | RSEDEKSDSSDSEYISDDEQKSKNEPED TEDKEGCMQMDKEPSAVKKPKPTNPVEI KEELKSTSPASEKADPGAVKDKASPEPE KDFSEKAKPSHPJKDKLKGKDETDSP VHLGLDSDSESELVIDLGEDHSGREGRK NKKEPKPSPKQDVVGKTPPSTTVGSHS PPETPVLTRSSAQTSAGATATTSTSTV TVTAPAPAATGSPVKKQRPPLPKETAPA VQR\SCGTSSTVQQKEITQSPSTSTITLVT STQSSPLVTSSGSMSTLVSSVNADLPIAT ASADVAADIAKYTSKMMDAIKGTMTEI YNDLSKNMTTWKAQLAEDSQGLRIEIEKL QWLHQQL\SEMKNLELTMAEMROSL EQERDRLIAEVKKQLELEKQQA\VDETKK KQWCANFKKEAIFYCCWNTSYCDYPCQ QAHWPEHMKSTQSA\YCSSSRKADAE\ VNTETLKLSPSQGSS\STQSAPFRKRPAP SKEK\ETFSLRKAKESGSTLDL\SGSRET PS SILLGSNQSGSDHSR\SNKSSWSSSDEKRG S\TRSDHN\TPSTQHGRSLLPGKESRAGTP FLGTSK |
| 4881 | 12932 | A | 5754 | 1 | 191 | MQK*ITAWAPAPMKIKIIASPERKYSVWI GGSIWPQLST\FQQMWISKQEYDESGPSI VHRKCF |
| 4882 | 12933 | A | 5755 | 2 | 1203 | LSRRCQLSHSVLPPLRRRVSLPVAMEEEI AALVIDNGSGMCKAGFAGDDAPRAVFP SIVGRPRHQGMVMGMGQKDSYVGDEA QSKRGILTLKYPIEHGIVTNWDDMEKIW HHTFYNELRVAPEEHPVLLTEAPLNPKA NREKMTQIMFETFTNPAMYVAIQAVLSL YASGRTTGIVMDSGDGVTHTVPIYEGYA LPHAILRLDLAGRDLTDYLMKILTERGY SFTTTAEREIVRDIKEKLCYVALDFEQEM ATAASSSSLEKSYELPDGQVITIGNERFR CPEALFQPSFLGMESCGIHETTFNSIMKC DVIDRKDLYANTVLSGGTTMYPGIADR MQKEITALAPSTMKIKIIAPPERKYSVWI GGSIASLSTFQQMWISKQEYDESGPSIV HRKCF |
| 4883 | 12934 | A | 5756 | 3 | 412 | SRFPEGLFQPPFPGMKSCGIHETTFHSH/ IKFDVAIRKDLYANTLLPGGNHQVSGAL LTGMQKEIHAPAAQATLRFKIIAPPGSAS TRW/VGVSIGLASLSTFQQMWISKQE\ YDESGPLHSSTAKCFLNGLSQIA |
| 4884 | 12935 | A | 5757 | 1 | 2297 | MGRDWSNLESLEEDRKMRESLEHARDL LNCCDQNAHDHMDSEVQAEV\SEGDEE LIGKWSKAYCHRCEQKDDLKWELIFKRE AEHKSLEILQPDHVVEKKNPGGGRNQST SSSWVGTVAEITIEAVKCKIQVLQQA DDAEERAVERSQREFREERRARE\QAEAE VASLNRRIQ\LVVEELDRAQERLATALQK LEEAEK/SLADESERRY*RLFENRALKRL KEKIGTSREIQLK\EAKHIAEEVADARKYEE VARK\LVIEGDLERTEVERA\ELAESRCR EMDEQIRLMDQNLKCLSAAEEKYSQKE DKYEEEEIKILTDKLKEAETRAEFAERSVA KLEKTIDDLEDNTNSTSGDPVEKKDETPFG VSVAVGLAVFACFLSTLLLVLNKCGRR NKFGINRPAVLAPEDGLAMSLHFMTLGG SSLSPTEGKSGSLQGHIIENPQYFSDACV HHIKRRDIVLKWELGEGAFGKVFLAECH NLLPEQDKMLVAVKALKEASESARQDF QREAELLTMLQHQHIVRFFGVCTEGRPL LMVFEYMRHGD\LRFLRSHGPDAKLLA GGEDVAPGPLGLGQLLAVASQVAAGMV YLAGLHFVHRDLATRNCLVGGQLVVKI GDFGMSRDIYSTDYRVGGRTMLPIRW MPPESILYRKFTTESDVWSFGVVLWEIFT YGKQPWYQLSNTAIDCITQGRELERPR |

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| | | | | | | ACPPEVYAIMRGCWQREPSNATASRMC TPGCKPWPRHLLSTWMSWARGPAQGLG VVSRTGACQHP |
| 4885 | 12936 | A | 5758 | 3 | 636 | WAWNQAEEVASVNGRIQLVEELDCA QERLATALQKLEEAGKAADESERGMKV IENRALKDEEKMELQEIQLEAKHIAEEA DRKYEEVARKLVIIIEGDLERTEVERAELA ESRCREMDEQIRLMDQNLKCLSAAEEK YSQKEDKYEKEIKNLTKLREAETRAEF AERSVAKLEKTIDDLEDKLKCTKEEHL TQRMOLDQTLDDL NEM |
| 4886 | 12937 | A | 5759 | 1 | 239 | QCCSGGTHGNPAIGDRMQKQILPWAPA QMKIRFMAPPERKYSVWIAAPILASLSTS SRMWISKQEYDESGPSIVHRKCF |
| 4887 | 12938 | A | 576 | 22 | 413 | |
| 4888 | 12939 | A | 5760 | 3 | 1458 | ADPPPVHTRRQLTMDDDDIAALVVDNGS GMCKAGFAGDDAPRAVFPISVGRPRHQ GVMVGMGQKDSYVGDEAQSKRGILTLK YPIEHGIVTNWDDMEKIWHHTFYNELRV APEEHPVLLTEAPLNPKANREKMTQIMF ETFNTPAMYVAIQAVLSLYASGRTTGIV MDSGDGVTHTVPIYEGYALPHAILRLDL AGRDLTDYLMKILTERGYSFTTTAEREIV RDIK/EEAVLRRPGLRARDGHGVASSSSLE KSYELPDGQVITIGNERFRCPEALFQPSFL GMESCGIHETTFNSIMKCDVDIRKDLA NTVLSGGTHQFPLPCRPGC*KKITALEP ATMKIRIIAPPEAQSTPLWNRGAPILAS LVHLPKMWQDQKSREYDESGPLPFVHR KICFF |
| 4889 | 12940 | A | 5761 | 171 | 324 | |
| 4890 | 12941 | A | 5762 | 3 | 383 | |
| 4891 | 12942 | A | 5763 | 2 | 314 | FFFFISALKALFAFLQILLFQVNVLRITAH IVISFINLLSVTPSKAFLLLAFIFCREDYSF TAYATISYLKIGPKANLLNNEAYVITMQ VTKSTQNSFRVNGY |
| 4892 | 12943 | A | 5764 | 1 | 176 | MRTFALLTAMLLLV/HAQAEPLQARAD EAAAQEQPGADDQEMAHFTWHESAA LPLSA |

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| 4893 | 12944 | A | 5765 | 1 | 2674 | GKHKLLSTGPTWPWSIREKLCLASSVMR SGDQNWVSVSRAIKPFAEPGRPPDWFSQ KHCASQYSELLETTETPKRKRGEKGEVV ETVEDVIVRKLTAERVEELKKVIKETQER YRRLKRDAELIQAGHMDSRLDELCNDIA KKKLEEEAEVKKRATDAAYQARQAVK TPPRRLPTVMVRSPIDSASPGGDYPLGDL TPTIMEEATSGVTPGTLPTVTSFPGIPD TLPPGSAPLEAPMTPTVDDSPQKKMLGQ KATPPPSPLLSELLKKGSLLPTSPRLVNES EMAVASGHLNSTGVLLLEVGGVLPMIHG GEIQQTPTNTVAASPAASESVSQATIVMM PALPAPSSAPAVSTTESVAPVSQPDNCVP MEAVGDPHTVTVMDSSEISMIINSIKEE CFRSGVAEAPVGSKAPSIDGKEELDIAE KMDIAVSYTGEELDFETVGDIAHEDKV DDHPEVLDVAAVEAALSFCENDDPQSL PGPWEHPIQQUERDKPVLPAPEMTVKQE RLDFEETENKGIHELVDIREPSAEIKVEPA EPEPVISGAIEIVAGVVPATSMPEPRLSQ DLDEELGSTAAGEILEADVAIGKGDETPL TNVKTEASPESMLSPSHSGNPIDPLEAE TQHKFEMSDSLKEESGTIFGSQIKDAPGE DEEEDGVSEAASLEEPKEEDQGEGLSE MDNEPPVSESDDGFSIHNLQSHLAD SIPSSPASSQFVCSQDQEAIAQKIWKK AIMLVWRAAANHRYANVFLQPVTDIA PGYHSIVQRPMDLSTIKNIENGLIRSTA EFQRDMLMFQNAVVMYNSDHDVYHM AVEMQRDVLEQIQFLATQLIMQTSSEGI SAKSLRGRDSTRKQDASEKDGGRGR CAIEADMKMKK |
| 4894 | 12945 | A | 5766 | 1 | 419 | YANVFLQPVQDDIAPGSPSIGQRVPMDL ST/KKNI*NG*SEAPADFQR*HMLMFQ LLMYHSSDHYFYHIAVEMQRDVLEQIQ QFLATQLIMQTSSEGISAKSLRGRDSTR QQDASEMDGGTRGRVCAIEADMKMK K |
| 4895 | 12946 | A | 5767 | 2 | 111 | ISAKSARGRDSTRKQDASEKDSVPMGSP AFLSLF |
| 4896 | 12947 | A | 5768 | 3 | 2884 | GKHKLLSTGPTWPWSIREKLCLASSVMR SGDQNWVSVSRAIKPFAEPGRPPDWFSQ KHCASQYSELLETTETPKRKRGEKGEVV ETVEDVIVRKLTAERVEELKKVIKETQER YRRLKRDAELIQAGHMDSRLDELCNDIA TKKKLEEEAEVKKRATDAAYQARQAV KTPPRRLPTVMVRSPIDSASPGGDYPLGD LPTIMEEATSGVTPGTLPTVTSFPGIP DTLPPGSAPLEAPMTPTVDDSPQKKMLG |
| 4897 | 12948 | A | 5769 | 3 | 627 | PRGENRFKAQPEWRKTPCQMMLSQSTF RKTYIGKIFTILALPYVGKELNMIML PDETTDLSTVEKDSHAKFVWTSLDM MAEEEVKLSIPRFKLEESYDMESVLRNL GMTDAFEAGARANFSGMSQTDLSLVQR SCTKSICGRSNEGRPREAASPPKVAIWM MRCAVFCPPPPAPDHPFLFIQHRKTN GULFCGRFSSP |
| 4898 | 12949 | A | 577 | 1 | 2148 | |
| 4899 | 12950 | A | 5770 | 3 | 626 | YNLVTR/LAVLSFEKDDDHNGHIDFITA ASNLRAKMYSEPADRFKTKRIAVKJILV KPTTTGTVSGLVCFEMIKVTGGYPFAAY KNCFLNLSHS/IFVVFTETTEVRKTKIRNG ISFTIWDRTVHGKEDFTLLDFINAVKE KYGIEPTMVVQGVKMLYVPVMPGHAK RLKLTMHKLVKPTTEKKYVDLTVSFAPD IDGDEDLPGTSK |
| 4900 | 12951 | A | 5771 | 92 | 265 | SFELFADKVPKTA/WLDGKHVVFGKVKE GMNIVEAMERFGSRNGKTSKKITADCG QLE |

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| 4901 | 12952 | A | 5772 | 1 | 1310 | GNSPPSELKWKAKSEDLRHRGLKAQAEI KGSTQQIGFTTDPMARSSPYPTDVARV VNAPIFHVNSDDPEAVMYVCKVAAEWR STFHKDVVVDLVCYRRNGHNEMDEPMF TQPLMYKQIRKQKPVQLQKYAELLVSQG VVNQPEYECVSMHGVRNKPSYNSTKSS MDGLILHPATGLVFVLSKQCEEIHQPVV WTCEQREAEENATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVGRAAACGNGA OKVGRGRENFPCL*ATGEKIGFWL*GVP CFHRLFPRVLCVQGGELQQRH*WPLVG KPHSMGKKI*KIEELPSLKHTGSPGILSP WQNAGPQTNGFPFSICTAKTNEWLEW PSHVVFVHK*KEGWMNIVEAHWSRFGS RNGKTQQRSPFADCGQLLISLTCVFILT TKIISFCRLRRAPLQPHLLAVS |
| 4902 | 12953 | B | 5773 | 47 | 204 | XQHTFCKRCGVQSFYTPRSNPGGFGIAP HCLDEGTVRSMVTEEFNGSDWEKA* |
| 4903 | 12954 | A | 5774 | 2 | 402 | CGDRGALRPPSCAGRSGPGRPPRPPRP LPWHPAPPAHGAPLARPGARARRSEKPP SEKPRLRSSPRAQEEGPGEPPPELALLP PPPPPPPTA\PRRPRRP\PGGRAAGALG DVPEAAEAYLERVPPSSC |
| 4904 | 12955 | A | 5775 | 2 | 241 | FSCLSLKSWDYRALPPSPANLFLVETG FHHVQGASLKLTSQDPPASASQTVGIT GMSHHAWPVSSFYIWSHWAPRNS |
| 4905 | 12956 | A | 5776 | 22 | 643 | VVEFPVLTMAATSGILSALGNFLAQMIE KKRKKENSRLDVGGLRYAVYGFFFTG PLSHFFYFFMEHWIPPEVPLARVRRLLL DRLVFFAP\AFLMLFLLIMNFLEGKASVT FAAKMRGGFWPAAEDETCTRVWTPLOF ININYPVFESSGCFGQPGQLFWYAYL ALLGEVTRWENIRCTCGRGSGGLHPPK REQKPIQSGCH |
| 4906 | 12957 | A | 5777 | 23 | 448 | ELESRSVTQAGVQWCDLGSILQPPPL/SF KQFSLSLLSSWDYRHHVPPCANVCILVE MGLVGQAGLELLISSDTPISVSQSAGIUSV SHGTQPHIGNFLEQLKVVLCTYTSFLCFT KSSTVKHIQLIILITLRNTKNKARI |
| 4907 | 12958 | A | 5778 | 25 | 396 | ISGRSTFSLFSRQGLSALSPRE\CSVAISA HCNLRLPSSNAGTTGA*HHTRLILYF/LA EMGFHHVGQAGFEVLTSSNPPASASTSA RITGMSNRT\GHLFNHP*MCYKYRCGS LAGRGGSRW |
| 4908 | 12959 | A | 5779 | 80 | 460 | YISLNVTTHLIFFFFLRQGL\CSVTQAGV QWCNLGSLQPLPPRFKNWDYRCVTPH LANFVFLVEMGF/LPASASQSAGITGVSH CTQLGVFICICYGSSHGVRQSWHQFCSS KLLVKSGRVGVGLLG |
| 4909 | 12960 | A | 578 | 222 | 666 | SLCFCFLEVSLPACQETYGKSPFWLSIPF EDIARNLMKRTVCAKSIFELWGHGQSPE ELYSSLKNYPVEKMVPFLHSDSTYKIKIH TFNKTLTQEEKIKRIDALEFLPFEGKVNL KKPQHVFVLEDYGLDPNCIPENPHNIYF GRW |
| 4910 | 12961 | A | 579 | 1664 | 1844 | WQKLLFLFGTESCSVARVGVQWRHLSS PKPPPPGSSNS/PASASRVATGAHLHAR LIFVFL |
| 4911 | 12962 | A | 5792 | 16 | 301 | IFASTAPKRSWARLGPPQILVSVATKASF GAPTIPSR\PGPQSVFANSDLFPAPPQIPSR PVRIPP\GIPPGVPRRPPAAPSRPTIIRPAEP SLLD |
| 4912 | 12963 | C | 5793 | 78 | 209 | MSVFXXXXXXXXXXXXXXXXXXXXXNEET NHPLGVVYRLSDSTQYI* |
| 4913 | 12964 | A | 5794 | 119 | 231 | |

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| 4914 | 12965 | A | 5795 | 69 | 909 | EWCLLSPEGHTFHLLIWGITELKTKRRGR KPSRPPMCYGKCARCIGHSLVGLAILCI AANILLVYFPKGETKNASVNLHLSRVVWF FSGIVGRL/VLLMLPAQHFLVHWGLEQD DCACGCCGHENCGKRCAMLSSVIGWLS IGIAGSGLLWSIV/VQPLGLARKDPLCLD S/LSGQWKLOPLPSTEGPVTFWITSTWSE CTEPKHIVKWNVSLFSILLALGGPELILC LIQVINGS/VLGGICG/FCCSHQQYGLAK RTNPGTEPOSFLYFHCNLSYLHLYSIC |
| 4915 | 12966 | A | 5796 | 1 | 200 | RGPVLLDTS/TWARCNEPKPI/VEWNDTL FSN/LLASGGIEFILCLIQVINGVLGGICGF CCSHQQQYDC |
| 4916 | 12967 | A | 5797 | 2 | 424 | RLSLTLVAQAAVQWHNLGSLQPPPPGFK RFSCLSLPSSQDHRHTPPCPANFSVFLVE TRLHHAGQAGLKLPTSG/DTSSASQSAR ITGVSHRARCWDSNSTIFLGLANSNWR NVFLIVGGERIKGKHTHFNTHSMSEFEE |
| 4917 | 12968 | A | 5798 | 46 | 626 | |
| 4918 | 12969 | A | 5799 | 1 | 1004 | MWLILAGLAWAGLWVSDGLKDVLVMA KGKSRRGKSAPKHIMSLGPLLMIAFAICH FASVMGFHYLEVNLRLQQCFKYLIETA FAVLVQSVLRIYSSRIWDKTSLECLKVLT GHTGSVLCLQYDERVIVTGSSDSTVRVW DVNTGEVLNLIHHNEAVLHLRFSNGLM VTCCKDRSIAVWDMASATDITLRRVLVG HRAAVNVVDFDDKYIVSASGDRITKNR DKAEVAYTNLVWSTSTCEVRTLNGHK RGIACQYRDRLVVS GSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGA Y/DMGFSSLELLATWLPNA*GSSFTAEL |
| 4919 | 12970 | A | 58 | 1107 | 1365 | HSGSAGMHWNLFLVHCMQAHILFDRL LHMM*CNGRGP*FALCTRCSQ*DSGAN WDK*KNILPLRNFGWLGFNRDLGSRGW VPEV |
| 4920 | 12971 | A | 580 | 3 | 439 | |
| 4921 | 12972 | A | 5800 | 1 | 3084 | |
| 4922 | 12973 | A | 5801 | 3 | 265 | |
| 4923 | 12974 | A | 5802 | 242 | 401 | DLYAATYSHSHT/ILVWSTSTCEVRTL GHKRGIAQLQYRDRLVVS GSSDNTI |
| 4924 | 12975 | A | 5803 | 2 | 385 | FVFAAARGERGGAAGVMEPDSVIEDKT IELMLPKCMFGILLKKA GYSKRKESWK MLDCCLFSD*SERENPHSFWIGGSEVQNI FQNTSVMEDQNEDESPKKNLWQISNGT SSVIVSRKRPSEGNH |
| 4925 | 12976 | A | 5804 | 1 | 1248 | |
| 4926 | 12977 | A | 5805 | 2 | 1653 | RGGAAGAAMEPDSVIEDKTIELMCSVPR SLWLGCANLVESMCALSCLQSMPSVRC LQISNGTSSVIVSRKRPSEGNH YQKEKDL IKYFDQWSESDQVEFVEHLISRMCHYQH GHINSYLPMLQORDFITALPEQGLDHIAE NILSYLDARSLCAAELVCKEWQVISEG MLWKKLIERMVRTDPLWKLSERRGW DQYLFKNRPTDGPPNSFYRSLYPKIIDIE TIESNWRGCRHNLQRIQCRSENSKGVYC LQYDDEKIISGLRDN SIKIWDKTSLECLK VLTGHTGSVLCLQYDERVIVTGSSDSTV RVWDVNTGEVLNLIHHNEAVLHLRFS NGLMVTCKDRSIAVWDMASATDITLR RVLVGHRAAVNVVDFDDKYIVSASGDR TIK V WSTSTCEVRTLNGHKRGIAQLQY RDRLVVS GSSDNTIRLWDIECGACLRVL EGHEELVRCIRFDNKRIVSGAYDGKIKV WDLQAALDPRAPASTLCLRTLVEHSGR VFRLQFDEFQIISSHDDTILIWDFLNVPP SAQNETHSPSGVITYYISR |

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| 4927 | 12978 | A | 5806 | 1 | 180 | NFKRFHKTIAIETASYWPK/DRHINQRN/ RESPVINPTTYGQLIVDKGAKNTQWGKD NYFN |
| 4928 | 12979 | A | 5807 | 1 | 355 | |
| 4929 | 12980 | A | 5808 | 81 | 474 | LGERRRASLSLSLTPGRRRGFKVATQER NPQRAQMRLARRQKKGVVFWGDFLTE LQ/MGLDSAIPGRPWMATPNKRSKEVRV LQEMQLLQVAAMNYRLRPLEKFVITYFT RMEQLSDKESYKLSQCLEPENQ |
| 4930 | 12981 | A | 5809 | 3 | 383 | |
| 4931 | 12982 | A | 581 | 1 | 691 | MDQDSASTKTCPGTHRKSQPRSRREQHG ALGAANAHDTVRDGERYDRWSGPRRRE QHGAALGAANAPDTRDGERSLRRDWR DCAEATADVSGVRSLSRLLSARRLALAL AKAWPTVLQTGTRGVHFTVDGNKRASA KVSIDSISAQYPVVDHEFDVAVVGAGGA GLRAAFGLSEAEFDACVTCLFPTRSHT VAAQLENYGMPFSRTEDGKIYQRAFGG QSLKFGKGRQA |
| 4932 | 12983 | A | 5810 | 1 | 148 | |
| 4933 | 12984 | A | 5811 | 3 | 1219 | PGAMATLSFVLLLGAVSWPPASASGQE FWPGQSAADILSGAASRRRYLLYDVNPP EGFNLRRDVYIRIASLLKTLKTEEWVLV LPPWGRLYHWQSPDIHQVRPWSEFFDL PSLNKNIPVIEYEQFIAESGGPFIDQVYVL QSYAEGWKEGTWEEKVDERPCIDQLLY SQDKHEYRGRWFWGYEETRGLNVSCLS VQGSASIVAPLLRNTSARSVMLDRAEN LLHDHYGGKEYWDTRRSMVFARHLREV GDEFRRHLNSTDDADRIPFQEDWMKM KVKLGSALGGPYLGVHLRRKDFIWGHR QDVPSLEGAVRKIRSLMKTHRLDKVFVA TDAVRKEYEELKKLLPEMVRFEPTWEEL ELYKDGGVAIIDQWICAHASS*SAAGEPE TSCAGAGGTGRPLT |
| 4934 | 12985 | A | 5812 | 75 | 130 | IHRE*VPAAQGELRGAAE |
| 4935 | 12986 | A | 5813 | 1 | 1940 | MATLSFVLLLGAVSWPPASASGQEFWP GQSAADILSGAASRRRYLLYDVNPPEGF NLRRDVYIRIASLLKTLKTEEWVLVLP WGRLYHWQSPDIHQVRPWSEFFDLPSL NKNIPVIEYEQFIAGAQLSHAASVFPKC FSEMDLKWMSFVPPQLEPLHPKKAATP GCYSDRTRLPVRKAVLRSGRRTACGVCF VVSQCSARDKELHLRDAPSFRFVPAPEFH LRGAPSRFVPAPELHLRGAPSRFIPAAFE QILIADLLGVTVPSPWCGSGQSGGPFIDQ VYVLQSYAEGWKEGTWEEKVDERPCID QLLYSQDKHEYRCLLRLPLPQGWRS QSQVSIKGSDDTRPPVEKLSVNSLHVS SARAAGSKAWQGSASIVAPLLRNTSAR FERWDYSLQRVFSVGVDFRIDGVTFHSH PWFCDRPADVFTRAAACKAGTCLQETQ SLLTWDFVQTRRSMVFARHLREVGDEF RSRHLNSTDDADRIPFQEDWMKMKVKL GSALAGGPYLGVLHRRKDFIWGHRQDVP SLEGAVRKIRSLMKTHRLDKVFVATDA VRKEYEELKKLLPEMVRFEPTWEELELY KDGVAIIDQWICAHARFFIGTSVSTFSF SDS*GKEKFLGLDPKTDVQQVLRPREG V |

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| 4936 | 12987 | A | 5814 | 3 | 1286 | PGAMATLSFVFLLLGAVSWPPASASGQE FWPGQSAADILSGAASRRRYLLYDVPNP EGFNLRRDVIYIRIASLLKTLKTEEWVLV LPPWGRLYHWQSPDIHQVRIPWSEFFDL PSLNKNIPVIEYEQFIAESGGPFIDQVYVL QSYAEGWKEGTWEEKVDERPCIDQLLY SQDKHEYRGWFWGYEETRGLNVSCLS VQGSASIVAPLLRNTSARSVMDRAEN LLHDHYGGKEYWDTRRSMVFARHLREV GDEFRRHLNSTDDADRIFFQEDWMKM KVKLGSALGGPYLGVHLRRKDFIWGHR QDVPSLEGAVRKIRSLMKTHRLDKVFVA TDAVRKEYELKKLLPEMVRFEPTWEEL ELYKDGGAHNDQWICAHARCLPTSLSAE SGSGGFQRFCKPKYSVSEQMVACVHSGH FHTVCLLV |
| 4937 | 12988 | C | 5815 | 164 | 391 | |
| 4938 | 12989 | C | 5816 | 321 | 341 | MAALAS* |
| 4939 | 12990 | A | 5817 | 128 | 526 | FFFFIFKTASHSVVQAGVQWRSLSMQP PPPGKQFSLSLGWSWIKGHLPHPSNFC IFSRDGVSPCWLGWSQTPGLRPQSPKC LGLTGCEATSPWPASLKFKNVFLPG YVYLLHVLGPRSCYLOKW |
| 4940 | 12991 | A | 5818 | 3 | 273 | RRPRQRPTDQTQWFSILPDFSLDLQEGPS VESQTHSDPHIPPVDPTTHLTFNHLISVC VSLTSLPHLGSPCLWSPALVSQEAASH QDRR |
| 4941 | 12992 | A | 5819 | 1 | 861 | MLDSSLALGGLVLLRDSVEWEGRSLLK ALVKKSALCGEQVHILGCEVSEEEFREG FSDINNRLVYHDFRDPLNWSKTEEAF PGGPLGALRAMCKRTDPVPVIALDSLS WLLRLPCTTLCQVLHAVSHQDSCPGDS SSVGKVSVLGGLHEELHGPVPGALSSL AQTEVTLGGMGQASAHILCRRPRQRP NYQTQWFSNLPDFQPGSPRGALCRVPA LIPHIPPKEREARDSLILPFQFSSEKQQA LLRPRPGQATSHIFYEPDAYDDLQEDP DDDLI |
| 4942 | 12993 | A | 582 | 306 | 458 | IYIFLLNCIFLIHIIYFETESCSVAQAGWV QWHDLGSLQALPPGFTPF |
| 4943 | 12994 | A | 5820 | 2 | 494 | LGLLHEELHGPVPGALISLAQTEVTLG GTMGQASAHILCRRPRQRPTDQTRVSI LPDFSLDLQEGPSVESQPYSDPHIPPVSK NAKARTKCSLVSGHGRENKSCRGWG WGQGF*GWGRVAASFVPQVDPTTHLTF NLHLSKKEREARDSLILPFQFSSEK |
| 4944 | 12995 | A | 5821 | 1 | 498 | VRKVSVLGLLHEELHGPVPGALSSLAQ TEATLGGYH/VGQASAHMLCRRPRQRP TDQTQWFSILPDFSLDLKEGPSVESQPY DPHIPRVDPTTHLTFNLHLASKKEREARD SLILPFQFSSEKQQAALLRPRPGQATSHIF YEPDAYDDLQEDPDDDLNLPQOI |
| 4945 | 12996 | A | 5822 | 3 | 322 | HERQMALLKANKDLIPDGMTLTPLLQP LGFEDPVVCEQDVVTAGQDVWVYYDR DYGQQTGEQERDKALQELRQELNTL ANPFLAKYRDFLKSHELPSHPPSS |
| 4946 | 12997 | A | 5823 | 3 | 276 | |
| 4947 | 12998 | A | 5824 | 151 | 204 | SGEPFISGRFWWLQDG/DLMTLPRLVS NSWLKQSSHLGLLKHWDMSEAPHLAK NFLKAYEVVSLSFHVEGSGGCRMA |
| 4948 | 12999 | A | 5825 | 175 | 456 | IHFVLISAHAVGCEGILWGGWSLRGVGV PHSSAKRS*VGIRGPGKGRPGAQLPAGR ARASTEVPISGAPCPLLGAKNDRGLHAP KRTGTGPSNH |

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| 4949 | 13000 | A | 5826 | 188 | 269 | IHFVLISAHAVGCEGISPIEEMGVVSALSIQ EACSPGLQWATSFLASAWVSAPLLQMA HICPIILLGSLKGARATNRFQSLFVQGV SFPARFPHLDLLQ*P*KNDWTDVSHLE QRGTNPG*RQE*SGPLQPWRAGFLDGQC |
| 4950 | 13001 | A | 5827 | 1 | 542 | |
| 4951 | 13002 | A | 5828 | 2 | 889 | RGLRIPTWALQELAGRVTRRGPEGEGR REPGGSASPMRAAFPAGGAGGSVEPPSA RPAPQPAGTAARSEEAPARAQAAGMAG PGWGPRLDGFILTERLGSPTYATVYKA YAKKDTREVVAIKCVAKKSLNKASVEN LLTEIEILKGIHHPHIVQLKDFQWSDNIY LIMEFCAGGDLRSFIHTRRILPEKVARVF MQQLASALQFLHERNISHLDLKPQNILL SSLEKPHLKLADFGFAQHMSPWD\EKH VLRG\SPLYMAPEMVCQRQ\YDARVDL WSMGVILYGETSFPCFSP |
| 4952 | 13003 | A | 5829 | 297 | 331 | |
| 4953 | 13004 | A | 583 | 47 | 358 | SLLTPLVSPVPACPCPSKSEVSVPOEHPLP CRPLFRVWRNRQSRGCPQGVHYGAGA WGLLPVWKSCPPAKTCCKWGLP/CPPC GRSCLHSGAALCLLCGSA |
| 4954 | 13005 | A | 5830 | 3 | 405 | |
| 4955 | 13006 | A | 5831 | 3 | 408 | |
| 4956 | 13007 | A | 5832 | 1 | 530 | |
| 4957 | 13008 | A | 5833 | 198 | 1175 | RANPFRMGNHAGKRELNAEKASTNSET NRGESEKKRNLGELSRTTSEDNEVFGEA DANQNGTSSQDTAVTDSKRTADPKNA WQDAHPADPGSRPHLIRLFSRDAPGRED NTFKDRPSEDELQTIQEDSAATSESLDV MASQKRPSQRHGSKYLATASTMDHARH GFLPRHRDTGILDSIGRFFGGDRGAPKRG SGKVPWLKPGRSPLPSHARSQGLCNMY KDSHHPARTAHYGSPLPQKSHGRTQDEN PVVHFFKNIVTPRTPPPSQGKAEGQRPG FGYGRASDYKSAHKGFKGVDAQGTLS KIFKLGGDRSGSPMARR |
| 4958 | 13009 | A | 5834 | 1 | 651 | MGNHAGKRELNAEKASTNSETNRGESE KKRNLGELSRTTSEDNEVFGEADANQN NGTSSQDTAVTDSKRTADPKNAWQDAH PADPGSRPHLIRLFSRDAPGREDNTFKDR PSEDELQTIQEDSAATSESLDVMSQKR PSQRHGSKYLATASTMDHARHGFLPRH RDTGILDSIGRFFGGDRGAPKRGSGKRLT PPGKNCSLRVPAPEVTRPDPR |
| 4959 | 13010 | A | 5835 | 3 | 208 | |
| 4960 | 13011 | A | 5836 | 71 | 394 | APSARDVSRCAHRARPGAIMLLPSAAD GRGTAITHALTS\LEDKKELSESEDEEL QLEEFPMKTLDPKDWKNQDHYAVLGL GHVRYKATQRQIKAARKYLVLK |

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| 4961 | 13012 | A | 5837 | 146 | 1910 | APSARDVSRCAHRARPGAIMLLPSAAD GRGTAITHALTSASTLCQVEPVGRWFEA FVKRRNRNASASFQELEDKKELSEESQD EELQLEEFAMLKTLDPDWKNQDHYAV LGLGHVRYKATQRQIKAAHKAMVLKH HPDKRKAAGEPIKEGDNDYFTCITKAYE MLSDPVKRRAFNSVDPTFNSVPSKSEA KDNFFEFTPVFERNRSWSNKKNVPKLG DMNSSFEDVDIFYSFWYNFDSWREFSYL DEEEKEKAECRDERRWIEKQNGATRAQ RKKEEMNRIRTLVDNAYSCDPRIKKFKE EEKAKKEAEKKAKAEAKRKEQEAKEKQ RQAELEAARLAKEKEEEEVRQQALLAK KEKDIQKKAIKKERQKLRNSCKIEINEQ IRKEKEEAARMRQASKNTEKSTGGGG NGSKNWSEDDLQLLIKAVNLFPARTNSR WEVIANYMNIHSSSGVKRTAKDVIGKAK SLQKLDPHQKDDINKKAFDKFKKEHGV VPQADNATPSEFEGPYTDFTPWTTEEQ KLLEQALKTYPVNTPERWEKIAEAVPGR TKKDCMKRYKELVEMVKAKKAAQEQV LNASRAKK |
| 4962 | 13013 | A | 5838 | 1 | 1909 | DVSRCAHRARPGAIMLLPSAADGRGTA ITHALTSASTLCQVEPVGRWFEAFVKRR NRNASASFQELEDKKELSESEDEELQLE EFPMLKTLDPKDWKNQDHYAVLGLGH VRYKATQRQIKAAHKAMVLKHHPDKR KAAAGEPIKEGDNDYFTCITKAYEMLSDP VKRRAFNSVDPTFNSVPSKSEAKDNFF EVFTPVFERNRSWSNKKNVPKLGDMS SFEDVDIFYSFWYNFDSWREFSYLDEEE KEKAECRDERRWIEKQNRATRAQRKKE EMNRIRTLVDNAYSCDPRIKKFKEEKA KKEAEKKAKAEAKRKEQEAKEKQRAE LEAARLAKEKEEEEVRQQALLAKKEKDI QKKAIKKERQKLRNSCKTWNHFSDNA ERVKMMEEVEKLCDRLELASLQCLNET LTSCCTKEVGKAALEKQIEEINEQIRKEKE EAEARMRQASKNTEKSTGGGGNGSKN WSEDDLQLLIKAVNLFPAGTNSRWEVIA NYMNIHSSSGVKRTAKDVIGKAKSLQKL DPHQKDDINKKAFDKFKKEHGVVPQAD NATPSEFEGPYTDFTPWTTEEQKLLEQ ALKTYPVNTPERWEKIAEAVPGRTKKDC MKRYKELVEMVKAKKAAQEQVLNASR AKK |
| 4963 | 13014 | A | 584 | 1248 | 1667 | TNTGGWGPRHHAFVQHTLELLSLLCLNC GFLVYPFFLSWTVMYGSVNLVNLKYG FQGIIVFYCYVIKKLKKIWLCLPRPRVP WLPTSDPSLRSPSSMVLNQICRVYSATK RGSVTGSWAYPCVLSRGMSELCKSRA |
| 4964 | 13015 | A | 5840 | 3 | 231 | SFFETESCSVAHPGAQWCDISSLP PPPG SSDCPASASRVAGITGTHHAWPIFV VETGFHCLPQPPIVLGLQA |
| 4965 | 13016 | A | 5841 | 2 | 300 | RRRLALSPAGVHWHGLGSLQPPPPWFER FSCLGLLSGWDCRRAPPRPASFFVFLVET GFRHVKGKGLDFLT/S/GDPPALASQGA WIAGVSHRTRPQIHFF |
| 4966 | 13017 | A | 5842 | 227 | 290 | |
| 4967 | 13018 | A | 5843 | 1 | 225 | HCNFFLPVQAILGSSNSRASASRVAGTTG ALQHMQILFCILVETGFHRVAQAGDLL SLTIHPPRPPKVLGLQA |
| 4968 | 13019 | A | 5844 | 3 | 147 | LEIFFFFSFTFF/CRWGLTMFIRLVNFW PQMILLPLPLPPKVLGLQA |
| 4969 | 13020 | B | 5845 | 47 | 241 | GGKDFNMPLTISRITPGSKAAQSLSQ DLVVAIDGVNTDTMTHEAQNKIKSASY NLSLTLOK* |

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| 4970 | 13021 | A | 5846 | 3 | 408 | CGGIPSQATIFTLSTLISSVTSLNSTSFSTK VHTLSQNLVVFREPLKLTFLTL*ASAAF IALSN*SRT*RASWGVIC*DCMSSSRPPE DCFPK*YFCITDMPWLRKNNFFSTFQSK CRF*GTPICQKDKTSKK |
| 4971 | 13022 | A | 5847 | 1 | 2209 | AAADSTMSYSVTLTGPGPWGFRLOGG KDFNMPLTISRTPGSKAAQSQLSQGDLV VAIDGVNTDTMTHLEAQNKIKSASYNLS LTLQKSKRPIPISTTAPPVQTPLPVIPHQK DPALDTNGSLVAPSPSPPEARASPGTPGTP ELRPTFSPAFSRPSAFSSLAESDPGPPRA SLRAKTSPEGARDLLGPKALPGSSQPRQ YNNPIGLYSAETLREMAQMYQMSLRGK ASGVGLPGGSLPIKDLAVDSASPVYQAV IKSQNKPEDEADEWARRSSNLQSRFRIL AQMTGTETFMQDPDEEALRRSSTPIEHAP VCTSQATTPLLPASAPPAASPSAASPP LATAAAHTAIASASTTAPASSPADSPRPQ ASSYSPAVAASSAPATHTSYSEGAAPAP KPRVVTASIRPSVYQVPASTYSPSGA NYSPTPYTPSPAPAYTPSPAPAYTPSPVPT YTPSPAPAYTPSPAPNYPAPSVAYSGGP AEPASRPPWVTDDSFQKFAFGKSTTSIS KQTLPRGGPAYTPAGPQVPPLARGTVQR AERFPASSRTPLCGHCCNNVIRGPFLVAM GRSWHPPEFTCA YCKTSLADVCFVEEQN NVYCERCYEQFFAPLCAKCNKIMGEV MHALRQTWHTTCFVCAACKKPFQNSLF HMEDGEPYCEKDYINLFSTKCHCHFP VEAGDKVIEALGHTWHDTCFCAVCHV NLÆGQPFYSKKDRPLCKKHAHTINL |
| 4972 | 13023 | A | 5848 | 1 | 537 | RTRGGDVKTDLNNIEEFLEETLTPEKYPI LAAKHREYNTEDIDIFYKFSAYIKNTKQQ NNAALERGLTKALKKVDYDNLTPPQE RDAYTCGEDKGTRRKFLADGDELTLAD CNL/LPKLHVVKIVGKKYRNYHIPADMT GLWRYLKNAYARDEFTNTCAADSEIEL AYADVAKRLSRS |
| 4973 | 13024 | A | 5849 | 1 | 654 | WEGPTCSMCKVIGIHNACEEAPLHVSFH GQKTELNNCISMLVAANDRVHTIITQLE DSRRVTKENSHHVNRKLSQKFDTLYAIL DEKKSELLLRISQEQEKKLIFIEALIQYQ EQLDKSTKL VETAIQSLDEPGGATFLLTA KQLIKSIVEASKGCQLGKTEQGFMNMF FTLDLEHIADALRAIDFGTDEEEEFIEEE DQEEEEESTEGKEEGHQ |
| 4974 | 13025 | A | 585 | 334 | 696 | IKPEMEAGISVTLGLDRNTRVQVGCREL RSTKYISGWASCTSIQPSGREL/VCVVGE CLPLPVVPNWIGGGYGTKYWSRRSSQ EWAVCSMDKTRYPEDSQLQCQDGSTR YKITVSSLPAS |
| 4975 | 13026 | A | 5850 | 141 | 626 | LLWILIAAPPPPPVIRNGARGCSPSTTIP NAWGQEPPrPRERPPPPSRDAIAGATPS FLPPPLRNHRDSIHHCSGL/CLDDFESK YSFHPVEDFPAPPEYKHFSEDVPSKTNR AARGVAPLPPLQVKPGLVPFLIKRMDL LFFSYGPLHSSSELLHDSS |
| 4976 | 13027 | B | 5851 | 23 | 160 | MQHVCAMRQVDIDAYTTCLYASGTPV PQLPLLMALLGLCTLVL* |

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| 4977 | 13028 | A | 5852 | 221 | 1645 | APRMRLLAWLIFLANWGGARAEPGKF WHIADLHLDPDYKVS KD PFQVCQSAGS QPRGPTQAPWGDYLCDSWALNNSIY AMKEIEPEPDFILWTGDDTPHVWDEKLG EAAVLEIVERLTKLIREVFPDTKVYAALG NHDFHPKNQFPAGSNNIYNQIAELWKP WLSNESIALFKKGAFYCEKLPGPSGAGRI VVLNTNLYYTSNALTADMADPGQQFQ WLEDVLT DASKAGDMVYIVGHVPPGFF EKTQNKAWFREGFNEKYLVVRKHHRV IAGQFFGHHHTDSFARMLYDYAGVSISA MFITPGVTPWRTTLPGVVNGANNPARRV FEYDRATLSLKDMVTYFMNLSQANAQG TPRWLELEYQLTEAHGVPHATAHSMHT VLGRIVGDKSTLQRYIVVNSVSYSG VCDEACSMQHVCMRQVDIDATTTCL YASGTTAVPQLPLLMLLGLCTTRAV TCQAHSSW |
| 4978 | 13029 | A | 5853 | 3 | 126 | AYGDSMCAKCVSDRIKHAFIKEQKIIV KVLKAQAGSQKAK |
| 4979 | 13030 | C | 5854 | 306 | 386 | MLFLKAIWGGSDSWSREAA CPLNCNL* |
| 4980 | 13031 | A | 5855 | 709 | 1199 | AGVGVRGTTGRLVVRKFLTIFGNPLFL VAPPKPHSEWSQRLTYRRRPSPYNTAL* QK/RRHRSHNQIPPRIVYLLYPRRLGKHP NSACGVCPRQEFEGVRAVRPKVLMRL SKTKKHVSRAVGGSNVCLNVFRDIKR AFLNEEQKIIVVKVLKAQAGSQKAK |
| 4981 | 13032 | A | 5856 | 1 | 219 | HRGYLLFNLFVEVISSEQSVLAPPVRR*T CIVANLRGVGDPDTSRHCAQGLGFKLLT LYSLVGSESWGGARA |
| 4982 | 13033 | A | 5857 | 112 | 312 | LCTVCLWALKAGVGPEPERLIYSVPVFV */HAVCAGIADGGSFSSKVRCLHFFYTG ISIKMFLYIK |
| 4983 | 13034 | C | 5858 | 133 | 237 | MFMDXXXXXXGGRFKGSLGGPKFTRAC KVKFFSL* |
| 4984 | 13035 | C | 5859 | 61 | 177 | MRIHKRLIDLHSPSEIVKQITSISIEPGVEV EVTIADA* |
| 4985 | 13036 | A | 586 | 258 | 382 | |
| 4986 | 13037 | C | 5860 | 100 | 153 | MSPPKSKGPFPRFPGRF* |
| 4987 | 13038 | C | 5861 | 142 | 195 | MSPPQSKGPFKFPGRF* |
| 4988 | 13039 | A | 5862 | 11 | 90 | |
| 4989 | 13040 | A | 5863 | 3 | 759 | TVPLEVLLRKVGAAGGARGVIRLLDW FERPDGFLVLERPEAQDLDFITERGA LDEPLARRFFAQVLA AVRCHSCGVVH RDIKDENLLAVLRSGELKLIDFGSGALL MDTVYTDGTRVYSPPEWIRYHRYHG RSDTVWSLGVLLYDMVCGDIPFEQDEEI LRGRLLFRERVSPECQLIRWCLSLRPSE RPSLDQIAAHPWMLGADGGAPEQ/DCDL RLCTLDPPDVASTSSSETLLRSLHLTGS |
| 4990 | 13041 | A | 5864 | 1 | 422 | |
| 4991 | 13042 | A | 5865 | 2 | 435 | ILAEFGSLHLEFLHLELSGNQVFAEKVR NIRKVLKIEKPFGLYPNFLSPVSGNWV QHHVSVGGLGDSFYEYLIKSWLMSGKT DMEAKNMYEAELET/HKLGPEAFWFNS GREAVATQLSESYILRPEVVESYMYLW RQTHNTK |
| 4992 | 13043 | A | 5866 | 1 | 837 | |
| 4993 | 13044 | A | 5867 | 1 | 415 | TKLGPEAFWFNSGREAVATQLSESYIIL RPEVVESYMYLWRQTHNPIYREWGW VVLAEKYCRTEAGFSIQDVSSTPNH DNKQQSFFLAETLKYLLFSWEDDLLSL EDWVFNTAEHPLPVNHSDSSGRAGGRH |

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| 4994 | 13045 | A | 5868 | 1 | 1187 | ESFHLNVSGEASLFEVNIRYIGGLLSAFY LTGEEVFRIKAIKRLGEKLLPAFNTPTGIPK GVVSFKSGNWGWATAGSSSILAEFGSLH LAEFLHLTELSGNQVFAEKVRNIRKVPQV SFEKPFGLYPNFLSPVSGNWVQHVSFG GLGDSFYEYLIKSWLMSAKTDLEAKNM YYG/APLEAIETYLLNVSPGGLTYIAEWR GGILDHKMGHLACFSGGMIALGAEDAK EEKRAHYRELAVQITKTCYESYARISDTK LGPEAFWFNSGREAVATQLSEE/ITYILR PEVVESYMYLWRQTHNPYSYREWGWE VVLAEKCYCRTEAGFSGDSKTCYSRHPQ PRTTSRQSFFLAETLNRCLVSACNGPDTG LEARDTAESSETVISPAVKGSRGKAMVR ETD |
| 4995 | 13046 | A | 5869 | 1 | 1561 | MIFVVIILMVVLSPEGGSGLDSSPFLSEA NAERIVQTLCTVRGAALKPYPTGPNFR YSHGVPPHLFAYFPFGSTVSQDNSFISQ LQHIFERVQRQADFMPRWQMLRVLEEEL GRDWQAKVASLEEVFPAASIGQVHQG LLRDGTEVAVKIQYPGIAQSIQSDVQNL AVLKMSAALPAGLFAEQSLQALQQLA WECDYRREAACAQNFRLANDPFFRV PAVVKELCTTRVLGMELAGGVPLDQCQ GLSQDLRNQICFQLLTCLRELFEFRFMQ TDPNWANFLYDASSHQVTLLDFGASREF GTEFTDHYIEVVKAAADGDRDCVLQKS RDLKFLTGFETKAFSDAHVEAVMILGEP FATQGPYDFGSGETARRIQDLIPVLLRH RLVSP/PEGDLWPWHRKLAAGAFACAH LRDHIACRDHKPGHLPPLGQSPARRSH CRQPPHQRGTGWPWPHDSLHGGFSPQSR PYPVAVPLIPSPSALGQRSPLGLPSLAWL SSLAPKTOESLGLGNSP |
| 4996 | 13047 | A | 587 | 1637 | 1832 | VFSTRCGTHPPVCLAEFVKRLRYCEYLG KYFCDCCHSYAESCIARILMMWDFKK YYVSNFSKTA |
| 4997 | 13048 | A | 5870 | 1 | 1532 | MPQALERADGSWAWVLLATMVTQGL TLGFPTCIGIFFTELQWEFQASNETSWFP SILTAVLHMAGPLCSILVGRFGCRVTVM LGGVLASLGMVASSFSHNLSQLYFTAGF ITGLGMCFSFQSSITVLGFYFVRRRVLAN ALASMGVSLGITLWPLLSRYLLENLWGR GTFLVFGGIFLHCCICGAHRPVATSVAPE TKECPPPPETPALGCLAACGRTIQRHLA FDILRHNTGYCVYILGVMWSVLGFPLPQ VFLVPYAMWHSVDEQQAALLISHGFSNI FLRPLAGLMAGRPAFASHRKYLFSLALL LNGLTNLVCAASGDFWVLVGYCLAYSV MSGIGALIFQVLMDIVPMDQFPRLGLF TVLDGLAFLISPLAGLLDATTNNF*DVF QQCPSFFP*SKAPLLKGGSFPPPPQKKEQ GKQAVAADAALERDLFLEAKDGPQKQR SPAEIMCQSISRQPRPAGVNKHLWGCPAS SRTSHEWLFWPKAVLQAKQALGWNSP T |
| 4998 | 13049 | A | 5871 | 946 | 1279 | QTELGVRFPTLPFLGARGCSGRFVLF VDFRVQPGFRKENLIQGDLLFFMNRQSS RQPRPAGVNKHLWGMSCP/ASRDPAMK WLLWPKAVLQAKQALGWNSPYLECP V |
| 4999 | 13050 | A | 5872 | 3 | 297 | ESCSVTQAGVHW/CNLGSLQSPAPDSSD SPSSVSRVAGITGMCHHAQLIFVVFVETG FHHGEAGLCLRLPKCWDYRCEPPRLHL GLQLNFTYKDRCLA |

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| 5000 | 13051 | A | 5873 | 276 | 880 | KADSEQHGEAKRRYSSSLAKKEVSKAPE DKKKRLEDKRRKKEDKERRKKDEEKVK AEEESKKKEEEEKKKHQEEERKKQEEQA KRQQEKIEAAAHMKEKEESIQLHQEAW RHHLKKELCSKNQNPAGSRPKENFFSRL DSSLKKNTAFVKKLKTPEQQRDSLSHD FNGLNLSKYIAEAVASIVEAKLKISDVNC AVHLCS |
| 5001 | 13052 | A | 5874 | 2 | 619 | LDLDFNAILIVTSLAPFFQDCMSENALH ELNIELLRNKLYKSYLEAFYKFCCKNHGD VTAEVMCPILEFEADRRAFIITLNSFGTEL GQEDRETLYPNLGQLLSEGFALALAE DFDQMKNVADHYGVYKPLFEAVGGIGG KTLEDVFYEREVQMNVLAFNRQFHYGV FYAYVKLKEQEIRNIVWIAECISQRHRTK INSYIPIL |
| 5002 | 13053 | A | 5875 | 1842 | 2306 | GPRRLAAFLTSAGDGVYTRPVVFDCTC ATFHREDAYRLPFIPTNHHTASPE*VPP HPHLGALQLPGDPSHDIHSIGTPNSNADA PKAGGCKWTQTRSVVPNSALGRKGSTH LPRIYTFTLALPETKLSNCPKAPPIGLEH TSLAWALGTAD |
| 5003 | 13054 | A | 5876 | 301 | 471 | |
| 5004 | 13055 | A | 5877 | 269 | 394 | |
| 5005 | 13056 | A | 5878 | 524 | 604 | |
| 5006 | 13057 | A | 5879 | 187 | 401 | VSCPGSNSPLGSSSASGASSLNFLPSVPV R*SVSGLNLRVPAMARAVTISGDVTKA WVSGFASLRPVKFL |
| 5007 | 13058 | A | 588 | 1 | 856 | MKRSMILTIFHSERJILRNRQPPKESWE DIEDFGETHDLFLKQYGFENGIPVHDTI ARVVSCISPAKFHECFINWMRDCHSSND KDVAIDGKTLRHSYDKSRRRGAIHVISA FSTMHSLVIGQIKTDKKSNEITAPELLN MLDIKGIITTDAMVNCIVKVTGVFAING DQRVAEPDSGALCQVRYPGNHRNDQRY LFRHSDSELLHWMVALDAVVRVKCL WMSLHKVYSCIPELPEPQESAGVHSGSQ YA*CNRTPHGQKPGTSAPGSSGVWRIT SV |
| 5008 | 13059 | A | 5880 | 667 | 888 | AHTVHIRRSASRLPAGPASRLVDLSH*DL GHVP/AGFFLIMNVQQEGLADLSTSAHL LGAPLVKGSRPHAWADAW |
| 5009 | 13060 | A | 5881 | 1 | 163 | GLVDESFDVTSPTGPSSADATTSVRAAK KRAPYTLVGSISEPGLGLISWWTSN |
| 5010 | 13061 | A | 5882 | 183 | 426 | |
| 5011 | 13062 | A | 5883 | 1 | 1152 | MHNSDGIEVMRQQKAEIGRVGGLEGIQL GVTEVIVNGARMLESYNCKAELGATGL VNYQISVKCSNQFKLEVYLLNAENKVV DNQAGTQGQLKVLGTNLWWPYLMHEH PAYLYSWEGRPDGAQAVGALTPGTAV EVWLTAQKSLGP/SDFYTLPVGLRTVAV TESQFLISGKPFYFHGVNKHEDADIQK GFNWPLLVKDFNLLCWLGANTFCTSHY PYTEEMLOICYRYGIVVIDECPAPSGHT GPSVPSLLARWQLFNNVSMHHHMWV EEPVLDRKNHPAMVMWSLAKEPASFLE SAGYSFKSLTMEQTARVLDLDTGEAVLQ YRSLPRGAHKTGKKRRISSYNVDLTSC QLAKEKCLKGPSSFLQSRQERMNSELRD N |
| 5012 | 13063 | A | 5884 | 401 | 882 | CTNTPPTWTRGRMVIAHTKALDPSQPVT FVTNVTYAADKGALYVDVTPLNSYYS YRNYGHLAELQLQLAAQFENWCKTSQ SHYSERVWSGNAL*GFHQDPPLMFQ*RG PGKVLLQYHLGLDQKRRKYVVGELIW NFADFMTNQCVSFLVGNENSANL |

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| 5013 | 13064 | A | 5885 | 197 | 1184 | ETSHQVMDRSNPVKPALDYFLNRLVNY QISVKCSNQFKLEVCLLNAENKVVDNQA GTQGGQLKVLGANLWWPYLMHEHPASL YSWEGRPDGAQAVGALTPGALAVEVR LTAQKSLGP/SDFYTLVPGLRTPVPTESQ WALYVDVIRVNSYYSWYRNYGHLELIQ LQLPAQFENWCKTSQSHYSERVWSGNA YRVSPGGGNLPHALPCCSQNLALPTFSP GTVVISLALSLIGLWAQETGVLFIVVSQD PPLMFSEYQKSLLEQYHLGLDQKRRKY VVGELIWNFADFMTNQCKWQFSAWDN VPVLIFSGCLAHS GHFGCKNIGNKGGKL V |
| 5014 | 13065 | A | 5886 | 1 | 657 | |
| 5015 | 13066 | A | 5887 | 76 | 614 | VCQYCTARMADFGISAGQFVAVVWDKS SPVEALKGLVDKQLQALTGNEGRVSVENI KQLLQCLVPGSTTLHSAEILAEIARILR PGGICLFLKEPVETAVDNNSKVKTASKL CSALTSLVGLVEVKELQREPLTPEEVQSV REHLGHESDNLLFVQITGKKPNFEVGSS MQLKLSITKKS |
| 5016 | 13067 | A | 5888 | 102 | 1292 | ACQYCTARIVDFEISAGQFVA*VWDKSS PVEALKGLVDKQLQAF/TPGNEGRVSVENI IKQLLQSAHKESSFDIHLVGLVPGKAPL WHS*DFWAGNPPGFLRPGWMFFFLKE PVETAVR*Q*AKWKASKLCSALTSLGL V/EKLELQREPLTPEEVQSVREHLGHES DNLLFVQITGKKPNFEVGSSRQLKLSITK KSSPSVKPAVDPA*AAKLWTL*ANDMED DSMCIFCGCSLTHRWPLEHVRLNMMI NQKEDRVDITFFLDSKFPLEACSHFSFSL AETTTVSLIALNTLQDLIDSDELLDPEDL KKPDPASLRAASC GEGKKRKACKNCTC GLAELEKEKSREQMSSQPKSACGNCYL GDAFRASCOPYLGMPAFKPGKVLSD SNLHDA |
| 5017 | 13068 | A | 5889 | 1 | 747 | MGFRYVAQAGLELLSSDPSIPSSKTLQEQ NDQSYPTLVPFPEVALHTLLWGEDANN SKVKELQREPLTPEEQSVREHLGHESDN LLFVQITGKKPNFEVGSSRQLKLSITKKS SPSVKPAVDPA*AAKLWTL*ANDMEDDS MDLIDSDELLDPEDLKKPDPASLRAAS CGEGKKRKACKNCTCGLAELEKEKS EQMSSQPKSACGNCYRGAMPSCGASCP YLGMPAFKPGKVLSDSNLHDA |
| 5018 | 13069 | A | 589 | 148 | 333 | |
| 5019 | 13070 | A | 5890 | 2 | 152 | YRHMAPHTNFKK/FFCRDGGVLMLPR LVFNSWPQGILLPQPKVLGLQV |
| 5020 | 13071 | A | 5891 | 1 | 581 | EKQSCSKSCGETFNSITKRRHHCKLCGAVI CGKCSEFKAENSRQSRVCRDCLTQVPA PESTEKTPTADPQPSLLCGPLRLSKSET WSEVWAAIPMSYPQVLHLQGSQDGR PRTIPLPCKLSVPDPEERLDSGHVWKLQ WAKQSWYLSASSAELQQWLETSTAA HGDTAQDSPGALQLQVPMGAAAP |
| 5021 | 13072 | A | 5894 | 1 | 303 | PCGARQCGGPPRL/CSSRRTSQELLSK PVPPPAPGGPASRVGRGSVSGALSPAWN GERQHHRGVVLTHPQSPNHQAGSPNPN TRQALATLSVPNKPPIE |
| 5022 | 13073 | A | 5895 | 1 | 284 | ATESCSVAQGVQWCDLSSLQAPPGFT PFSSLSLQGSWDYRSPPPHPANFFVVLVE /MASASQSAGITGVSHRTRPRIAIFNLTEN TNGSVDED |
| 5023 | 13074 | A | 5896 | 3 | 338 | GIHGWSYGGYLSLMLMQRSDFRVAIA GAPVTLWIFYDTGYTERYMGHPDQNEQ GYYLGSVAMQAEKFPS/EIYPQERHSIRV PESGEHYELHLLHYLQENLGSRIAALKVI |
| 5024 | 13075 | A | 5897 | 1 | 1200 | |

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| 5025 | 13076 | A | 5898 | 2 | 594 | NRGSCHRGLKFEGAFKYKMQQIEIDDQV EGLQYLASRYDFIDLDVRVGIHWSYGG YLSLMALMQRSDFRVAIAGAPVTLWIF YDTGYTERYMGHPDQNEQGYLGSVA MQAEKFPSEPNRLLLLHGFLENVHFAH TSILLSFLVRAGKQYDLQIYPQERHSIRV PESGHEHYELHLLHYLQENLGSRIAALKV I |
| 5026 | 13077 | A | 5899 | 74 | 248 | KTLWMVNRTVLAGICSQQLSAGTAT/DV SKHRLQGFIPCRIPS/ASPQTQRKFSLQFH RNC |
| 5027 | 13078 | A | 59 | 582 | 1303 | GACSRAGLWLLGQGLLPRIYQLSEDCV SWSCHQPLSPQSLIWARTESSPDTQS GEDRKTSFVGHQPTALGGLGQSIESLMS SEAETEERRCTWMQLSETNRTLFLFGVT KYTAGPYECEIWNSSGASRSDPVTNLNLL HGLDALTISSSYTYHTGEVPKLSCLIDT HPLAEHSWLIGGKFQSSAQVFIPQITKT YRGVYVCFIHNSATGGTNLIKRIVPDHS LRSALSLEVTGS |
| 5028 | 13079 | A | 590 | 311 | 576 | |
| 5029 | 13080 | A | 5900 | 258 | 552 | CMVFHD/VSGACCCNGETTGKISGGGNQ LGSSPIGGPNPS/SGSSQTSISGDVVEACC SVLSMVCADPVYKVYVAALLLERELPG VFSGKIFNLLSDCLLW |
| 5030 | 13081 | A | 5901 | 1 | 1660 | |
| 5031 | 13082 | A | 5902 | 1 | 1947 | MALRRLSHDVSGALLANGESTGNSGG SSGSSPSGGATSGSSQTSISGDVVEACCS VLSMVCADPVYKVYVAALQCMLLVTL EDPSSHFRMRRLM/AYADEVEIAEAIQ LGVEDTLDGQQDSFCHLFPPTTIWKPQR TVP/LECTIHLEKTGKGLCATKLSASEDI SERLASISVGPSSSTTTTTTEQPKPMVQ TKGRPHSQCLNSSPLSHSQLMFPALSTP SSSTPSVPAGTATDVSKHRLQGFIPCRIPS ASPQTQRKFSLQFHRNCPENKDSKLS VFTQSRPLPSSNIHRPKPSRPTPGNTSKQ GDPSKNSMTLDLNSSSKCDSFGCSSNS S/NCCYTSDETVFTPVEEKRLDVNTEL NSSIEDLLEASMPSSDTTVTFKSEVAVLS PEKAENDDTYKDDVNHQKCKEAMEA EEEEALAIAMAMSASQDALPIVQLQVE NGEDIIHQDMTFFRHIIPPIQWIYKKESA NLLIDSTGQRLRIADFGAAARLASKGTG AGEFQGQLLGTIAFMAPEVLRGQYGRS CDVWSVGCAIEMACAKPPWNAEKHSN HLALIFKKLLDFANTACDGDKESEVEDV ETDSGNSPEDLRKEIMIGLQYQAEIPPYL GEYDGNKDSPPQPKMTGVQNAKEVLS T |
| 5032 | 13083 | A | 5903 | 1 | 4491 | PSPEAGGGGALKASSARAAAAGLLRE AGSGGRERADWRRRQLRKVRVELDQL PEQPLFLAASPPASSTSPSEPADAAGSG TGFQPVAVPPPHGAASRRGAHLTESVAA PDGASSPAAAEPGEKRAPAAEPSAAA PAGREMENKETLKGHLKMDDRPEERMI REKLKATCMPAWKHEWLERNRGPGV VVKPIPVKGDGSEMNHAAESPGEVQAS AASPASKGRRSPSPGNSSPGRTVKSESPG VRRKRV |
| 5033 | 13084 | A | 5904 | 1940 | 2062 | |
| 5034 | 13085 | A | 5905 | 785 | 892 | |
| 5035 | 13086 | A | 5906 | 1 | 2745 | |
| 5036 | 13087 | A | 5907 | 1 | 3297 | |
| 5037 | 13088 | A | 5908 | 1 | 2202 | |
| 5038 | 13089 | A | 5909 | 1 | 2868 | |

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| 5039 | 13090 | A | 591 | 279 | 602 | FFLSEILSVSLTFFIISNYYYYSQVINS LAVY RHRETDFGVGV RDHPGQ/PWQNPISHEK LDNLIHIIIGFLRRYTFNILFCTSCLCVSILT FCRGILVITNKNKLYKTK |
| 5040 | 13091 | A | 5910 | 1 | 3237 | |
| 5041 | 13092 | A | 5911 | 1 | 2001 | |
| 5042 | 13093 | A | 5912 | 1 | 2982 | |
| 5043 | 13094 | A | 5913 | 1169 | 3269 | VHCRFWILALCQMSRLQKSPLL FNIVLE VLAKAIKQEKEIKGIQLGKEEVKLSLFAD DMIVYLENPTVSAQNLLKLMSNFSKVSG YKINVQKSQAFLYTNNRQTESQIMSGLP FTITSKRITYLGIQLTRDVKDLFKENYKP LLKEIKEDTNKWKNIPCSWVGGRINLVK MAILPKVIYRFNAIPKLPMTFFTELEKTT LKFIWNQKRALIAKSSLSQKNKTGGITLP DFKLYYKATVTKTSWYWYQNRDIDQW NRTEPSEIMPHIYNLIFDKPKDNKQWG KDSL FNKWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLHVRPKTIKTLEENLGN TIQDIGMGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQPTWEKEI FATYSSDKGLISRIYNELKQIYKKKTNNPI KKWAKDMNRHFSEEDIYAAKHKMKKC SSSLAIREMQIKTTMRYHLTPVRMVIKK SGNNRCWRGCGEIGTLLHCWWDCCLV QPLWKS VWQFLRDLELEIPFDPAPILLGI YPEDYKPCCYKDTCTRMFIAALFTIAKT WNQPKCPTMIDGIKKMWHIYTMYYAA IKKDEFMSFAGTWMKLETILRKLSQGG KTKHRMYSLIGGNLTMRTFGHSAGSHH TPGPIMRCGAGGGIALGEIPNVNDEL MG TANQHGTCIPMQQNCTLCCTLKLKV |
| 5044 | 13095 | A | 5914 | 2821 | 5794 | |
| 5045 | 13096 | A | 5915 | 457 | 651 | |
| 5046 | 13097 | A | 5916 | 3 | 637 | KGDHVKHYKIRKLDNGGYIITRAQFET LQQLVQHYSERAAGLCCRLVVPCHKGM PRLTDL SVKTKDVWEIPRESLQLIKRLGN GQFGEVWNGTWNNGNTKVAIKTLKPGT MSPESFLEEAQIMKKLKHDKLVQLYAV VSEPIYIVTEYMNKGSLLDFLKDGEGR ALKLPNLVDMAAQVAAGMAYIERMNYI HRDLRSANILVGNGLICK |

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| 5047 | 13098 | A | 5917 | 1 | 2523 | MHWKRPWQVGGYLTAAATDTVQMLNY MSVRQLSYLNFPNTWQFLSWSQMPTQQ AYPCVTHHTPPVLGQMACCISNQRRTA ALIGTRPERNVHVNLRQGFVNAHEP WVNEKVARQEPEDAGRGAVNRAWGFS PRLIHWSEGPQAAALGDRDPRWLPYHH AAALSGSHAAALSLAPSRSSALAVLIALL PAAQLHHHVPRSKACDIAYVGGHRRQV WYGGQEDGQQILVVPVLLSTTQQKVSAL WADRLEVRALLARSLAARLAPPSVHPCW V/VTFPSAVAWINAGSLDLFLKDGEGRA LKLPNLVDMAAQVAAGMAYIERMNYIH RDLRSANILMGNGLICKIADFGLARLIED NEYTARQDPTRSRGHRSSAMNPYGSRA GRGRVESGLTLQMAATQVTVQWSAHLV SGEAVAWNTFPTANQDRKELAALSCSCP STLCFMLLGLYPTLDHLQVRQSHCLTVS CAWQGLKPLFLWLAINKAEIEICLTLLKY WQADCELLASAYQHAWHTCARTQSSNL SIADIESLELVVKTFFHQKKIFGLTSYSG MFVGTWNGNTKVAIKTLKPGTMSPEFL EEAQIMKKLKHDKLVQLYAVVSEPIYI VTEYMNKGGDEGTREEIGQVKAPRRDN IPKPSAAHAAQLVMWHEVRLTRALCPF WGWLDSWHHFCVELHPTHPLITQKPKG KELTDVVHRSQFSGAQSRVESIWIQRSM TKTPGAKLQKQAYQGVSNPHHHHTGQ QLKAVPHPLMEAPDAIDGYRKILVNFTKI YSAFAVTNSDYEWQPTLVAIGYRCGDP QGTERRTQKPTEVTTQLQPQPWLLRG HVGLVLLDHPFKEKP |
| 5048 | 13099 | A | 5918 | 74 | 1002 | SNESNAVALSTVERTARRDAPQHGTQPR GLPRSSEHPAQRATAATGKARQRRKTTA SAGAREGRRRLAGTTSIPGP/FSAPVHR HRPQEPRQGPRTPRRAEEKRDQMASHV ECRPLGVFECELCTLAPYSYVGQKPPN TQSMVLLEESYVMKDPFTSDKDRFLVLG SCCSLCSRLVCVGPVGRMEVEQHGFHSV PSVLRVTPSEKSLSICHLRLTHTKGSCINS QGDEMGQGRSLRSVAWEYLRLMEELV VQEKLGKEDCKGNSARLGEKESSIKEDP QPARFSDGPGLECCSDVTERDDLQQG SS |
| 5049 | 13100 | A | 5919 | 3 | 401 | RSRGTRAAMASHVECRPLGVFECELCTL TAPYSYVGQKPPNTQSMVLLEESYVMK DPFTSDKDRFLVLGSCCSLCSRLVCVGP VG\CSLFYSKRFLPCVRENINAFQEIQR DLEKRKAPSKRTPSQGSRT |
| 5050 | 13101 | A | 592 | 66 | 1474 | TAPPPSPSPSLLSPCNGVHHVSTQPSCP GRGKMSKLLNPEEMTSRDYYFDSYAHF GIHEEMLKDEVRTLTYRNSMYHNKHVF KDKVVLGVGSGTGILSMFAAKAGAKK VFGIECSSISDYSEKIIKANHLDNIIITFKG KVEEVELPVEKVDIIHSEWMGYCLFYES MLNTVIFARDKWLKPGGLMFPDRAALY VVAIEDRQYKDFKIHWWENVYGFDMTC IRDVAMKEPLVDIVDPKQVVTNACLIKV WTLIRGGPGCAGSPAVPPWSPGNAGSCT APTWARAKVVRLRYEPEVRLEGHATLV TEGTTKERYQGPWKEPGAWLIGPEKVM EKSVLTPNVILDASYCWELAYQKIGEGV VWFIYITGGPKTQIAVLVQQEVDIYTV KTEELSFTSAFCLQIQRNDYVHALVTYF NIEFTKCHKKMGFSTAMEEPCIPFVLSK EKVNNVVVVTAQVESVLDEGEAG |

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| 5051 | 13102 | A | 5920 | 96 | 615 | NIILRNSIITSRKIKYTTLSSTHISFLFPQISP QMSLIGFFYESEANKGSHFPFGYVVSCLNL AETT/SLFYIICFLKSPDQGGQNAQTMAY NITPLRRAVECVQDQFGFINYEVGDSK KLLFFHMKEV/SRDGQCSAWNVPSSLR GPKAIVAAPRPDRIVSRLKNITLDDAS DPR |
| 5052 | 13103 | A | 5921 | 1497 | 2853 | EMVLVSSSVWIVMFVCSSTSVMKFWMG SSHIADEVFTVVPDMLSAQRNHAIRIKK LPKGTVSFHSRSHRFLGTVEKEATFSNP KTTSPNKGKEKEAEDGIIAYDDCGVKLTI AFQAKDVEGSTSPQIGDKVEFSISDKQRP GQQVATCVRLGRNSNSKRLGYVATL KDNFGFIETANHDKIEIFFHYSEFGDVS LELGDMEVYSLSKGKGNKVSARKVNT HSVNGITEEADPTIYSGKIRPLRSVDPT QTEYQGMIEIVEEGDMKGEVYFPGIVGM ANKGDCLQKGESVKFQLCVLGQNAQTM AYNITPLRRATVECVKQDQGFINYEVG DSKKLFFHVKKVQDGMELQAIGDEVEF SVILNPAATGKVQAPCNVWRVCEGPP RLQAPRPDRVGSIRLKNITLDDASAPR LMVLRQPKGDQITSMGFGAERKIRQA GVID |
| 5053 | 13104 | A | 5922 | 23 | 206 | |
| 5054 | 13105 | A | 5923 | 1 | 267 | ALFRDKLKHMGKSTRKLFELARAFSEK TKMRKSKRKHLKHQSRGAAASTANL LDDVEGHACDENFRGQASRRAPQGGG RPCREGQ |
| 5055 | 13106 | A | 5924 | 1 | 267 | FFFFLTDILL/CLFLRWSFTVTQAGVQ WSDLGSLQPPPRLKQFSLCLSSWDH KCLAPRANFCSFSKDGVSPPWPGWSQT PHLR |
| 5056 | 13107 | A | 5925 | 1 | 325 | MGTSSGSWPRWSVTAMPPTSMRPCSRR SSSCWPCIPRLPASTAP*SMRPHSGPRMT TRSCCLKT/RSYADGYSPPLNVAQRVVA/ W*GTQEKVMPPGRLAIPQRHRAGQQR |
| 5057 | 13108 | A | 5926 | 366 | 489 | QETTWPDLTKWLP*RPWMGMSSGF ARWSVTAMPPTSE |
| 5058 | 13109 | A | 5927 | 228 | 754 | |
| 5059 | 13110 | A | 5928 | 1 | 2709 | |
| 5060 | 13111 | B | 5929 | 76 | 925 | XQCFFLSADSRIAELLTELHQLSKQTQEE RSRSEHNLVNIQK THERMQTENKISPY RTKLRGLYTTAKADAEACNLRKALD MIAEIKSLLEERRSAKAGLYNDSEPPR KTMRRGVLMILLQQSAMTLPLWIGKPG DKPSQPSSPLVLAASKALQVLLGFLLYN LPCLSHRHHPQFLSRLRLPLYSQDCISQ CLNLVFLADVWFGLPSIYLVFLIILYEG LLGGAAYVNTFHNLIALETSDEHREFAMA ATCISDTLGISLGLLALPLHDFLCOLS* |
| 5061 | 13112 | A | 593 | 379 | 475 | DLQGVNHLRPGVQDQPGQHGETLSLLK IQNN/LARRGGGRL/QSQLRLRLRQDNRL NPGGGGCSEPRSRHCTPAWVTEQDPISK QNKRRQANFLIWEDFPYIPQGTCLIFTAQ KLPRCK |
| 5062 | 13113 | A | 5930 | 3 | 1066 | GSWGYQPTGLYAPTRRGLNVILDWVQA HFPTDDFALAEFDGTNL YEHSDPREGYH QDWNTLIYNYGRREVSNFLVGNALYWI ERFGIDALRVDASMIYRDYSRKEGE WIPNEFGGRENLEAIEFLRNTNRILGEQV SGAVTMAEESTDFPGVSRPQDMGGLGF WYKWNLGWMHDTLDYMKLDPVYRQY HHDKLTGILYNYTENFVPLSHDEVVH GKKSILDRMPGDAWQKFANLRAYYGW MWAFFGKKLLFMAAKIAGLYNDSEPPR KTMRRGVLMILLQQSAMTLPLWIGKPG DKPPPLCGAIPASGDYVARPGDRLLARL |

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| | | | | | | KPLNGERAVDLSLEGGQVTAIATQQGM R |
| 5063 | 13114 | A | 5931 | 53 | 506 | FFVFLVEMGFHHVQAGLELLNSSDLPS SASQSAG/IYRCEPLCPAFFFFSETESRSV AQAVVQWCDLSSLQPPPHFKRFFCLSL LSSWDYRHVPPCLANFCIFVEAGFHHV GQAGHKLLISSDPPASVSQSAGITGMSHC IQPHSPVFS |
| 5064 | 13115 | A | 5932 | 1 | 346 | SANATTKTSETNHTSRPRLKNVDRSTAO QLAVTVGNVTVIITDFKIEKTRSSSTSSST VTSISAGSEQQNQSSSGVQRAPDKGLPP RSLPTPKGDMSAVNDEIFPEIATWNCEK L |
| 5065 | 13116 | A | 5933 | 1 | 915 | MGKEKTHINIVVNGHIDSGKSTSTGHLY KCGGINKRSIKKFEKKAEMGKGSFKSF VCDSSWYIPGHRDFITNIFTGTSQADCAV LVVAAGVGEFEAALLQDVYKIGIGTV PDGQVETVALKPGVVITFAPVNTTTEVK SVKMHHEALSEAFSGDNVGFHVKNVSV KDIHCSNNAGNCKNDPPMEAAGFTAQVI VLNHPGQ/DCHMAHIAACKFAELKEKIDR SSGKKLEDGPKFLKSGDVAIIMVPGKP MCVESFSDYPPLGCFAACDMRQTVALG VIKAADKKAAGAGKVTKYPOKAQKAK |
| 5066 | 13117 | A | 5934 | 1 | 759 | |
| 5067 | 13118 | A | 5935 | 30 | 706 | KLPLKAKMGKEKTHINIVVIGHVDSGKS TTTGHLYKCGGIDKRTIEKFEKEAAEMG KGSFKYAWVLDKLAERERGITIDISLW KFETSKYVYTIIDAPGHRDFIKNMITGTS QADCAVLIVAAGVGEFEAVIFKNGQVTR EHALLAYTLGGKQLIVGVNKMDSPEPPY SQKKYEEIVNEVSTYIKKIGYNPDTRAFV PISGLNGDHMLEPRANMPWFKGWKSHP |
| 5068 | 13119 | A | 5936 | 1 | 706 | QSEQPCALPSRESTKLGGIGTVSSAPMET VGFNPGMVVTFAPSPR*QRKVKSAMH HEALSEALSQEQLGASNVKNVFCQGM FRPWQTVAG*PAKNDPTOWEASWLSLL QVILNHPRPK*GAGPMPLYLDCHTAHI ACKFAELKEKIDRRSGKKLEDGPKFLK SGDAAIVDMVPGKP/MCVESFSDYPPLG RFAVRDMRQTVAVGVKAVDKKAAGA GKVTKSAQKAQKAK |
| 5069 | 13120 | A | 5937 | 364 | 458 | VIEHLVSQDGLDFL/NLVICPPRPPKVLGL QA |
| 5070 | 13121 | A | 5938 | 1 | 266 | EMESRSIARMECSGISAHCKLRPLPGSH HSPASVSRVAGTTGTCHHARLIFYF/LL ETGFHCVSHDGLHLL/NLVICPPRPPKVL GLQA |
| 5071 | 13122 | A | 5939 | 1 | 201 | PPTGP/PKLPDPVHLPPFGPPPSAWALPG MSPSPDPDRNKLRIIRILKNASLSYLQVE VFPYPKMP |
| 5072 | 13123 | A | 594 | 2 | 307 | QAGV**WDLGSLQPLPRLKQFS/CILNP GNLSKEP*STKETQONIFVGHISQTSKF AISLIQHPINMRSGTKTFMMV*GNKQRS KFIWTFKIFPDMPLPS |
| 5073 | 13124 | A | 5940 | 2 | 142 | ESIQDYKHLCDLSFCQLPPDPPLTVPQ THNARDQWLQDAFHISL |

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| 5074 | 13125 | A | 5941 | 1 | 432 | IHDELSRAARA/VDGPRHAAGAANAGPA AGPRRPVNLDLSALAALRKEMLSAIVGLR QLDMSLLCQLWGLYESIQDYKHLCDL SFCQDLSSSLHSDSSYPDAGLSDDEPP DASLPDPPLTPVQTHNARDQWLQDAF HISL |
| 5075 | 13126 | A | 5942 | 3 | 696 | VSMGALGLEGRGRLQGRGSLLLAVAG ATSLVTLALLAVPITVLAVALVPDQGG/ LGFQKLPEEEPETDLSPGLPAHLIGAPL KGQGLGWETTKEQAFLTSQTQFSDAEG ALPDGLYYLYCLVGYRGRAPPGGDP QGRSVTLRSSLYRAGGAYGPGTPELLLE GAETVTPVLDPARRQGYGPLWYTSVGF GGLVQLRRGERVYVNISHPDMVDFARG KTFFGAVMVG |
| 5076 | 13127 | A | 5943 | 1 | 743 | MGALGLEGRGRLQGRGSLLLAVAGAT VSLVTLALLAVPITVLAVALVPDQGGV TETADPGAQAQGLGFQKLPEEEPETDLI PGLPTAHLIGAPLKGHGLGWETTKEQA FLTSQTQVSDAEGALPDGLYYIYCLV GITGARAPPGGDPQGRSVTLRSSLYRAG GAYGPGTPELLLEGAETATPVLDPARR QGFVPLWYTSVGFGLVQLRRGERVYV VNISHPDMVDFARGKTFFGAVMVG |
| 5077 | 13128 | A | 5944 | 1 | 588 | MGFLHVGQAGLKLLTSGHYQKKRMFSE NEENVKRMKTSEQINENICVSLERQTAF EQVPESFEHLPLPEPPAPLPVLDKTRD TLPPQKPELKVKRVFRPNGLALTWNITKI NPKCAPEEKVYPLFLCHENSNNKLIWKKI GEIKALPLMACTLSQFLASNRYFTVQ SKDIFGRYGPFCDIKSIPGFSENLT |
| 5078 | 13129 | A | 5945 | 3 | 495 | EDTGTFRIVESAGAVKKARGFLEFVEDF IQVSKNLIGKVIGKNGKVIQEIVDKSDMV PVRJEGDSENKLPREDKDDRDSRHQRDS RRCPGGRCRSVSGRRGRGGPRGGKSSIS SVPKDPDSNPYSVLDN/TESDQTADTAS KSHHSTNRHTRSRRRRRTDEDAVL |
| 5079 | 13130 | A | 5946 | 1 | 2065 | MAELTVEVRGSNGAFYKGFIKDVHEDSL TVVFENNWQPERQVPFNEVRLPPPPDIK KEISEGDEVEVYSRANDQPCGWWLAK VRMMKGEFYVIEYAACDATYNEIVTFER LRPVNQNKTVKKNTFFKCTVDVPEDLRE ACANENAHKDFKKAVGACRIFYHPETT QLMILSASEATVKRVNLSMDHLRSIRTK LMLMSRNEEATKHLECTKQLAAAFHEE FVVREDLMGLAIGTHGSNIQARKVPGV TAJELDEDGTFRIVGESADAVKKARGFL EFVEDFIQVPRNLVGKVIGKNGKVIQEI DKSGVVRVRIEGDNENKLPREDGMVPP VFVGTKEISGNVQVLLYHIAYLKEVEQ LRMERLQIDEQLRQIGMGFRPSSTRGPEK EKGYATDESTVSSVQGSRSYSGRGRGR GPNYTSGYGTNSELNPNSETESERKDELS DWSLAGEDDRDSRHQRDSRRRPGGRGR SVSGGRGRGGPRGGKSSISSVQYRSNIH NCSTLKRIFLASDMNIVLKDPSNPYSLL DNTESTDQTADTASESHHSTNRRRRRSR RRTDEDAVLMDGMTESDTASVNENGLD DSEKKPQRRNRRRRRFRGQAEVDRQPAI DFIYKEVEKVVSLLWQAKDVIEEHGPSEK AINGPTSASGDDISKLQRTPGEEKINTLK EENTQEA AVLNGVS |

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| 5080 | 13131 | A | 5947 | 1 | 1876 | MADVTVEVRGSGAFYKGFIDVHEDS LTVVFENNWQPERQVPFNEVRLPPPD KKEISEGDEVYSRANDQEPGWWLA KVRMMKGEFYVIEYAACDATYNEIVT RLRPVNQNKTVKKNITFFKCTVDVPED REACANENAHKDFKKAVGACRIFYHPE TTQLMILSASEATVKRVNLSDMHLSIR TKLMLMSRNEEATKHLECKQLAAAFH EEFVREDLMGLAIGTHGSNIQARKVP GVTAIELDEDGTFRYGESADAVKKAR GFLEFVEDFIQVPRNLVGVKNGKVIQ EIVDKSGVVRVRIEGDNENKLPREDGMV PFVFGTKESIGNVQVLEHYHAYLKEVE QLRMERLQIDEQLRQIGSRYSRGRGR RGPNTSGYGTNSELNPNSETESERKDEL SDWSLAGEDDRSRHQDRSRPPGGRG RSVSGGRGRGGPRGGKSSISVLDKPD NPYSLLDNTESDQTADTDASESHSTN RRRR/SIRRRRTDEDAVLMDGMTDSDT ASVNENGLVTVAADYISRAESQSIQRNLP RETLAKNKKEMAKDVIEHGPSEKAING PTSASGDDISKAT/RVLRGEEKINPLKEE NTQEA AVLNGVS |
| 5081 | 13132 | A | 5948 | 1 | 392 | TESERKDELSDWSLAGEDDRSRHQDRS WRRPGGRGRSVSGGRGRGGPRGGKSSIS SVLKDQPSNPYSLLDNTESDQTADTD SESHSTNRRRRSRRRRTDEDAVLMDG MTESDTASVNENGLGKRCD |
| 5082 | 13133 | A | 5949 | 269 | 973 | PAACPSPANNICFYGECSYYCSTEHALC GKPDQIEGASLGAFPLSLAKRKTWRN PWRRSYHKRKAWEVDPDYCEEVKQT PPYDSSHRILDVMDMTIFDFLMGNMDR HHYETFEKFGNETFIIHLNNGRGFGKYSH DELSILVPLQCCIRKSTYLRQLLQAKE EYKLSLLMAESLRGDQEPVLYQPHLEA LDRRLRVVLKAVWDCVERNGLHSVVD DDLDEHRAASAR |
| 5083 | 13134 | A | 595 | 374 | 665 | GAQGLSLSPRECNAILAHCNLCPLGSS NSPGSAS*VAGTIGMHHRMLFVFLVE SGFHHVGOAGLELLTSSDPPASASQAGI RGISRRAGLDF |
| 5084 | 13135 | A | 5950 | 1 | 106 | |
| 5085 | 13136 | C | 5951 | 146 | 280 | MVFKDQKMRFCFCNXXXXLMNLXXX XXXVLEKKGGSPFVFL* |
| 5086 | 13137 | A | 5952 | 2 | 1929 | MAAAVDSAMEVVPALAEAAPEVAGL SCLVNLPGVELEYILCCGSLTAADIGRVS STCRRLRELQSSGKVVKEQFRVRWPSL MKHYSPTDYVNWLEEYKVRQAGLEA RKIVASFSCRFFSEHVPCNGFSDIENLEGP EIFFEDELVCILNMEGRKALTWKYYAKK ILYYLRQQKILNNLKAFLQPPDDYESYL EGAVYIDQYCNPLSDISLKDIAQIDSIVE LVCKTLRGINRRHPSLTFIAGESSMIMEIE LQSQVLDAMNYVLYDQLKFKGNRMDY YNALNLYMHQVLIIRRTGIPISMSLLYLT ARQLGVPLEPVNFPSSHLLRWQGAEGA TLADIFDYIYIDAFGKGKQLTGKECEYLIG QHVTAAALYGVVNVKKVLQRMVGNLL SLGKREGIDQSYQLLRDSDLYLAMYP DQVQLLLLQARVYFHLGWPEKSFLV LKVLDILQHIQTLDPGQHGAIVGYLVQ HTLEHIL/ERKKEEVGVEKLRSEKVR DVCYSNGLHYGRHKRYGLN*LC*FYGW GPHLAWMGHELDNRNMNVHSLPHGH QPFYNVLVEDGSCRYAAQENLEYNAEP QEIHPDVGRVYSQRFTARTHYIPNAEL EIRYPEDLEFVYETVQWNYKCKRKENIE |

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| 5087 | 13138 | A | 5953 | 3 | 364 | FFSPETESHCIAQAGVQWQMLGSLQSP PFSCSLPSSYDYRHAPLHRANFLFLR DGVSACWPATAPGLLLIFFGRAPWLMV IPAPREAEAGGSLEARSSRPASLFQVSFFS FFFHMF |
| 5088 | 13139 | A | 5954 | 2 | 114 | FFFFGRDK/SLTMLPRLVSNCWAQGILPS WPPEVLRQA |
| 5089 | 13140 | A | 5955 | 3 | 139 | FFFFFETETHTVARAGVQWCHLASLQPL PAGSSHSPAAAASHVAS |
| 5090 | 13141 | A | 5956 | 274 | 363 | |
| 5091 | 13142 | A | 5957 | 7 | 1047 | |
| 5092 | 13143 | A | 5958 | 7 | 960 | |
| 5093 | 13144 | A | 5959 | 2973 | 3400 | GIIFMCPDMYTSTKTLKACLFALFFFIYP IYFFLVGIMEEYIKMCNIPQVGIFSKYLP *SLSV*FFFETESCFVTQAGVLWCYLSL QPPPPGFKRFSCLSLSSWDYRHLPPCPA NFC/IFSRDGVSPCWPG*SQTPDLR |
| 5094 | 13145 | A | 596 | 1 | 685 | EIKYHSLPRLECRGEISAH*NLCLPGSSDS PATAS*VAGITGMRHYAQLIFLFLVET*F HHVGQGWSRTPDSNDPPASASQAGDY RRD |
| 5095 | 13146 | A | 5960 | 6459 | 7074 | LEARAGSYRDLPGSHYLLAFFFFFRRS LTLFSQAGVK/WCDLGSSQPPSPGFKQF SCLSLSSWDYRHAPPYRG*SFFFFFFFVF LVETGVSPCWARL/VLNARPQVIHPPRAS QSAIGTTAVSHHAQPLCLFIYLFYFY/CIF LRLSFALGPQARVQWHNLSSLQPPPPGF KQFSCSLPSSWDYRWPPHPANFVLL RYLR |
| 5096 | 13147 | A | 5961 | 1 | 361 | VCYPDRDCGESLVAASYRQVPVHOCGW FHPLKPA/SHPDTVECVFRKTPKIPQKHS GSPR/PPSPSYRGRFLFRFHPQHGAQGP SPPLGRKHRPSHTGSAALRACPPPGAA GLHSWGQL |
| 5097 | 13148 | B | 5962 | 27 | 288 | MRKVHVSTVTPNYAGGEPKRFRAYTR QQVLELEKEFHYNRYLTRRRRVEIAHAL CLSERQIKIWFQNRMMKWKDHLKLPNT KIRSGX* |
| 5098 | 13149 | A | 5963 | 1 | 825 | MSSFLNSNYVDPKFPCEEYSQSDYLP DHSPGYAGGQRESSFQPEAGFRRRAA CTVQRYAACRDGPPPPPPPPPPPPGGL SPRAPAPPAGALLPEPGQRCEAVSSSP PPCAQNPLHPSPHSACKEPVVPWMR KVHVSTGRYSLSEVGSWGGVEVEEEK EEESNPNYAGGEPKRSRTAYTRQQVLEL EKEFHYNRYLTRRRRVEIAHALCLSERQI KIWFQNRMMKWKDHLKLPNTKIHSGG AAGSAGPPGRPNGGPRAL |
| 5099 | 13150 | A | 5964 | 656 | 1164 | |
| 5100 | 13151 | A | 5965 | 1 | 4033 | MWRRKHPRTSGGTRGVLSGNGRVEYGS GRGHLGTFEGRWRKLPKMPEAVGTDPS TSRKMAELEEVTLDGKPLQALRVTDLK AALEQRGLAKSGQKSALVKRLKGALML ENLQKHSTPHAAFQPN SQIGEEMSONSFI KQYLEKQQELLRQRLEREAREAAELEEA SAESEDEMIHPEGVASLLPPDFQSSLERP ELELSRHSRKSSEEEKGDSDEKPRK GERRSSRVQARA AKLSEGSQPAEEEEED QETP |
| 5101 | 13152 | A | 5966 | 3 | 5979 | KSSSISEEKGDSDEKPRKGERRSSRVQ ARAAKLSEGSQPAEEEEEDQETPSRNLV RADRNKLT EEEEEEEEEEDDEEEEGD DEGQKSREAPILKEFKEEGEIPRVKPEE MMDERPKTRSQEQEVLERGGFRTRSQEE ARKSHLARQQQEKEMKTTSPL EEEEREI KSSQGLKEKSKSPSPRLTEDRKKASLV ALPEQTASEETPPPLLTKEASSPPHPQL HSEEEIEPMEGPAPA VLIQLSPNTDA |

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| 5102 | 13153 | A | 5967 | 16 | 208 | LLPYSTNPPASASRLAVIAGVHHHTQLAF FLVETGSHCVTQSGKLFPASSNPPTGLT MLGLQV |
| 5103 | 13154 | A | 5968 | 1 | 932 | MKFLLDILLPLLVCSLESFVKLFIPKR RKSVTGEIVLITGAGHGIGRLTAYEFAKL KSKLVLDINKHGLEETAACKCKGLGAK VHTFVVDSCNREDIYSSAKKVKAEGDV SILVNNAGVVYTSDLFATQDPQIEKTFE VNVLAHFWTTKAFLPAMTKNNHGHIVT VASAAGHVSVFLLAYCSSKFAAVGFHK TLTDELAALQITGVISLCLCPNFVNTGFI KNPSTSLGPTSSCSRVPKLVPEEVVNR MHGILTEQKMIFIPSSIAFLTTLERILPERF LAVLKRKISVKFEAVIGYKMKPH |
| 5104 | 13155 | A | 5969 | 1 | 1202 | IHTGENPYECHECGKAFSRKYQLISHQRT HAGEKPYECTDCGKAFLKSQLIHHQRT HTGEKPFECSECQKAFNTKSNLIVHQRT HTGEKPYSCNECGKAFTKSQLIVHKGV HTGVKPYGCSQCAKTFSLKSQLIVHQRS HTGVKPYGCSECGKAFRSKSYLIHMR HTGEKPHCECRECGKSFSFNSQLIVHQRIH TGENPYECSECGKAFNRKDQLISHQRT AGEKPYGCSECGKAFSSKSYLIHMRTHS GEKPYECNECGKAFIWKSLIVHERTHA GVNPYKCSQCEKSFSGEITPSLLHORMH TTEKPYECSECGKAFIRNSQLIVHQRT GEKPYGCNECGKTFSQKSILSAHQRTHT GEKPCCKCTECGKAFCWKSQIMHQRT VDDKH |
| 5105 | 13156 | A | 597 | 3 | 198 | GIPGSSFCGLCGDVPKPV*RADGSC*DG VAPRLLRPRGFRGRCGPVLDLAGQRG AESGCRG |
| 5106 | 13157 | A | 5970 | 153 | 571 | LLVFYLPPTSLKGGRLQDMSLLCQLYS LYESIQEYKACQAASSPNWTYALENGF FDEEEYFPEQNSLHRRDRGPRLSLP VAPPSPAATGFWSRGSWEGCDCWEAL PTGHAIVICCFCKKAPPLWTVLGHGRG |
| 5107 | 13158 | B | 5971 | 223 | 347 | XNYIRVFGGGTKLTVLGQPKAAPSVTLF PPSSEELQANKATL* |
| 5108 | 13159 | A | 5972 | 2 | 283 | LHSRLDGAACLPGHCHGSRVEVTYETH QCGLVGLKLLRGGREQSDRGSLGLT*DG GQLGPPAEQRTTQAVIPCCAVIMSLRL EPTDGGGG |
| 5109 | 13160 | A | 5973 | 3 | 231 | RRQAQIAAGRVLVVALFGGCGGLHSRL DGAACLPGHCHGSRVEVTYETHQCGL VGLKLLRGGREQSDRGSLGLT |
| 5110 | 13161 | A | 5974 | 2 | 385 | APFMRDPAAVASVGF/PLLGRQAQVAAG RILVVALFGGFGGLHSHLDGAACLPGH CHGSRVEVTYETHQCGLVGLKLLRGGW EQSDRGSLGLTEDGQVGAASEDSIISWP KHAVIVSLILRLEPGDE |
| 5111 | 13162 | A | 5975 | 3 | 539 | RRQAQITAGRVLVVALFGGCGGLHSRL DGAACLPGHCHGSRVEVTYETHQCGLV GLKLLRGGREQSDRGSLGLT*DGQGLP SAEHLITTTIPHLTVIVGLIPGLDPGDGQ GGRVPRAGAENRSGIPAGRSAS**MTNT GARPGFCWYHCTLLSPIFSPQVILAVFP GATDTEGG |
| 5112 | 13163 | A | 5976 | 1 | 351 | RGGWEQSDRGSLGLTEDGQLGASSEH RTMQAVIPCCTVIISLILRLESTDGQGG*G ARLGARESVD*GPLIITIDEEFGGPSWD LLVPVYNINSDVGVASRTRDGDPLPGGP RR |
| 5113 | 13164 | B | 5977 | 78 | 448 | XQRVTISCTGSSSTIGAGYDVHWYQQLP GTAPKLLIYGNSNRPSGVDRFSGSKSGT SASLAITGLQAEDEADYYCQSYDSSLG YWVFGGGTKLTVLGQPKAAPSVTLFPPS SEELQANKATL* |

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| 5114 | 13165 | A | 5978 | 1 | 393 | RVLVVALFGGCGGLHSRLDGAACLPGH CHGSRVEVYETHQCGLVGLKLLRGGR EQNDRGGSGLT*DGQLGPSAEHPSGTT TSSI*TAIISLGLSLEPINCQGGRGTLGSI EIYNKPLRADYRPHKS |
| 5115 | 13166 | A | 5979 | 3 | 389 | LPGGPGTMVAFGGGLPTVQGRVQALAP VLVGACLEGCGGLHSRLDGAACLPGHC HGSRVETVYETHQCGLVGLKLLRGGR QSDRGGSGLDLGRSAWSLRRIHPDKDH WCLLIDSNSQPRLLPGRH |
| 5116 | 13167 | B | 598 | 188 | 246 | MAWLPGSCARVAFPAAGAAAR* |
| 5117 | 13168 | A | 5980 | 1 | 908 | AGHRGRRAFRGKGQGGQGRSRLGAGFSG WDKRWWVKGVSVRAEIEGVTGVPARD NSIQAGGREVGGYALRRRGRNERAEG VFSQDTSPIRASFTRRHPCASPSGPLS HWVPGFPHPTLRTQGRPPMCEIRKEERE QDFSLTMRIFIEKGWMTWDGGRDPSPG NLQLQAPVGGVVRVGGKAFRCRGHCLLH GAPFMRDPAAVASVGLPLLGRQAQVAA GRILVVALFGGFGGLQSHLDRAAICLP VCTGPRVKIHFKNHVGLVGLKLLRGGW EQSDRGGSGLTGDGQLGASSEHSTQ |
| 5118 | 13169 | C | 5981 | 60 | 392 | |
| 5119 | 13170 | C | 5982 | 176 | 385 | |
| 5120 | 13171 | A | 5983 | 1876 | 2540 | FLQLGSWLGRGSCQVSRGPGQPRSDNLL VEPKDLKGNLTHFTTLGGFHLLYMMIWI HPPINLCSGSNFFLFFFSLSRLGLALL PQAGVEWRDLGLLQPLPRLQSCPS GSSWDRRFMPWPANFCM/FL*RWGLT VLPRLVSNWAQ/CDPPVSASQSAGITIV SHHVQLEGSTSTFCCKHICFTPPFSPSLF ISHFYIDLLFYNKTLPLPKKKKK |
| 5121 | 13172 | A | 5984 | 1 | 393 | |
| 5122 | 13173 | A | 5985 | 1 | 1427 | MRERFRNLDEEVEKYRAVYNKLYEHT FLKSEFEHQKEEYARILDEGKIKYESEA RLEEDKEELRNQVLNVDLTCKSKRVEQL AREKVYLCQKLKGLAEVAELKAEN SEAQVENAQRIQVRQLAEMQATVRSLE AEKQSANLRAERLEK/DSLQSSSEQNTFL INKLHKAEREINTLSSKVKEKHSNKLEI TDIKLETARAKSELDRENRNKHSELDVYL HLDNEILKAAVEHHKVLLVKKDRELIRK VQAAKEEGYQKLVLQDEKLELENRLA DLEKMKVEHDVWRQSEKDQYEEKLRAS QMAEEITRKELQSVRLKLQQQIVTIENAE KEKNENSDLKQISSLIQVTSLAQSEND LLNSNQMLKEMVERLKQECRNFRSQAE KAQLEAEKTLEEKQIQWLEEKHKLHERI TDREEKYNQAKEKLQRAAIAQKKRSL HENKLKRLQEKVEVLEAKKEELETENQ VLK |

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| 5123 | 13174 | A | 5986 | 2 | 1831 | NYKTLIIICALFTLVTVLLWNCSSDKAI QFPRSSSGFRVDGFEKRAAASESNMYM NHVAKQQSEEAFFPQEQKAPPVVGGFN SNVGSKVLGLKYEEIDCLINDEHTIKGRR EGNEVFLPFTWVEKYFDVYGKVVQYDG YDRFEFSHSYSKVYAQRAPYHPDGVM SFEGYNVEVRDRVKCISGVEGVPLSTQW GPQGYFYPIQIAQYGLSHYSKNLTEKPPH IEVYETAEDRDKNKPNDWTVPKGCFMA NVADKSRFTNVKQFIAPETSEGVSLQLG NTKDFIISFDLKFLTNGSVSVVLETTEKN QLFTIHVVSNAQLIAFKERDIYYGIGPRTS WSTVTRDLVTDLRKGVGLSNTKAVKPT KIMPKKVVRLLIAKGKGLDNITISTTAHM AAFFAASDWLVRNQDEKGGWPIMVTRK LGEFGKSLEPGWYSAMAQQAISTLVR AYLLTKDHIFLNSALRATAPYKFLSEQH GVKAVFMNKHDWYEEYPTTPSSFVLNG FMYSLIGLYDLKETAGEKLGKEARSLYE RGMESLKAMLPLYDTGSRTIYDLRHFM LGIAPNLARWDYHTTHINQLQLLSTIDES PIFKEFVKRWKSYLKGSRAKHN |
| 5124 | 13175 | A | 5987 | 34 | 332 | LLRQGLALLPRLECSGTISAYCNLCPLGS NHPPVSVSQVAGTTGVHHAQLIFVFW VETGFCHVAQYGLEFLGSSNPPALTSPPSA GITGVSHCIWAQVF |
| 5125 | 13176 | A | 5988 | 3 | 395 | PAGGPAAGRAAARAGAMAKLLSCVLGP RLYKIYRERDSEAPASVPETPTAVTAPH SSS/WGYLSLSKVVPFPHYAGTLLLLLAG VACLRSGRWTPNPQYRQFITILEATHRNQ SSENKRQLANYNFDFRSW |
| 5126 | 13177 | A | 5989 | 3 | 414 | |
| 5127 | 13178 | A | 599 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDFSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGTG AQLSELHCDKLHVDPENFKLLGNVLVTV LAIHFGKEFTPEVQASWQKMTGVASA LSSRYH |
| 5128 | 13179 | A | 5990 | 3 | 784 | LIALRTCTESPGTTHASADAWEAALLSC VLCPRLYKIYRERDSEGAPISETETPTAD TAPHSSSWDTYYQPRALEKHADSILALA SIFWPISYYSCTF AFFYLYRKGYLSLSKV VPFPHYAGTLLLLLAGVACLRGIGRW NPQYRQFITILEATHREPSLQKTKRQLAN YNFDFRSWPVDHFWEEPSSRKESRGGPS RRGVALLRPEPLHRGTADTLNRVKKLP CQITSYLVAHTLWRRMLYPGSVYLLQK ALMPVL |
| 5129 | 13180 | A | 5991 | 461 | 660 | |
| 5130 | 13181 | A | 5992 | 1 | 1774 | MSSSEEVSWISWFCGLRGNEFFCEVDED YIQDKFNLTGLNEQVPHYRQALDMILD EPGIGRWTPNPQYRQFITILEATHRNQSSE NKRQLVYYYFFDFRSWPVDHFWEEPSSR KESRGGPSRRGVALLRPEPLHRGTADTL LNRVKKLPCQITSYLVAHTLGRMLYPG SVYLLQKALMPVLVQGAARLVEKCNV RRAKLLACDGNEIDTMFVDRRGTAEPQ GQKLVICCEGNAGFYEVGCVSTPLEAGY SVLGWNHPGFAGSTGVPPQNEANAMD VVDQFAIHRLLFFHPQDIIYALAIGGFTAT WAAMSPDVSAMILDASFDDLPLALK VMPDSWRGLVTRTVRQHLNINNAEQLC RYQGPVLLIRKTQDGNLTPTVPKDCSN RANCLLVKALQHRYPGVMAEEGLLVA RQWLEASSQLEESIYSRWEEVEDWCLA SVLRISYQAEHGADFPWASVGEDMSAD GRRQAGPLFPGLGKASCHNFGGPTHCT PLPSPQNFPRCPWHPLGTQLGLIMEEWG ERRHEERPFLFVILLCFMAVYKFCGKGV |

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| | | | | | | GGPFLLTTVPLARFSPFMWLYLTFSNIH PALHEMG |
| 5131 | 13182 | A | 5993 | 3 | 180 | |
| 5132 | 13183 | A | 5994 | 1 | 1015 | MIAPLGLGV LARDQYRQAALADWDLKL DGGRQSTGA VSLKEIIGLEGVELGADGK TVSYTQFLPTNAFGARRNTIDSTSSFSQ FRNLSHRSLSIGRASGTQGS LDTGSDLGD FMDYDPNLLDDPQWPCGKHKRV LIFPSY MLCTQLPCSQAFCSTVHSSDLSLHERN EHPCKKHNC LLQEGHSPLQAPGFRRALV VAPMQVFLLMALGVTTVIDYVKPSDL KKDMNKFFKEKFPHIKLTLNKIRTLKRE MRKLAQEDCALEEPTVPMAFVYFEKLA LKGKLNKQNRKLCAGACVLVSSQYKFG SDLKKHEVKHLIDKLAEEKFRLNRARTGF AF |
| 5133 | 13184 | A | 5995 | 48 | 327 | EELEALRRQRLAELQAKHGDPGDAIAQ QEAKHREAEMRNSILAQVLDQSARARIV SEQGLIEILKKVSQQTEKTTTVKFNRKRV MDSDEDDDY |
| 5134 | 13185 | A | 5996 | 52 | 281 | VSKLKHLKPEKTKAVENYLIQMARYG QLSEKVS LDSLEELYCYLLYQNMASKGQ LHLHWITEFLTLRRNCWRE |
| 5135 | 13186 | A | 5997 | 1 | 280 | GNPLFLELHWNPSLRQACDRIYRVGQ QKQDVSI PRFVCGGTVEESILHFQEKIDL AKQFLSGSGESVTKLTSLDLRVLIGIYPP VDRVSE |
| 5136 | 13187 | A | 5998 | 36 | 512 | LFVLLQVNVSGNELCLMTSHLESTRGHA AERMNQLKMVLKKMQEAPESATVIFAG DTNLRDREVTRCGGLPNNIVDVWEFLG KPKHCQYTWD TQTELLILGITAAACKLR FDRIFFRAAAEEGHIIPRSLDLLGLEKLD CGRFPSDHWGLLCNLADIIL |
| 5137 | 13188 | C | 5999 | 205 | 519 | MGKEGVHGGLINKKCYEMAFPLQAFPV LTSSVPSPLPTALHPFXXHTHTNHFI WAITPYPLLLPKPHGLGARAGWDTSPY PYPSRVWLENFCFLGFFSE* |
| 5138 | 13189 | A | 6 | 144 | 398 | |
| 5139 | 13190 | A | 60 | 713 | 811 | IPGRPWRL*A*PVT LRLQTQATCGG*MV RASL |
| 5140 | 13191 | A | 600 | 3 | 496 | HSLFGTSEVINKLRSPDAMGHFTEEDKG TITSLWGKIVNVEDAGGETLGRLLVVP WTQRRFFDSFGNLSASAIMGNPKVKAH GKKVLTSLGDAIKHLG*SQGAPFAQA*S ELHCDKAALLDPEELSSFLGEMLLGDPF LGNPIFGQKNFTPEGCKAFLGQKDG |

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| 5141 | 13192 | A | 6000 | 3 | 939 | FLKLHLQSSVSGLASGGGREWGAGSGV RGLLHSERSRGPDSACPELSASPRPASR GSSSPVRGRQQRPRAAPVAAPWPCWN AYIDNLMADGTCVTGAIVRYQDSEPPV WAAVPGKTFVNNTPA*GGLSLVGKDR SSFLR*MGLTLWGGQKCSVIRGLTCLQD GEF/SAMDRLRYQEPPGGAPTFQCSLFTKT DKDG*VLADGAKEGVHGGLTNNKKCYE MASHLSGFPSTDHRLSLPLHRSPTAFAPL SSPYTHHPFLFFGPLPHTPYCCQNHMGL GGQGLMGQTPSPTHIPSRVWYGKLLFFG VFFFSE |
| 5142 | 13193 | A | 6001 | 172 | 407 | |
| 5143 | 13194 | A | 6002 | 1 | 185 | ESSCLSLPSSWDHRHGRPWLADFSVFF/C YRNSLTMLPRLGLNSWPQAILPPWPKV LGLQA |
| 5144 | 13195 | A | 6003 | 1 | 618 | |
| 5145 | 13196 | A | 6004 | 1 | 478 | HPVRRFFVHRGPH/VDFSLEVVSQWYELV VFTASMEIYGSAVADKLDNSRSILKRRY YRQHCTLELGSYIKDLSVVHSDLSSIVIL DNSPGAYRSHPDNAIPIKSWFSDPSDTA LLNLLPMLDALRFTADVRSVLSRNLHQ HRPLTGTGGTLGEPNQCL |
| 5146 | 13197 | A | 6005 | 2 | 833 | WNSAELGRGGPGAGGAGVIGMMRTQC LLGLRTFVAFAAKLWSFFIYLLRRQIRTV IQYQTVRYDILPLSPVSRNRLAQVKRKIL VLDLDETLIHSHDGVLRTVRPGTPPDF ILKVVIDKHPVRRFFVHKRPHVDFLEVV SQWYELVVFTASMEIYGSAVGRNLWD NSRSIL*GGRYVYRQPAPLELGSYIKGPL CWFHSDLSIVILDNSPGAYRSHPGYGG RDNAIPIKSWVSVTPSDTALLNLLPMLD ALRFTADVRSVLSRNLHQHRLW |
| 5147 | 13198 | A | 6006 | 2 | 258 | EAESRSVPRLECSGPILAGCMLHLPSC HFPASASQVAGTTARHHTQLIFAVLVE NGLC*PGWSRSPDLVIRLPWPPKVLGLQ A |
| 5148 | 13199 | A | 6007 | 60 | 429 | IRGOYMWGPVSSSLFCSMGYLVFGFFSFI FFFCDEVLLSTRLECNGTISGHCNLCPL GSSHSPVSASRVAGTTGARNKARLIFYF FLVEMGFHHISQDGLDLLNLVIRPPWPP KVLGLQA |
| 5149 | 13200 | A | 6008 | 1 | 1047 | SCGWTFTSMKLLRHRKHDDRRFTC PVEGCGKSFTRAEHLKGHSITHLCTKPFE CPVERCCARVSARSSLYIHSKKHVQDVG APKSRCPVSTCNRLFTSKHSMKAHMVR QHSRRQDLLPQLEAPSSLTSSSELSSPGQ RELTNMDLAALFSDTPANASGSAGGSDE ALNSGILTIDVTSVSSSLGGNLPANSSSL GPMEPLVLVAHSDIPPSLDSPLVLGTAA TVLQQGSFSVDDVQTVSAGALGCLVAL PMKNLSDDPLALTSNSNLAHHITPTSSS TPRENASVPELLAPIKVEPDSPSRPGAVG QQEGSHGLPQSTLPSPAEQHGAQDTLS AGTGNFYLV |
| 5150 | 13201 | A | 6009 | 66 | 423 | MEVACRQSTSWQPMDLASSSDFRPRMQ NPTTNRHSQANSCLQGDSPRRMSASKR YFEKTNAICRPSSFTKHSRESSGSPGVSRS CTGTRF*NVTKQPYFTSSKHKRTGKVKV RISVV |
| 5151 | 13202 | A | 601 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDLKGTF AQLSELHCDKLHVDPENFKLLGNVLVTV LAJHFGKEFTPEVQASWQKMTGVASA LSSRYH |

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| 5152 | 13203 | A | 6010 | 44 | 283 | FSCLILHDAFPCLILHDAFPCSLCSVTGSL VLSRVPLRGTHQKSAIATSTKIALSNM/KI LKHHTDAYFKKQQLFFDVSKK |
| 5153 | 13204 | C | 6011 | 107 | 118 | MAV* |
| 5154 | 13205 | A | 6012 | 197 | 683 | SLEVPLGFLLYLSFILLYSCFPLSNRVLLC HRDPFLSFLDLFLPAFSPDYVQFLFL*CA PQFSIRH*TL*MLHCKCLDFFFFFFFETR FHSPSLRLECSGMISAYCSVTSWTQVRG TTGTCHHAWLVFIFSVETGFHHVAQPD QLLPVRPPKVLRLQV |
| 5155 | 13206 | A | 6013 | 1 | 415 | LWREGPKWN/AARLNESTTFVSVSRPTIA CGMVGTIVRFYIKSPHLFKYAADPRDK HWLAEQHMRATGGKMAFYLLIEDIP GPCGPVMITEDALDLKLEGIEPLSLPSW MVEKMRKYMETLRTENEHRAVEAPQ T |
| 5156 | 13207 | A | 6014 | 1 | 1256 | |
| 5157 | 13208 | A | 6015 | 2 | 1594 | GRPARGAPQRGQTPEAGADKRATAGLC GGGGGRRRHRASGRRRAGRGPAGLKS QQQRAVPKRAVARGGRQVYSAIALLEP AGSEIADDLSILYSNRAACYLKEGNCSCG CIQDCNRALHLPFSMKPLLRAMAYET LEQYGKAYVDYKTVLQIDCGLQLANDS VNRLSRILMELDGNWREKLSLIPAVPAS VPLQAWHPAKEMISKQAGDSSSHRQQGI TDEKTFKALKEEGNQCVDKNYKDALS KYSECLKINKECAIYTNRALCYLKLQ FEEAKQDCDQALQADGNVKAIFYRRAL AHKGLKNYQKSLIDLNKVILLDPSIIEAK MELEEVTRLNLKDKTAPFNKEKERRKI EIQEVNEGKEEPGRPAGEVSTGCLASEK GGKSSRSPEDPEKLPIAKPNNAIEFGQII NALSTRKDKEACAHLLAITAPKDLPMFL SNKLEGDTFLLLIQSLKNNLIEKDPSLVY QHLLYLSKAERFKMMLTLISKGQKELIE QLFEDLSDTPNNHFTLEDIQLKROQYEL |
| 5158 | 13209 | A | 6016 | 1 | 449 | MAEGEITTFALTEKFNLPNGYKPKLL YCSNGGHFLRILPDGTVDGTRDRSDQHI QLQLSAESVGEVYIKSTETGQYLAMDT DGLLYGSQTPNEECLFLERLEENHYNTY ISKKHAEKNWFVGLK\GPRTHYGQKAIL FLPLPVSSD |
| 5159 | 13210 | A | 6017 | 1 | 153 | |
| 5160 | 13211 | A | 6018 | 1 | 528 | |
| 5161 | 13212 | A | 6019 | 223 | 513 | QRGPLPEDPSGWHSGWDKGQERPAHRH QMRNVCSWKGWRRITITPIYPRSMQRR GLLASRRMGAANAVLGLTMARKQSC*A MAEGEITTFALTEKFNLPNGYKPKLL YCSNGGHFLRILPDGTVDGTRDRSDQH QTPNEECLFLERLEENHYNTYISKKHAE KNWFVGLKKNKNGSCKRGPRTHYGQKAIL FLPLPVSYNSRDLFWEG |
| 5162 | 13213 | A | 602 | 38 | 538 | APSPDAMGHFTEEDKATITSLWGKVN EDAGGETLGRLLVVYPWTQRFDSFGN LSSASAINMGNPKVKAHGKVLTSLGDA IKHLDDLKGTFAQADVNCTCDKALHVD PENFKLLGNVLTVLGNPIFGKEFTPEG CKASWAERWVTWSWPVPCSSRIPLKPL CP |
| 5163 | 13214 | A | 6020 | 1 | 812 | MAEGEITTFALTEKFNLPNGYKPKLL YCSNGGHFLRILPDGTVDGTRDRSDQHS GLNYSWTMHQRLQALRTNDHFAGAHA VPSDAQVMGMDAGVYTSSKTIAAFVIVL LYHSQVHLSVSLIMQKPQVQGPWLALS QQLQEDVGLENWNEVTLESWTPSQLHK PLSLVQLQLSAESVGEVYIKSTETGQYL AMDTDGLLYGSQTPNEECLFLGLEE NHYNTYISKKHAEKNWFVGLKKNKNGSC |

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| | | | | | | KRGPRTHYGQKAILFLPLPVSSD |
| 5164 | 13215 | A | 6021 | 1 | 1471 | MESMFSSPAEALQRETGVPGLLTPLPD LDGVYELERVAGFVRDLGCERVALQFP DQLLGDAVAVAAARLEETGSKMFILODT AYGSCCVDLGAEQAGAQAHLHFGPAC LSPPARPLPVAFVLSSTFCGLGTLQDLW GPKPRQSACGAA\GEPACAHLEALAT LLRPRYDLLVSSPAFPQVGSLSPEPMP LERFGRFPLAPGRRLEEYGAIFYVGGSK ASPDPLDPLSRLLLGWAPGQPFSSCCP DTGKTQDEGARAGGLRARRRYLVERAR DARVVGLLAGTLGVAQHREALAHLRNL TQAAGKRSYVLALGRPTAKLANFPEVD VFVLLACPLGALAP\QLSGLRFQILAPCE LEAACNPAWPPGLAPHLTHYADLLPGS PFHVALPPESELWETPDVSLITGDLRPPP AWKSSNDHGSALTPRQLELAESSPAA SFLSSRSWQGLEPRLGQTPVTEAVSGRR GIAIAYEDEGSG |
| 5165 | 13216 | A | 6022 | 1 | 343 | PTRPPTRPRTHGQECPLLDPVDFLLFRTR AGDPLRRVSSSFNKNLIFFSIKPQPPCL AFHPRDPPGSKRPLFWDPFKGPPILAPI LSLTQIFFRWSCFFPKSRIAQQWALS |
| 5166 | 13217 | A | 6023 | 3 | 919 | |
| 5167 | 13218 | A | 6024 | 3 | 275 | GLRLGKIGRDCLIGYGASMLLLERLMIS SDAFEVDVCGQCGLLGYSGWCHYCKSS CHVSSLPUFYACKLLFQELQSMNIPLK LSKYNE |
| 5168 | 13219 | A | 6025 | 455 | 679 | |
| 5169 | 13220 | A | 6026 | 1 | 2064 | MTASIRRYHTCATDGEPSVVLVGGDGD LTLVAALGLDLGLPFMLLPMEWMR VAITYAEHRRSLTVDSGDIRQAARLLP/ GPEHCFSSFRRLDARAATEKFNQDLGFR MLNCGRTDLINQAIEALGPDGVNTMDD QGMTPLMYACAAGDEAMVQMLIDAGA NLDIQVPSNSPRHPSIHPDSRHWTSLTFA VLHGHISVVQLLLDAGAHVEGSAVNGG EDSYAETPLQLASAAGNYELVSLLSRG ADPLLSMLEAHGMGSSLHEDMNCFSHS AAHGHRGIWGLVTLGPLACLEEDHETP SPRVQSSPSGQEGTGGQLRNVLRKLLT QPQQAADVLSLEILAEGVEESDASSQ GSGSEGPVRLSRTRTKALQEAMYSAEH GYVDITMELRALGVPWKLHIWIESLRTS FSQSRYSVVQSLRDFSSIREEEYNEELV TEGLQLMFDILKTSKNDSVIQQLATIFTH CYGSSPIPSIPEIRKTLPARLDPHFLNKE MSDVTFLVEGKLFYAHKVLLVTASNRF KTLMTNKSEQDGDSSKTIIESDMKYHIFQ MMMQYLYYGGTESMEIPTDILELLSAA SLFQLDALQRHCEILCSQTLMESAVNT YKYAKIHNAPELALFCEGFFLKHMKALL EQ\MPSGSSSTAAAKCRAWIHCRTRC PWQSACTLSTSPPGSAA |
| 5170 | 13221 | A | 6027 | 2 | 144 | LFYEMESCSIAQAGVQWLSLGLLQAPPP GSCHSPASASCELMFFKI |
| 5171 | 13222 | A | 6028 | 163 | 465 | |
| 5172 | 13223 | A | 6029 | 1 | 1614 | |
| 5173 | 13224 | C | 603 | 83 | 349 | |
| 5174 | 13225 | A | 6030 | 163 | 1917 | |

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| 5175 | 13226 | A | 6031 | 133 | 424 | PFLCDLFHLVIFISDSLFLMVIDFVNGTFM ISFINRILLGQNDRGIVFSTDDYFHHQDG YRYNVNQLGDAHDWNQNRGLFWAKCP RIEYLARSQKT |
| 5176 | 13227 | A | 6032 | 3 | 270 | FKMESGSVAKLECRGTISAHCNLRPPGS SDPPASASQIAATTGVHHNRLIPAFLVE TGfCHVDQAGLELLT/LVIHPPRPPKVLG LQA |
| 5177 | 13228 | A | 6033 | 407 | 720 | RHNSSNFFFFFFFETESRSIAQACMQWC YLSSLQSLPPGFKRFSCLSLPSSWDDRC PPCLANFVFLVETGFCHVGQAGLELLIS GDPPASASQSTGITGMI |
| 5178 | 13229 | A | 6034 | 1 | 135 | KEAPGLKKENN\CFVCAICQINMEGKTL SKKDRPICKSHAFFHV |
| 5179 | 13230 | C | 6035 | 96 | 410 | |
| 5180 | 13231 | C | 6036 | 108 | 422 | |
| 5181 | 13232 | A | 6037 | 2 | 195 | CLPRFMPILPASTSQVAGNTGAHHHARLI FVFLVEVGFHHVVGAGLL/ISLPQMIHPP RPPKVLGL |
| 5182 | 13233 | A | 6038 | 251 | 377 | LGLAQTILDNPLLGEGLECAPTGPLEPP LAYTVNLILKSKARTEPQKQYFSSHAK NGG*REGVAA*APTGPLEPLAYTVNLIL KSKA |
| 5183 | 13234 | A | 6039 | 175 | 393 | ARPTFRLYLSLPVSQAGQQREAER/HPRL VPTGPTHREPSVRYDNLNRHIVDLSVAP RGEESRRQGLVVHL |
| 5184 | 13235 | A | 604 | 295 | 448 | NQTCVCWHACAYVSSNRVPWSIGSAIRS VCCYPLPPALCAPCL*ISTALD |
| 5185 | 13236 | A | 6040 | 1 | 537 | |
| 5186 | 13237 | A | 6041 | 1 | 1555 | MPYSLNLAIRDTFVNASRTLYSSSPRVLS NNSDANLELINTWVAKNTNNKISRLDS LPSDTRLVLLNAIYLSAKWKTTFDPKKT RMEPFHFKNSVIKVPMMNSKKYPVAHFI DQTLKAKLSRGDSLKEPTSAIESSRHP RSEPSLEPESFRSPTFGKSFHFDPLSSGSR SSSLKSAQGTGFELGQLQSIRSEGTTS YKSLANQTRNGSLSYDSLTPSDSPDFES VQAGPEPDPLGYTSPFLSARLAQOREA ERHPRLVPTGPTHREPSVRYDNLNRHIV ASLQEREKLLRQSPPLPGREEEPGLDGS IQSTPGSGHAPRTSSSSDDSKRSPLGKTP LGRPAVPRFGKPDGLRGRGVGFPEPGPT APYLGRMSYSSQIAQPGVSETEEVDLRP LLTPKDEVQLKTTYKSNGQPKSLGSAS PGPGQPPLSSPTRGGVKKVSGVGGTTYEI SEFDHHCWPVNNCIGRRNYRYFFLFLS LTAHIMGVFGFLLYVLYHIEELSGVRT AV |
| 5187 | 13238 | A | 6042 | 1 | 627 | TRREAERHPRLVPTGPTHREPSVRYDN LSRHIVASLQEREKLLRQSPPLPGREEEP GLGDSGIQSTPGSGHAPRTSSSSDDSKRS PLGKTP LGRPAVPRFGKPDGLRGRGVG SPEPGPTAPYLGRMSYSSQKAQPGVSE TEEVALQPLLTPKDEVQLKTTYKSNGQ PKSLGSASPGPGQPPLSSPTRGGVKKVSG VGGTTYEISV |

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| 5188 | 13239 | A | 6043 | 3 | 2265 | PTWLERGGGEPAARPQTPOPTAPESRGP SGASALRCRGPTARSLPAASMLGAPDES SVRVAVRIRPQLAKEKIEGCHICTSVTPG EPQVFLGKDKAFTFDYVFDIDSQEQIYI QCIEKIEGCFEGYNATVFAYGQTGAGK TYTMGTGFDVNIVEEELGIISRAVKHLF KISIEKKHIAIKNGLPAPDFKVNAQFLEL YNEEVLDLFDTRDIDAKSKSNIRIHED STGGNLYCGRLPTRTVNTESEMMQCLK LGALSRTTASTQMNVSQSSRSHAFTIHVC QTRVCPQIDADNATDNKIISESAQMNEFE TLTAKFHFVDLAGSERLKRTGATGERAK EGISINCGLLALGNVISALGDKSKRATHV PYRDSKLTRLLQDSLGGNSQTIMIACVSP SDRDFMETLNTLKYANRARNIKNKVMV NQVAELVSKSMHFVVKSHDFRWSSWST KPGKRIIDEEGVESINDMFHENAMLQTE NNNLRVRJKAMQETVDALRSRITQLVSD QANHVLARAGEGNEEISNMHSYIKEIED LRAKLLESEAVNENLRKNLTRATARAP YFSGSSTFSPITLSSDKETIEIDLAKKADLE KLKRKEKRKKKSVAGKEDNTDQDEKK EEKGVSERENNELEVEESQEVSDHEDEE EEEEEEEDDIDGGESDESDESDEKANY QADLANITCELAIKRKLIDELENSQKRLQ TLKKQYEEKLMMMLQHKIRDTQLERDQV LQNLCSVESYSEKKKK |
| 5189 | 13240 | A | 6044 | 2 | 323 | EDQGLYSIRMEGARGCLAKSLAL*GAGR GFYSGERTWTLSPSGNCAPYQRGGW WSHA*AHSNLNGVWHHGGHYRSRYQD GVYWAEFRGGAYSLRKAAMLIRPLKL |
| 5190 | 13241 | A | 6045 | 3 | 902 | PFFCSTISYRLCPEGAAGQKKVLPPLV PVVPVRLVGSTRDTSRMRDPAPEPQRDQ TORQQEPMASPMPAGHPADPTKPVGPW QDCAEARQAGHEQSGVYELRVGRHVVS VWCEQQLEGGGWTVIQRRODGSVNVFT SWQHYKAGFRPDGEYWLGLEPEHHHL TSRGDHELLVLKEDWGGRGARAHYDG FSLEPESDHYRLRLGQYHGDAGDSLW HNDKPFSTVDRDRDSYSGNCALYQRRG WYHYHAICAHSNLNGVWHHGGHYRSRY QDGVYWAEFRGGAYSLRKAAMLWPLK L |
| 5191 | 13242 | A | 6046 | 3 | 218 | KAVSLSVTQAGVQWALISLQSPPPFRNRF SCLSLPSSWDYRQVPPRPANFCIFSRDRV SPCWPGWSPTPNLK |
| 5192 | 13243 | A | 6047 | 1 | 297 | MVVSIFYFPTHPSFPVLLCLVLCPGRLIL RDCNPPRLPFVIDFCLGLVNGMPWHSF GGKKREDNVFLHCSHSDLG YVLLAGTA SLQDFSFFQKSPPP |
| 5193 | 13244 | A | 6048 | 1 | 8157 | |
| 5194 | 13245 | A | 6049 | 1126 | 1355 | |
| 5195 | 13246 | A | 605 | 43 | 208 | ARTLIEVIGLSHHNQKAHAMLNNAF*SSI RASP*RSYG*SSLWNQTSRFQIPAPT |

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| 5196 | 13247 | A | 6050 | 1 | 1627 | MGSRCLNPPPPAHSDTTGKDSFGNIRGA ETGQGASACSVTSARVTCGAGSEPHSHR NPGISAQVGLAPSYGAARGRRRLALQQ SPQERRHVGWNSTRGLLPASLPGTASSQ SASATASAAALPKVTGPLARNPTPWTA AAALATRGQRPEKGLFPGPAPFSLGKRK RGRGRTWERRRRVSIETSTCFRPGCERL GAAAGANLSQLASSQRPLRERWVLYTHI MAAAGAPDGMEEPGMDTEAETVATEAP ARPVNACLEAEATAGAGAGTVAEDSGTA RGSLLQAPAPAPAQAPGDPVSQASVSNGE DSGGSADSELVDLRIWNKTKHDVKFPL DSTGSELKQKHSITGLPPAMQKVMYKG LVPEDKTLREIKVTS GAKIMVVGSTINDV LAVNTPKDAQQDAKAEENKKEPLCRQ KQHRKVLDKGKPEDVMPVKGAQERLP TVPLSGMYNKS GKGKVRLLTFKLEQDQLW IGTKERTEKLPMGSIKNNVSDPIEGHED YHNDGRFQLAPTEAISYYWVYVWPTQY VDAIKDTVLGKWQYF |
| 5197 | 13248 | C | 6051 | 47 | 298 | |
| 5198 | 13249 | B | 6052 | 64 | 362 | XCVWHRRKVAVNLAKLKLFRHYVVMV ICYVYFTRIAILLQVAVPFQWQWLYQPT GNNPYLQLPQEDEEDVQMEQVMTDSGF REGLSKVNKTASGRELL* |
| 5199 | 13250 | A | 6053 | 1 | 342 | |
| 5200 | 13251 | A | 6054 | 1 | 485 | |
| 5201 | 13252 | A | 6055 | 696 | 3195 | SGRRTPMASCRQRRCPFSSTWSCPPAS WPLASSGCPSSAGTRTASFkihWLMaAL AFTKSISLLFHSVRALDRGAAGAPITSFES HPPSSLFNFLTTHLMVTVRVNPPPPPSA SHPSVRLTVRLSIHPQINYYFINSQGHPIE GLAVMYIYIAHLLKGALLFITIALIGSGWA FIKYVLS DKEKKVFGVIPMQVLANVAYI IIESREEGASDYVLWKEILFLVDLICCGAI LFPVWVSIRHLHGCVWHRRRMVAVNLA KLELFRHYVVMVGARLTHSGFGGITGL LHAHPSPSAAAPSRGPHPGSPARILQSSP MPARAPTVLAPRLAPLQVICYVYFTRII AILLQVAVPFQWQWLYQLLVEGSTLAFF VLTGYKFQPTGNNPYLQLPQEDEEDVQ MEQVEAHTLKLKLVKDIKSTVSNVSEMK ENMDKELKQIMRMiyERRICVADPFEVT VMQDFFIDLRLPYSVVRNEQVEIRAVLY NYRQONQELKVRVELLHNPAFCSLATTKR RHQQTVTIPPKSSLSVPYVIVPLRPACRK WKSRLLSITHSSVTVSGKGQKEDIPPAD LSDQVPDTESETRILLQGTPVAQMTEDA VDAERLKHILVTPSGCGEQNMIGMTPTV IAVHYLDETEQWEKFGLEKRQGALELIK KGYTQQLAFRQPSAFAAFVKRAPSTWL TAYVVKVFS LAVNLIAIDSQVLCGAVKW LILEKQKPDGVFQEDAPVIHQEMIGGLR NNNEKDMALTAFLVLSLQEAKDICEEQV NIHNRYAATRQLMVAKISGKFSKMDKS KTAGLADCHSVLDVSNKGVL RDVASTS SGIVDWRGSQIQT |
| 5202 | 13253 | A | 6056 | 1 | 516 | LRQPTRPVFGVIPMQVLANVAYIIESRE EGASDYVLWKEILFLVDLICCGAILFLV WSIRHLKDASGTDGKVPVNLPLKLFRLH YYVIPAPTPCAPLQVICYVYFTRIANPL QVAVPFQWQWLYQLLVEGSTLAFFVLT GYKFQPTGNNPYLAVAPGGRGCSRSWS K |

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| 5203 | 13254 | A | 6057 | 3 | 528 | LSCRVQSVAPPRPRPALPVSAVPGTGT LTPALLHP/WLADCDVSDSSCSLAATLL ANHSLRELDLSNNCLGDAGILQLVESVR QPGCLLEQLVYVQRAGRVPPLPREE GGGGGGHWAHASLLACVQPVQFTGLR RWRTGLQGPGETSTSLRGHLLRLFLL AAALDDRP |
| 5204 | 13255 | A | 6058 | 1 | 334 | |
| 5205 | 13256 | A | 6059 | 225 | 843 | WTRCWSRLRASGSSCEGRRAAPPRPCA RYEGGYQRSCGSESACGRRVLGSSLRQ HQGSCRNTRAGMFCGRQYIPHPAASPR RPLGRSRNTQMGTPLSRVLLRSCRKKID/ SLKQKVTHLRGLQIPHEPELMRKEISRLN KTVGRENK*LSRSEAGAGGLQEARDAA LERVQMLEQQVSVPRAPDGTQMSAGR WWPKSWDRLG |
| 5206 | 13257 | C | 606 | 892 | 1269 | |
| 5207 | 13258 | A | 6060 | 300 | 957 | GSTKVHAETHALGCSVADSTSRTHOQL HRGAHWGEVGTWRWHTSVQSVIEKLQ EENRLKQKVTHVEDLNKQWRYNASR DEYVRGLHAQLRGLQIPHEPELMRKEIS RLNRQLEEKINDCAEVKQELAASRTARD AALERVQMLEQQILAYKDDFMSEADR ERAQSRIQEELEKVASLLHQVSWRQDSR EPDAGRIHAGSKTAKYLAADALELMVP G |
| 5208 | 13259 | A | 6061 | 2 | 271 | FFETESRSVARLECSGAISAYCTLCPLGS SDSIASASRVAGITGEHHHARLILVFLVE MGFHHVQGAGLGLLDLVHPPRPVKVLG LQA |
| 5209 | 13260 | A | 6062 | 3 | 376 | DYSLGLPVVTTGCWGHMSNAPLRWALN PSYWGKNQLLCPESLALCCGLCCCKPRFL EVTSVRSADLYLSSPCLVRRCPFRGKE KPAVGMRMPDNKGWRRALSSSLSPRVP APVAASVLTVMN |
| 5210 | 13261 | A | 6063 | 2 | 70 | |
| 5211 | 13262 | A | 6064 | 3 | 258 | ADPPSPSFCFCFFFETESCSVTRLECSG AILAHCNLC/LPTCHHAWVIFVFLVETEF HHVGEDGLNLL/NFMIYLP RPVKVLGLQ A |
| 5212 | 13263 | A | 6065 | 1 | 408 | |
| 5213 | 13264 | A | 6066 | 3 | 25 | |
| 5214 | 13265 | A | 6067 | 3 | 503 | |
| 5215 | 13266 | A | 6068 | 1 | 1740 | MAAVVAATRWQQLLVLSAAGMGASG APQPPNLLLLMDDMGWDLGVYGEPS RETPNLDMAAEGLLFPNFYSANPLCSP SRAALLTGRLPINRGFYTTNAHARNAYT PQEI VGGIPDSEQLPELLKKAGYVSKIV GKWHLGHRPQFHPLKHGFDEWFGSPNC HFGPYDNKARPNI PVYRDWEMVGRYYE EFPINLKTGEANLTQIYLQEALDFIKRQA RHHPPFLYWAVDATHAPVYASKPFLGTS QRGRYGDVREIDDSIGKILELLQDLHV ADNTFVFFTS DNGAALISAPEQGGSGNPF LCGKQTTFEGGMREPALAWWPGHVTA GQVSHQLGSIMDLFTSLALAGLTPPSDR AIDGLNLLPTLLQGRMLDRPIFYRGDTL MAATLAGQHKAHFWTWTNSWENFRQG IDFCPGQNVSGVTTHNLEDHTKLPLIFHL GWDPERFPLSFASA EYQEALSRTSVV QQHQEALVPAQPQLNVCNWAVMNWAP PGCEKLGKCLVTPESIPKKCLWVPLAPA QTQARPRISSWPCKCLEEGWLWPRSSPN PAPSQTDSTCRRRGCTISNLPRT |
| 5216 | 13267 | A | 6069 | 3 | 2945 | |
| 5217 | 13268 | A | 607 | 187 | 363 | MPLRLPIQDVY*IGGIGTALVGRVESGAV NYGLVGSSVH*AVQSVALDFRFNSWML YSQ |

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| 5218 | 13269 | A | 6070 | 2 | 3078 | |
| 5219 | 13270 | A | 6071 | 3 | 3204 | AGRGRLWGGTASREPQKSAGKFPRWGA FRASRTALGPGARSQERGPGGGNAPRPP PPRLPPAAVLAAA VAAAAALPRRGAAL KGGTPPPGALAAARAPREPVAAMPPRAPP APGPRPPRAAAATDTAAGAGGAGGAG GAGGPGFRPLAPRPWRWLLLLALPAACS APPPRPVYTNHWAVQVLGGPAEADRVA AAHGYNLQGIGNLEDYYHFYHSKTFK RSTLSSRGPHFTFLRMDPQVKWLQQQEV KRRVKRQV |
| 5220 | 13271 | A | 6072 | 3 | 3002 | |
| 5221 | 13272 | A | 6073 | 1 | 1181 | MEVSRAGLSTVLEAVLCPADLTAASLDA ASPMSSSHLPVLGYPVGKSGARPGSTQ EVVLTAAAVTQEVVLTAAAVTQEVVLT AAAVTQEVVLTAAAVTQEVVLTAAAVT QEVVLTAAAVTQEVVLTAAAVTQEVVLT TAAAVTQEVVLTAAAVTQEVVLTAGA ENKPVSAPHSSSTCARTGSPGRPLHTQSP PRGHILFGKEKVCYKFKHDILKHLTQLT VDGIVSIPLVQVLRRTALTSAEHSQR VVYLEHVVRTSISHPRRGDLQIYLVSPS GTKSQLAKRLDLSNEGFTNWEFMTV HCWGEKAEGQWTLEIQDLPSQVRNPEK QG/DVFCTKCHSHQSFEESQDTKSVAW EGWGCTHGVHCEVPKNLGIRSGKHHPL KIKLV |
| 5222 | 13273 | A | 6074 | 3 | 656 | RSAFELWTQEGGLPSPSGW/VIIQSLKNL NRTDSRGRSSPLISCLATGAGTSRHLLP LDWMSTIGCPGSQASRPESLNTSGFP GFPAPHPRWWAFSGPQSHINQIPKSP CVGSLLQRAYTNTLPFLPLQFLRSPTKES TYSQLHPSGSPGGGPGPRLGLTSPKAS EQPLPGFDWEGQGSRRAGADGSGRES SGTPGTAVLQRSSCGTSC |
| 5223 | 13274 | A | 6075 | 3 | 873 | AAEGLPPVRIPPFSETTANGTISFTEMVQ DMGAGLAVVPLMGLLESIAVAKAFASH NNYRIDANQELLAIGLTNMLGSLVSSYP VTGSFGRTA VNAQSGVCTPAGGLVTGV LVLLSLDYLTSLFYYPKSAVGAVIIMG RGPVAVSTPRSFARNALGFLKRLDLLPLCVT FLLCFWEEQDGLAGALGSLMLLHSAA RPETKGSEGPVLVLQPASGLSFPAMEAL REEILSRALVSPRCLVLECTHVCSIDYT VVLGLGELLQDFQKQGVALAFEGQLQVP RLRVLLSR |
| 5224 | 13275 | A | 6076 | 3 | 256 | HASGMKNDLVYTGVDPETLPNRNGDGV /PTGLSPDPQFRTRKIQASLLTLEETMKQ LEEEEFRRLLKPLLANLGNSVPHPGCT |

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|------|-------|---|------|-----|------|---|
| 5225 | 13276 | A | 6077 | 1 | 1966 | MAEPLLRKTFSRLRGREKLPRKKSDAKE RGHPAQRPEPSPPEPEPQAEQSGAGAEG PSSPEASRSPARGAYLQSLPSSRRWVLG GAKPAEDTSLGPGVPGTGEPAGEIWINP IPEEDPRPPAPEPPGPQPGSAESEGAPQG AAPASPPT/NSLPHQVPGPRQAPLHKDEE AAGTAAPPEPARPPGWQGAREGCPCGL RHQPLPPGQQRGGPRAGSRAWGHPEPE GRLPQRRGLTGAPSWAPITHLLPALRGG SRSPGTGRTLGPPQPAPVRSRGAAASA GGHPQGPLLPTASGWGGQGNRATARG AGLPAAGPHLPPGAGGRQAPARPGACV GPWREKAPALCPGHRAAAHGLPRCQA QQLAVRLEPQGLLYAKLTLSEQQEAPAT AEPRVFGPLPLLLVERERPPQVPLIJKC VGQIERRGLRVVGLYRLCGSAAVKKELR DAFERDSAACVCLSEDLYPDINVITAVPSL ALEASGALTRGDPVFTGILKDYRELPTP LITQPLYKVVLEAMARDPPNRVPPTTEG TRGLLSCLPDVERATLTLLDHLRLVSSF HAYNRMTQPQLAVCFGPVLLPARQAPT RPRARSSGPGLASAVDFKHHIEVLHYLL QSWPWPACPDNLQMSRLTCDPNDSHLCT CRWQTPKW |
| 5226 | 13277 | A | 6078 | 2 | 82 | |
| 5227 | 13278 | A | 6079 | 1 | 347 | FFFFFFFFLETASHSVAQAGGQGHDLSSL QPPPPRFKQFSCSLPSSWDHRHKPPHPV NFVFLVETGFHHVGQAGLELLTSSDPPA SASQMAGITGVSHCAWPITIFKQSNYGM L |
| 5228 | 13279 | A | 608 | 514 | 792 | DSRCPGAMACALRAPRITNPVSAQWDP ETGSAVAGEPWIWTQRERNQSALQRGNV PFCRCRDHEFTLDLGGQGGQIT*GQEFET SLANMAKPH |
| 5229 | 13280 | A | 6080 | 1 | 779 | |
| 5230 | 13281 | A | 6081 | 1 | 214 | HPTAAIVPPGPEAGLIYTPYEYPYTLAPA TSILEYPIEPSGVLVWLSQRKAKNSRTV LTEPSSDLNLTNA |
| 5231 | 13282 | A | 6082 | 3 | 435 | EPFPGGDCIPRATLESCRSMLMDTVGS GKLNLEQFHHLWNKIKGWQKIFKHYD TDQSGHHQTATKMRNAV/NTDAGHLN NQLYDIITMRYADKHMNIDFDSFICCFV RLEGMFRAFHAFDKDGDGIIKLVLEWL QLTMYA |
| 5232 | 13283 | A | 6083 | 2 | 339 | GKPTLREFTHL/WDKIKGWREIFNNITPS QSGTITGYEMRNA/VNDAGFHLNPLVD IINTSRTADNHMNIDFESFICCFVRLEG MFRAFHAFDKDGDGIIKLVLEWLQLTM YA |
| 5233 | 13284 | A | 6084 | 2 | 775 | PSASDQSTWYLDESTLTDNIKKTLHKFC GPSPVVFSDVNSMYLSSTEPPAAAEWAC LLRPLRGREPEGVWNLSIVREMFKRRD SNAAPLLEILTDQCLTYEQITGWWSVR TSASHSSASGHTGRSNGQSEVAHAACAS MCDEMVTWRLAVLDPALSPQRRREL TQLRQWQLKVIENVKRGQHKKTLERLFP GFRPAVEACYFNWEEAYPLPGVTYS GTDRKLALCWARALPSRPGASRSGGLEESR DRPRP |
| 5234 | 13285 | A | 6085 | 193 | 388 | |
| 5235 | 13286 | A | 6086 | 2 | 353 | AAAEDLSDALCEVDAVLADFASPFHER HFHYEEHLERMKRRSSASVSDSSGFS SDSEVADSLYRNSFSFSDKLNSTDPAL LSATVTPQAKLGDKELEAFIADLDKT LASM |
| 5236 | 13287 | A | 6087 | 315 | 411 | |
| 5237 | 13288 | A | 6088 | 2 | 283 | |
| 5238 | 13289 | A | 6089 | 3 | 189 | |

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| 5239 | 13290 | A | 609 | 1169 | 1335 | NFASDDKFSLP*DYTTFKVNWP GAVAH A*NPSNLGGQGGQIT*GQEFETSLANMA |
| 5240 | 13291 | A | 6090 | 1931 | 3137 | KMEISSLKEINMEPNHSETMFKKAKTK AKKKPRKRSDDSGGYNLSDIIQSPSSSTGL LKSCKTNSVESLPELLTSDSEGSYAGVGS PRDLQSPDFTTGPHSDKIEAKVKPYVNG TSPVYSREDLKPWEKSPILKISAPQIPSN RIDTTSSASWVAGSFSPVSPVVDLRTIM EIEESRQKCGATPKSHLGKTVSHGVKLS QKQRKMIALTTKDNNSGLNSMQTVICIP SDAP*TVNE*GSSLHSVSSKSFRDFLEE KKSVTSHSSGDHVKKVSFKGIENSQAPKI VRCSTHGTGPEGNHISDLPLLDSPNPWL SSSVTTPSMVAPVTFASIVGRGTSTKEAA LIRSREKPLALIQIEEHAIQDLLVFYEAFG NPEEFVIVERTPQGPLAVPMWNKHGC |
| 5241 | 13292 | A | 6091 | 336 | 410 | |
| 5242 | 13293 | A | 6092 | 40 | 921 | TEVPGVHSENDKNQKKKIRKLDPKKKQ VDTVQIHQSGKKGSSFLIFFSPLIILTVEL QVGNVVAQELSIQLELFWRTASQSVTE PTAGLCLLNPGEQEMRALRGRKPLLLI PSKQDLEWTSSKLQQTCS*GF*R*KEN* QTERSTPKPHLVGSSGQGNQAGEGNK GYPVKRGRSQIVPVC*HDCISRKPHCLN PK/YSL**ATAAKSQDTK/FNVQKSQAF LYTNKQTDQSIMSELPFTIASKRIKYL NPTYKGCEGPLQGLQTIAQRNKTEPNK WKNIPVMGEEPM |
| 5243 | 13294 | A | 6093 | 1 | 1960 | MPPHSEQPHSPSTRQKRKVPLFVRQCPSPF VIQAPKAKMDTFDGRKKQFTRFLFLFSM DQLGQGRFSMQTLFALAVYRKDSPLV ACQVQALGNLEPSSVEAHVSSHGAIADR KGWHVSLFSIQPGDCFPKALVEDSPDR ARRQSSKEEGWCRDRRLKFHSSKGA AAIVVKSCKYESPSFGVCFESLNPRLT SRREKTISSSKRCRQCHAEETT VFWAK ESQTGEQTGRGAGQRRMGMIICKACSM LPAERQDLRPTSLVISHGVSVKDRREHC QCPNYYPPLRNMSPLEHSIKICGGKKPQ NDSQRITITTKVIVNQDFKQDDTELSQG SRKETSEASLVTLWELVTAGQTPPLVTP RQTGSGVDLQQTPTDLQLRVLTIRKTN KQKGHPKPHLYVTIHKDQRTLHPKSTEY TFFSAPHPTYSKIDHIVGSKALLSKCKRT EITNCLSDHSAIKLELRIKLTQNRSTTW KLNNLLNDYWVYKEMKAEIKMFFETN ENKDTTYQNLWDTFKAMYSKFMALN AHKRKQORSKIDTLISQLTELEKQEQT KASRRQETTKIRAELEIETQKTLQKINE SRSWFFEKINKIDRTLARLIKKKREKNQI DTIKKIKVISPIPKYKLLFILFGTGTQIN |
| 5244 | 13295 | A | 6094 | 275 | 1839 | CPSVGFSLQAGVVFVGCKLLTAKDF*QQT QGFSQ/RLSQLHGHRAHQKKAISSKNE FTIMGQISEATSALFGEKESKEATLRGEG ARNRDDRVDNSCRLQPPGDGDEGQKV PVKYSAGDTQANRVWSGLQQTPTDLQL RVLTVRKTNKQKGHPHQNPICTSASSK TKEIQTIREYHKNLANKLENLEMDK FLDTYTLPRLNQEEVESLNRPIGSKIEAI NSLPTKKSPGPDFTAIFYQRYKEELRIK YLGJQLTRDVKDLFKENYKPLLNEIKGH KQMEHSMMLDRKNQYCENGHTAQEL EKTALKFIWNQKRAHIAKTILSQKNKAG GILPDFKLYYKATVTKTAWYRYQNRDI DQWNRTEPPEIIPHIYNHLIFDKPKNEK WGKDPLFNK WY WENWLAICRKLKLDSE LTPYTKINSRWIKDLNGRPKTIKLEENL GNTIQDIGMGKDFMTKTPKAMATKAKV GKWDLIKLSFCTAKETTIRVNRQPTW |

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| | | | | | EKIFAIYPSDKGLISRI |
| 5245 | 13296 | A | 6095 | 78 | 1986 |
| | | | | | EKTKSASDWCT*K*RGDGTLKLENTLQDI IQDNFPNLGRQANIQIEIQIMPQRYSSRR ATPRHIIVRFTKVMMKEKILRAAREKEIQ TTISEYYKHLIYANKLENLEEMGKLLDTY TLPRQNQEEVESLNRPIAGSEIEAINSLPT KKSPGPDGFTAKFYQRHKEELVPFLLKQ FQSMEKEVILPNSFYEAIIIPKPRDIT EKENFTPISLMIIDAKILNKILANRIQQHIK KLIHQDQVGFISGMQGWFNHKSXNVVIH HINRTKDRNHMISVDAEKAFNKIQQPF MLKTLNKLGIQLTRDVKDPFKENYKPLL NEIKEDTNKWKNIPIYSWIGRINIVEIAILP KVSLEERERQHDQTHVQSLEKLDLLEQE YNKLTMTQALAEKKMQELEAKLHEEEQ ERKRMQAKAAEHPRCLYLAIFSAKLN LQDKIRLELERIQAEESVKTLSTRETIEYK KVLDEQIERENSKNEESKHNLQELTSQL LAAENKCNLLEKQLEYMRNMIKHAEME RTSVLEKQTPLLIPRQRGSRVDLQQTPD LQLRVLTVRRKTNKQKGHPHQPICMSP SSKTKEERSSSPITERSWTENDFDELREE GFRRSNYSELKEELQTHGKEVKNLEKKI RRMAN |
| 5246 | 13297 | A | 6096 | 870 | 1860 |
| | | | | | TRKSRRNG*IPGHIHPKTKQEEAESLNR PITGSEIEAINSLPTKKSPGTDGFTAKFY QRYKEELVPFLLKLFQSIEKEEILPNSFY ASIIIPKPRDITTKENFRPISPMNIDAK TLNKTLANRIQQHIKKLIHHDQVGF/HC NARLVQHMQINKRNPAK*NRQKPHD YLNRCRKGL*QNSTALHAKTSQ*ISVGSS GQGNQAGEGNKGYSIRKRGSQMSLFAE DVIVYLENPVSDQNLKLIISNFSKVS KINVLNSQAFLYTNNRQTESQIMSEVPFT IASKRIKYLGIQLTRDVKDLFKENYKPLL KEIKEDTTFAHG |
| 5247 | 13298 | A | 6097 | 453 | 545 |
| 5248 | 13299 | A | 6098 | 1 | 235 |
| 5249 | 13300 | A | 6099 | 3 | 706 |
| 5250 | 13301 | A | 61 | 1 | 1194 |
| 5251 | 13302 | A | 610 | 24 | 452 |
| | | | | | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFGNLSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGT AQLSELHCDKLHVDPENFKLLGNVLVTV LAHFGKEFTPEVQASWQKMTGVAS LSSRYH |
| 5252 | 13303 | A | 6100 | 368 | 798 |
| | | | | | LSYIYMHPIQ/RAPRFIKQALRDSQRDL SHTIIMGDFNTPLSTLDRPTRQKVNKDIQ ELNSVLHQVDLIDYRTFHPKSTEYTF APHRTYSKIDHIVGSKALLSKCKRGEIT KIKLELRICKQTQNRSTTWKLNLLND Y |

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| 5253 | 13304 | A | 6101 | 1 | 666 | |
| 5254 | 13305 | A | 6102 | 412 | 681 | GDIIPKCSQPLNIHFHYVFKMR*GSSRPG RGPEIRCFSPAARLLLTAAHQWPQLWAI FQQVALLPHAGGADHVILFSPVSKAT EKIVG |
| 5255 | 13306 | A | 6103 | 489 | 585 | |
| 5256 | 13307 | A | 6104 | 1 | 1474 | MDMLDKGMIQVPVESLECEPHFVQEPV LPSELRSEKQEPWNQPSLDLEPSFATYM ACSMPLAERQDLRPTSLVISHGVSVKDR REHCQCPNYYPPLRNMSPLEHSIKICGGK KPQNDSSQRJTITTKVIVNQDFKQPDDTEL SQGSRKETSEASLVTLWELVTAGQTFQ DDRMGTAPVYSSQRRRRRRVISACPT PPLVTPTQTGSGVDLQQTPTDLQLRVLT RRKTNKQKGHPKPHLYVTIHKDQRTLH PKSTEYTFPSAPHPTYSKIDHIVGSKALLS KCKRTEIITNCLSDHSAIKLELRJIKLTQN RSTTWKLNLLNDYVWYKEMKAEIK MFFETNENKDTTYQNLWDTFKAMYSKG FMALNAHKRKKQQRSKIDTLISQLTELEK QEQTSHKASRRQETTKIRAELEIETQKT LQKINESRSWFFEKINKIDRTLARIKKK REKNQIDTIKWKIKVISPPIPQKYKLLFILF GTGTQIN |
| 5257 | 13308 | A | 6105 | 1 | 903 | |
| 5258 | 13309 | A | 6106 | 803 | 1184 | |
| 5259 | 13310 | A | 6107 | 1458 | 1568 | TQTNLQEKNOQTTSKSGQRV*TDTSRKK TFMQPTDT |
| 5260 | 13311 | B | 6108 | 24 | 2456 | MGVSSGDLKGLLHPRVRVGNEYVTKG QSVEQVVFVAVGALAKATYDRLFRWLVS RINQTLDTKLPRQFFIGVLDIAGFEIFEFN SFEQLCINFTNEKLQFFNQHMVFLEQE EYKREGIDWVFIDFGLDLQPCIDLIEKEE RLKPSRKKITKKHTKKRTASLILHAMICC RSLNSSKTKNTKCLNSINQRLKIWSLQK DLMCGTAGRCKTLHGTSQNLNTTAHVVL ALAGSPKDADDTSIYMFYQKHILYCIVD SECKSRDVLQSYFDLLGELMKFNVDFAK RFNKYINTDAKVLKQINSSLVDSNMLV RCVTLSLDRFENQVDMKAALLSIPGFVE RLCKLATRKVSESTGTASFLQEELEWYT WLDNALVLDALMRVANESEHNQVFW FEQHGLVSGAEKAPGTTIDQAPRIYRWS DLTRTQAQWQSAMTWMSAFTETFLTE RDKQSKWSGIPQLLLKLHTTSHLHSDFV ECQNILKPLLVIPRQTGSGVDLQQTLDL QLRVLTVRRKTNKQKGHPHQNPICMSPS SKTKEAKNLDKRLDEWLTRINSIEKTLN DLMELNTMARKLRDACTSFSSQFDQVE ERVSVIEDQMNMKREEKFREKRIKRNK QSLQEIWDCVKRPNRLIGVPESDGENG TKLENTLQDIIQENFPNLARQVNIQIEIQ RTPQRYSSRRGTPRHIIVRFTKVEIKEKIL RAAREKGRVTHKGKPIRLTAVLLAETLQ ARREWGPINFILKEKNFQPRVSYPAKLSF ISEGEVKSFTDKQMLRDFVTTRPALQEL LKEALNMERNNRYQLLQKHAKL* |
| 5261 | 13312 | A | 6109 | 82 | 1208 | LVEGKLTNRKNIHTKTPSVHHHHQRPKC GREMWGQSPHTESLLGHHLVELWEEGH CPLDPRMVDPPACTMYLEKQPOTLNASL /WKAARSQVPQGGGKGTKKSETEIQATI REYYNKHLAYANKLENLEETEKFLDTYTL PRLNQEEVESLNRRITGSKIEAIINSLPTK KSPGRDGFATAEFYQGYKEELVPFLKLKLF QSIEKEGILPNSFYEAHILIAKPGRDTATT TKNFRITSLMNIDAKILNKILENQIQQHIK KLJHNNQVGFIPGMQGWFNHKSINVIHH IKRTKNKNHMIISIDAGKAFDKIQPFML KTLNKLIDGMYLKIIRAIYDKPTANIILN |

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| | | | | | | GQKLEAFPLKTGTRQGCHSYSTLTPIQH SV |
| 5262 | 13313 | A | 611 | 3 | 552 | HSLFGTSEVINKLRSPDAMGHL/TPPEEDK ATITSLWGKVNVEDAGGETLGRLLVVYP WTQRFDSFGNLSSASAIMGNPKVKAH GKKVLTSLGRCHKSTWDDLKG/TPFAQA *SELHCGQACMWDPEELSSFLGKCCWV TRFWAIPFSAKEFHPWRLQGFPKSRRW QKMVTGVASALVPSRYH |
| 5263 | 13314 | A | 6110 | 1261 | 2396 | LNALYFLLLPDCPGQN**TASKTNKEEK REESNRCNKK**SNITTNPTEIQTIREYY KHL YANKLENLEEMDNFLDTYTLPRLN QEEVESLNRPI TGSEMEAI NSLPTKKSPG PDGFTADFYQSVGSSGQGNQAGEGNKG HSIRKRGSIQVPVCR*HDCISRKPRLSPK SP |
| 5264 | 13315 | A | 6111 | 1 | 819 | MCHSAIFTVLQPPLVVIPRQTGSQVDLQ QTPTDLQLRVLTVRRKTKKQKGHPHQN PICMSPSSKTKATFEDSVWHFAERIIPDP NVIKLRKEELTLNNIRQYYVLCERKDK YQALCNIYGSITIGQAIIFCQTRRNAKWL TVEMIQDGHQVSLLSGELTVEQRAFFAQ RFRDGGKTVLITNV CARGIDVKQVTIV VNFDPVKQGEEDYETYLQRIQRTGRF GKKRLAFNMIEVDELPSLMKIQDHFNSS IKQLHAEADMDEIEKIDY |
| 5265 | 13316 | A | 6112 | 1 | 1068 | |
| 5266 | 13317 | A | 6113 | 3 | 655 | LLSNDQRCISIFNKTREKASATRVYIVLD NSGFELVTDLILADFLLSSELATEVHFYQ KTIPWFVSDTTIHDFNWLIEQVKHSNHK WMSKCGADWEYIKMGKWVYHNHIFW PVPHEYCAMPOVAHDL YAE LQKAHLIL FKGDLNRYRKL TGDRKWEFSVPFHQALN GFHPAPLCTIRTLKAEIQVGLQPGQGEQL LASEPSWWTTGKYGIFQYDGPL |
| 5267 | 13318 | A | 6114 | 3 | 225 | GACGRPPFPRLPRGAPP/PAMAAPFSP PASAPGAAPTFPPLGPAWHPALFLTGIN LTCFSKEREKEAQS WY |
| 5268 | 13319 | A | 6115 | 2 | 624 | |
| 5269 | 13320 | A | 6116 | 2 | 594 | NRGSCHRG LKFEGAFKYKMGQIEIDDQV EGLQYLASRYDFIDLDRVGIHGWSYGG YLSLMALMQRSDFRVAIAGSPVTLWIF YDTGYTERYMGHPDQNEQGYLGSVA MQAEKFPSEPNRLLLHGF LDENVHFAH TSILLSFLVRAGKQYDLQSYQERHSIRV PESGAEHYELHLLHYLQENLGSRIAALKV I |
| 5270 | 13321 | A | 6117 | 4 | 310 | |
| 5271 | 13322 | A | 6118 | 1 | 601 | LQKWSLEYIQEIAGCRTVPVEVGSRYTD EEWSQTLMTVNEFISKYIVNEPRDVGYL AQHQLFDQIPELKQDISIPDYCSLGDGEE EETINAWFGPQGTISPLHQDPQQNFLVQ VMGRKYIRLYSPQESGALYPHDTHLLHN TSQVDVENPDLEKFPKFAKAPFLSCILSP GEILFIPVKYWHYVRALDLSFSV/SFWWS |
| 5272 | 13323 | A | 6119 | 3 | 306 | EIIAFS/DRAED/FRKLGCEVLGVSVDSQF THLAWINTPRKEGGLGPLNIPLADVTR RLSE DYGV LKTDEGIA YVCPAGWKPGS |

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| | | | | | | DTIKPNVDDSKKEYFSKHN |
| 5273 | 13324 | A | 612 | 251 | 488 | GGWITRSGDRDHPG*HGE/IPVY*KKLAG RGGGRLKSQLLGRLRQENGMSGGRAC SEPRSHCTPAWVTERLLKKKKK |
| 5274 | 13325 | A | 6120 | 1 | 774 | PTRTKGFAGQGSLSGAENAGPRVVIVRAS RGLPTQLSVMASGNARIGKPAPDFKATA VVD\GAFKEVKLSDYKGKYVVLFFVPLE LHFCGAPTEIIAFSNPCRGTSRKGLG*SAG ASRWDS\HFTHLAWINTPRKRGEALGP LWIPPALLNGEPERLV*GIYGRG*KTD*G AFAYKGASLFIRLGKGCFFAKITLLIDL VGTLP\DEGFCGLVQGLSQVHKTSHGG KFVPA\GWKALPVATD*APTWM TARKY FSKHN |
| 5275 | 13326 | A | 6121 | 3 | 306 | KNWPPPRFF/YKGPSSSSSSSSSSSSSS PLTPFFSSSPGVCPLKGSSSSSPPKPG RPPSSSQKGKPPFFKPPNFFPKNSPTPG GAPLKPFWKNF |
| 5276 | 13327 | A | 6122 | 1 | 200 | PPHNVPRRWSANLYLTP\SNMVLTLAIAL IGVCVFILAIIGILHWQEKKADDREKRQE AHRFHFDAM |
| 5277 | 13328 | A | 6123 | 2 | 297 | |
| 5278 | 13329 | A | 6124 | 1 | 211 | VSPHVLIRRQSSRHLGSLYLQAPFV*MA GCLLETGSHV*TYKDLHVTITRHLPLW KTRSTLNFQVARSS |
| 5279 | 13330 | A | 6125 | 1386 | 2151 | DYLCEKHQYRQLCGYLQPCQGS PCVWT PRAGSGRAALRTGMAVLARAAGQRLRA RLPPQAQRARAAAGALRERGLCAPRPP APGAGRQSPQSGELRVPSTTSSTCRSC WSARPWGSRRGRAVPQRRRNATATGSP RPLRRLPAASPRRGAASERPNWPDPPR PRTARSRALNLRSSSKVNATLVCHKET EAQRGVWTGETIPVRTCFGPLIGQQSHS MEVAEWTDKAVNHIWKAPRNTALKMT QTYNDPAD |
| 5280 | 13331 | A | 6126 | 1 | 1337 | MRNKAVGQARAPPAQLAGWAAPFKLL DGRPQVFPEMPQPVAGCTATGPREKLG GPGRPRGRVAASVQRLMNEMNLSPVGM EQLTSSSVSNALPVSGSHLGLAASPTHSA IPAPGILSYLADRPPPQYIHPNSINVDGNT ALSITNNPSALDPYQSNNGNVGLEP GIVSI DSRSVNTHGAQSLHPSDGHEVALDTAIT MENVSRTVSPISTDGM AEELTMDGVAG EHSQIPNGSR SHEPLSVDSVSNNLAADA VGHGGVPMHGNGLAELPVVMTDHIAS RVNGMSDSALS\SNHTVAMSTNSGPRE SSAVAPVASHFSVHVFLFSFIWVSPADAE TLGESLLGLTVYGSNDQDPYVTLKDTEQ YEREDFLIKPSDNLIVCGRAEQDQC NLEV HGNYIAVGNMTPVIEVWDLDIVDSLEPV FTLGSKLSKKKKKKKGKVKKLNI |

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| 5281 | 13332 | A | 6127 | 1 | 2412 | MKMNLSPVGMAQLTSSSVSNALPVSGS HLGLAASPTHSAIPAPGLPVAIPNLGPSLS SLPSALSMLPMGIGDRGVMCGLPERNY TLPPPPYPHLESSYFRITLPGILSYLADRP PQYIHPNSINVDGNTALSITNNPSALDPY QSNNGNVGLEPGIVSIDSRSVNTHGAQSL HPSDGHEVALDTAITMENVSRTVSPISTD GMAEELTMDGVAGEHSQIPNGSRSEPL SVDSVSNNLAADAVGHGGVPMHGNGL ELPVVMETDHIASRVNGMSDSALSDSIH TVAMSTNSVSVALSTSHNLASLESVSLH EVGLSLEPVAVSSITQEVAMGTGHVDVS SDSLSFVSPSLQMEDSNSNKENMATLFTI WCTLCDRAYPSDCPEHGPVTFVPTPIES RARLSLPKQLVLRQSVGAEVGVWTGET IPVRTCFGLIGQQSHSMEVAEWTDKAV NHIWKIYHNGVLEFCIITTDENECNMMM FVRKARNREEQNLVAYPHDGKIFFCTSQ DIPPENELFFYYSRDYAAQQIGVPEHPDVH LCNCGKECNSYTEFKAHLTSHIHNHLPT QGHSGSIGPSHSEKWKCSMCPQAFISP SKLHVYFMGHMGMKPHKCDFCSKAFSD PSNLRTHLKIHTGQKNYRCTLCDKSFTQ KAHLGVHMHVIHTGEKNLKCXY/CVVK LFYGGSRDLQGRHVLHVTQERQIKCPK CDKLAFLRTNHLKKHLNSHEGKR/DYVC EKCTKAYLTKYHLTRHLKTCKGPTSSF VQAPEEEEEEDDSEEDLADSVGTEDCRI NSAVYSADESLSAHK |
| 5282 | 13333 | A | 6128 | 1 | 1767 | MQALIPLESMSGMTQTSGVSTETGDVVK DMGVNNQSKEGRCPWKDHEAAPWISEK PKKRGNEGKSKKFKNNYSTQPARMERK EELNPPFEGKDGDGTSIPHSKEIGFTFP KMHDSFSHTPDPTVEAVDRKGGNFQ VNFVELGTLGENKISTVKASTVTEPPAK VTDVSCQEIQGAGFVPSVSEENKTD ANRYTAVADKPSERSNDGKSSGSAACE KLPTPTPVVKEGDSFPDTLAKNGQEAP AQISKSLMVDNYTKDGVPGQERPKGSA VVPSTSTGGVALPITTAIETVNIHGDHSL KNKAELADSMKNEAGIDEGHVIGESV HSGASKHSVEKVTELAKGHLLPG/CASR RPEPTRRGQSPRR/T/HADRGNFPAHPVN EEKETKEGSVAVQIPDLLEDKAQKLSFC EDQNAQDRNSKGSDSLNNKKVDLTLLSP KSENDKLKEISLACKITELESVSLPTPEIQ SDFLSKVEAPPSEVADTLVIMTASKGV RLPEPKDKILETPQKMTESKSTPGEK KEDKSRMAEPMKGYMRPTKSRGLTPLL PKSTIQEQERHKQLKSAGMNLPGWNV ACGF |
| 5283 | 13334 | A | 6129 | 893 | 3822 | GKGNHATVNLLSFLQRPQVGSVHPPVV G/HGNQRKSIHVDLSLEPQRDLGREAWDI ESTPIMMKKKKKKPKQKRYSQPRAGGP SDDDNADKPKGHPFAADTQKSGVLPSQ PTTMGTEYGLVSGENLKRECLVNSSAAR LVAENFVSESLRIPLYPSEEAPKTAISSQS KL RVEEESKSNKSVLQNDKKLLKQHE YKQPAPHLKTPVDKSQSVGPLNLKGPL AEVSAYNVETPLDIRLKEGCSFFLDQEV MGVV |
| 5284 | 13335 | A | 613 | 5987 | 6461 | GVNKSWNHWFHLGVREAEHAGVVRT PHHDLVLLPRGMAACALGACSLGAV PGHPVAGGVSHGCSSGTTYRGERHRV GRMRQKNRLNPGGGGCGEPRSRHYTPA WATVEQNSVSKQNKTKQNKHRLVHWN RKKWIYLLFALKKYKMSMLCRKS |

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| 5285 | 13336 | A | 6130 | 1 | 1965 | MQALIPLESQSGMTQTSQSVSTETGDIVVK DMGVNNQSKGRCPCWKDHEAAPWISEK PKKRGNEGKSKKFKNNYSTQPARMERK EELNPPFEGKDGDTGSIPHSKEIGFTFP KMHDSFSHTPDPTTVEAVDRKGGNFQ VNFVELGTLGENKISTVKASTVTEPPAK VTDVSCQEQIQGAGFVPSVSEENKTDA ANRYTAVADKPSKRSNDGSKKVKNSS PEKHILENKIDATKIHVPMETTQDQGIEG WPIWTKIEIL/RFTCPRTPELINKSSPLEV LESAACEKLPTPTQVVKEGDSFPDTLA KNGQEIAPAQISKSLMVDNYTKDGVPGQ ERPKGPSAVVPSTSTGGVALPITTAJETV NIHGDHSLKNKAELADSMKNEAGIDEG HVIGESVHSGASKHSVEKVTELAKGH LLPG/CASRRPEPTRRGQSPRR/T/HADRG NFPAPHPVNEEKETKEGSVAVQIPDLLED KAQKLSFCEDQNAQDRNSKGSDSLNNK VDLTLSPKSENDKLEISLACKITELESV SLPTPEIQSDFLHKSVEAPPSEVADTLVI MTASKGVRLPEPKDKILETPQKMTSE SKTPGEGKKEDKSRMAEPMKGYMRPTK SRGLTPLLKSTIQEQRHKLKLSAGMN LPWGNVCACGF |
| 5286 | 13337 | A | 6131 | 1632 | 2783 | VILLSKSLIQENFFFF*QSFALVAQAGV QWSNPCSLQPPPPGFNGFSLILPSSWD YRRVPPCPANFVFLVETGFHHVQAGL ELLTSGDPPTSASQAGITGVSHHAQPAE DIANNVTLFFPLHLFL |
| 5287 | 13338 | A | 6132 | 240 | 564 | NGWEFKHGSPWPGGFFFFFETESRSV A/TRLECSGVIPAHNRCLPGSSDSPASAS QLTGTGAHHHARLIFVFLVETGLRHLS QAGLELL/NLIHQPWNPQELGLQA |
| 5288 | 13339 | A | 6133 | 1 | 1898 | MAASGRGLCKAVAASPPAWRRDNTA RGGLKPEYDAVVIGAGHNLVAAAYLQ RLGVNTAVFERRHVIGGAAVTEIIPGFK FSRASYLLSLRPQIYTDLELKKHGLRLH LRNPYSFTPMLEEGAGSKVPRCLLGT MAENQKQIAQFSQKDAQVFPKYEEFMH RLALAIPLDAPVDMMAAFQHGSLLR MRSLSTLKPLLKAGRILGAQLPRYEV TAPITKVLDQWFESEPLKATLATDAVIG AMTSPHTPGSGYVLLHHVMGGLEGMQ GAWGYVQGGMGALSDAIASSATTHGAS IFTEKTVAKVQVNSEGCVQGVLEDGTE VRSKMVLSTSPQITFLKLTPEWLPEEF LERISQLDTRSPVTINVAVDRLPSFLAA PNAPRGQPLPHHQCSIHLNCEDTLLHQ AFEDAMDGLPSHSDLGSAKIHTPKDRKC IPGEKSEDEGRPVIELCIPSSLDPTLAPPG CHVVSFLTQYMPYTLAGGKAWDEQERD AYADRVFDCIEVYAPGFKDSVVGRI PPDLERIFGLPGGNIFHCAMSLDQLYFAR PVPLHSGYAGPLQGLYLCGSGAHPAPY SEILTSITKRVPIQHVHPQLRLWAVDLA PPQTFGAGSLEGARIY |
| 5289 | 13340 | A | 6134 | 163 | 513 | CLLFFLTPSHFSVFGTPVFDNRVYAPGF KDSVVGRDILTPDLERIFGLPGGNIFHC AMSLDQLYFARPVPLHSGYRCPLQGLYL CGSGAHPGGVMRAAGRNAAHVAFRD LKSM |

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| 5290 | 13341 | B | 6135 | 1 | 720 | MGCKHWMTCGRARKEGKDDSYMOTQ WLHRAFAAPPETCPFPLRDHIQTGRDL LGTFEKCWFVWGAEREVWRERHQREPG LRAAFAGQLEFPAGVGLAGPALGAAGQ PCWPRGNEGLSTRASGCGGCTGSSSSAS PPVLCSSHQALAAFLRGRSRDLQRAMP EPPTPSMGSCAAGASPTSTTPCSKEPSID HPRAEECECTARDWQAAPPAALVRDPL GEASWAPESGGDMESLYI* |
| 5291 | 13342 | A | 6136 | 133 | 311 | QLHADKVSRLFATHA/GVPWCDHGLFQP QPPPLKRSSCLSLWSSWDYRHAPHPAII CLLL |
| 5292 | 13343 | A | 6137 | 1 | 1098 | |
| 5293 | 13344 | A | 6138 | 2 | 241 | PPRFKRFSCGLSSSWDYRCTPPRSANFC NLVEMGFHHVQAGLELLTSDDPPTLAS QSAGITGVSHHAGPHRFLINYY |
| 5294 | 13345 | A | 6139 | 3 | 333 | YFISSHFISFHYVISFHLITFHLISFH/HHFI SSFHFISSFHLFISFH/HHHLNSFHLISSFH HFISFHLISYLSISFQF/HFHYFMSSHLISSF HLITSHHFNFIISSFH |
| 5295 | 13346 | A | 614 | 180 | 345 | GLSFHMLKKKVYKMYCIYMYICTHTHT HLI*MYINRPSLYDYQFLFYLSQLDSC |
| 5296 | 13347 | A | 6140 | 3 | 137 | GVSPCWPGWSRAPDLK*SAHLGLPKCW HYRRPIHDCGQAPHLHC |
| 5297 | 13348 | A | 6141 | 967 | 1386 | KKKKIFIGHQLRWL*RFFFFFFFETGSHS VPQAGVQWCDHGSLOPQSPWAQRSSNL SLPSSWDYRHLPPCLANF/FFVEMGLT MWPRLVLNSGVPDLPASVSQ/SAGITGV SHRNWWPMKIFFFQTASHVAQAGVQ WCNLGSLQALPPAFMPFSCLLPQPPSSW DYRSLPPCLANF/CFGFLVETGVSPCWPG WSRTPDLR |
| 5298 | 13349 | A | 6142 | 278 | 643 | GRQERGERERSSRPLGGRKCQ/HWLAVN AQKLLALQVEKAKVEGVGAPALGILV VAGCSFAIRRYQKKSDSLKQPQNPVLEA AVGVVPVEMSLPHASSSLTLVPCLRRLD PFLCFPLSLAKV |
| 5299 | 13350 | A | 6143 | 18 | 479 | QRTFCKGKWKGAAKILIDLNNLFLCKLE QKGTDLALVIAMENYGSLSKKGVLDLPA AVDLLAMSEKDIQDLKFGVEWDVDMVF ASFIHVASNVHEIRKAIANWSKVPTCPP ELGSYLPRGTETHSYFYISYSSDQIQICKP LHYSYGRNYDTL |
| 5300 | 13351 | A | 6144 | 3 | 282 | RSPPA\GSPPPSAPAPRLPPPPAPPPALPP ASRPTFPPLPVSLPVLSSRSLSLPPAFLF SFFCIGVLGLLHTRALSIAAYIKAGAIMQ LYC |

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| 5301 | 13352 | B | 6145 | 26 | 2671 | MAAPGAPAEYGYIRTVLGQQILGQLDSS SLALPSEAKLKLAGSSGRGGQTVKSLRI QEQQVQOTLARKGRSSVGNLHRTSSV PEYVYNLHLVENDFVGGRSPVKTYDM LKAGTTATYEGRWGRGTAQYSSQKSVE ERSLRHPLRRLEISPDSSPERAHYTHSDY QYSQRSQAGHTLHHQESRRAALLVPPRY ARSEIVGVSAGTTSRQRHFDYHRQYQ HGSVSDTVFDSIPANPALLTYPRPGTSRS MGNLLEKENYLTAGLTVGQVRPLVPLQ PVTQNRASRSSWHQSSFHSTRTLREAGP SVAVDSSGRRRAHLTVGQAAAGGSGNLL TERSTFTDSQLGNADMEMTLERAVSML EADHMPPSRISAAATFIQHECFQKSEARK RVNQLRGILKLLQLLKVNEDVQRAVC GALRNLFEDNDNKLEVAELNGVPRLL QVLKQTRDLETKKQITDHTVNLRSRNG WPGAVAHACNPSTLGGQGGRTSGVR DQPDQHGLLWNLSSNDKLNLMITEAL LTLTENIIPFSGWPEGDYPKANGLLDFDI FYNVTGCLRNMSAGADGRKAMRRCD GLIDSLVHYVRGTIADYQDDKATENCV CILHNLSYQLEAELPEKYSQNIYIQNRNI QTDNNKSIGCFGSRSRKVKEQYQDVMP EEKSNPKGVEWLWHSIVIRMYLSLIAKS VRNYTQEASLGALQNLTAGSGPMPTSV AQTVVQKESGLQHTRKMLHVGDPSVKK TAISLLRNLSRNLSLQNEIAKETLPDLVSH PDTVPSTDLLIETTASACYTLNNIQNSYQ NARDLLNTGGIQKIMASAGDAYASNKA SKAASVLLYSLWAHTELHHAYKKAQFK KTDVNSRTAKAYHSLKD* |
| 5302 | 13353 | A | 6146 | 2 | 355 | FYFLRWSFTLIAQAGVQWRDLGSPQPLP PRFKQFSCSLLSWDYRHAPPRPANFL CF/LVETRFLHAGQAGLELLTSGDPPTLA SQSAGITGASHRNPVQSILRLEGLLETIV QPPT |
| 5303 | 13354 | A | 6147 | 3 | 277 | FFLETEFRSTQSPRLECSGAISAHCNLQLP GPSHSPASASRAAETTLGLCHHARLIFVFL VEMRFHHVVGQSGLELRQAICLPRPPKVL GPQA |
| 5304 | 13355 | A | 6148 | 20 | 363 | LHHFPKPCPAHFSACIHWQHPHTCACT QAHMCKPKH/THTHACTH/ICVLSGTHP WVHTGVCARSSSSS/PSSSSSLRYTRQV HALLHTAQPQRLKASEPTPAQLQPGRQE GLTG |
| 5305 | 13356 | A | 6149 | 3 | 301 | STATWAGVQWCNLSLQPLPSGFKPFSC LSLPGSWDHRHLPPCPANFLYCFFLVEM GFHYVGQAGLKLLT/S/GDLCASAPQSAG STGVNHRVRLGLLIYP |
| 5306 | 13357 | A | 615 | 173 | 338 | GLSFHILKKKVYKYMCIYMYICTHHTH LI*MYINRPSLYDYQFLFYLSQLDSC |
| 5307 | 13358 | A | 6150 | 15 | 352 | DSIFTLVCAEHINFLRAGQHWGCVIDCL HYNKQAVTGDHSSYAERSSTPENGGRE GTREQGERGGTWGRGGG/QERPSIPDR QKNQGRGGGNPLSGRGKVKAITIILLI |
| 5308 | 13359 | A | 6151 | 20 | 415 | |
| 5309 | 13360 | A | 6152 | 24 | 156 | SSFVMELCPELVGSWSH*LQE*SRGPLR *RTHSSRYMVKRQE |
| 5310 | 13361 | A | 6153 | 128 | 880 | |
| 5311 | 13362 | A | 6154 | 310 | 719 | LRTYPTIRGPVREEKWGYVQTESRSVAW AGVQWHCFTELRFVLVSLTRMKPRTL AVSVPALKVARLEFVSSDVQRWGFHHV GPAGLELLTSSDLPVSASQMAGITGRH RAWPWEHVYMDVFVHLKQTEGNLLDL |
| 5312 | 13363 | A | 6155 | 1 | 169 | FFETGSCSVAQAGMQCDHGSLOPCPPG SWDPPALASQSAGITSMSSHHPKLF |

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| 5313 | 13364 | A | 6156 | 525 | 972 | NHLGGFKQILMPRLHPMPMKSFLGV SAR QLYFFFFFETESHIVQAGVQWRDLGS LQPLPPGFKQFSCSLPSSWNYRHTLPRP ANFLYFLVETGFHCVAQAGLKLLSSGNL PALASQSARITGMSHARLAVVFFKALL SSSRTRI |
| 5314 | 13365 | A | 6157 | 300 | 500 | DGLCSKQT*NGVPSITNPIKTANQHOGK KQHPIQGNRTAPSSSVSYMKRCELLPKG TGLEVVRESG |
| 5315 | 13366 | A | 6158 | 1 | 1889 | MGLLQGLLRVRKLLLVVCVPLLLPLPV LHPSEASCAYVLIVTAVYVWSEAVPLG AAALVPAFLYPFFGVLSNEVAEYFKN TLLLVGVICVAAAVEKWNLHKRIALR MVL MAGAKPGMLLCFMCCTLLSMW LSNTSTTAMVMPIVEAVLQELVSAEDEQ LVAGNSNTEEAEPISLDVKNSQPSLELIF VNEDRSNADLTTLMHNEENLNGVPSITNP IKTANQHOGKKQHPSQEKQVLTSPRK QKLNRYRSHHDQMICKCLSLSYSATI GGLTHIGTSTSLIFLEHFNNQYPAAEVVN FGTWFLFSFISLMLVVSFWFWMHWF LGCNFKETCSLSKKKKTKREQLSEKRIQ EEYEKLGDISYPEMVTGFFILMTVLWFT REPGFVPGWDSFFEKKGYRTDATSVFL GFLFLIPAKKPCFGKKNDGENQEHSLG TEPIITWKDFQKTPWEIVILVGGGYAL ASGSKSSGLSTWIGNQMLSSLPPWAV TLLACILVSIVTEFVSNPATITIFLPILCSLS ETMHINPLYTLIPVTMCISFAVMLPVGNP PNAIVFSYGHCCQIKDMVKAGLVNVIGL VIVMVAINTWGVSLFHLDTYPAWAR VSNITDQA |
| 5316 | 13367 | A | 6159 | 41 | 570 | SLHDSTADSIRTCQGVISTLKAHYLRRT FQHILEAADGEDPSYIKFEWRNYSIMDA VDMAIAWEELKPALMNSMWKKIWPEC VQAQRFSQADNIAQLQKNIVTLARNVAF EEVAEAAVDQLLSHEEDLSNEELMRLE QELAVGEEEREDGPWALWQLTTGRLSA ALSHFEAGL |
| 5317 | 13368 | A | 616 | 363 | 412 | |
| 5318 | 13369 | A | 6160 | 3 | 367 | HASAHAFGQLSCVSKLMRDVCGQPCFSP RGMV/LYLQWGRKYSRIGNSSWQIKEK VWRFSTAFCSVNEWKFADILSMADHLK KCSYNVVEKREEAIPLCMCVTRELKE GRSLRSVLKPVL |
| 5319 | 13370 | A | 6161 | 74 | 295 | AEDKSQMLLDLRWSYIRTSSSSADRSHA SGPRIAHKWSTVDRNRPRYDSNNELAEK EQLS*ICSICSRVFFKA |
| 5320 | 13371 | A | 6162 | 32 | 342 | |
| 5321 | 13372 | A | 6163 | 184 | 556 | |
| 5322 | 13373 | A | 6164 | 251 | 1133 | PND SKRLILFRTPWQCLSVRTVARRCT ALTFIASEEKVLVADKSGDVYSFSVLEPH GCGRLELGHL CMLLDVAVSPDDRFLTA ARDEKMRVSWAAAPHSESFCALGHTF VSRISVPHSARALLSSSGDGLRLWEY RSGRQPALLSPWPVCRSSVDPQAPQKFA ASRIAFWCQENCVALLCDGTPCGLHLP GRPQTAVGVQAAAGVPAPSVGRGFRGD PGAVGAPGLARKPPWC SYRHVGDQWQ SVPESTVLKKVSGVLRGNWPMLERLCR RRRQLSAVS YKAHVPTT |
| 5323 | 13374 | A | 6165 | 1 | 391 | APMAGCLSFYLIQGGDDKGFSLYTRDG AGLYKEIWKADRPGNAAWNLAEGEFNA PYPMEVIFEDAFNGPKGGYVALDDISFSP VHCQNQTELLFSAVEASCNYEQDL CNFY QDKKRPGWTRVKGKPNML |

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| 5324 | 13375 | A | 6166 | 3 | 1459 | KLPPPPGECTFEQDECTFT/AGEKKPEQL AQEEGETPTSYTGPKGDHTTGTVVSSH ASECPFGLNSDALLPKKICSLVLLTSFL AASADSGTMLLRWGCLKSKIKMSVGLV PSEISLLGLQMAAFLLHMAFPLCQCTPD MYLLLTVGNNHGRQKQIKGALLYWTF TTCRHCARNLNILSTCKDKVGEFAKLS KIELLEATEKSIGPPEMHKYHCELKNLRE KEKQLEDLLATKIASKVAKLGILLGMPT LEIGGKEGGWGTGYWLRAEKEDGDYL CIEGSEGLNTEKIVPVMQERNININKKD VHSETPAKGHQLQRPKVDKSMKMGRN QHKKAENSKTQITSSPPKDPKSSPAREQT CMENEFDKLTEVGFRRWAITNSPELKED VLTQCKEAKNLEKRLDKLLTRITSLEKS MNDLMELKNTGRELCEAYTSINSRIDQV EERISEIEDQLNEIKQDDKIREKRVKRNK QSPKKYGT |
| 5325 | 13376 | A | 6167 | 1 | 393 | |
| 5326 | 13377 | A | 6168 | 1 | 1137 | |
| 5327 | 13378 | A | 6169 | 1 | 1793 | MAETAVINHKKRKNSPRIVQSNLDEAA YSLSRDQKRMLYLFVDQIRKSDGTQEH DGICEIHVAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDEKGYESFP WFIKRCATAVGRQRTHADKERGAREKG GEKKAKAKKTSGRTRKGGGRERKKKGE QEGKDGQRNAQTKGEKQPHKANTPPK TLQQRKEKKTGDSHRRKKLKFKESEKVL SQEWEHDFVIETMATGARPQLLFSAVEA SCNFEQDLNCFYQDKEGPGWTRVKVKP NMYRAGDHTTGLGYLLANTKFTSQPG YIGRLYGPSPGNLQYCLRFHYAIYGLK MSDTLAVYIFENHVVQEKIWSVLES GVWMQAEITFKKPMPTKVVFMSLCKSF WDCGLVALDDITIQLGSCSSSEKLPPPPG ECTFEQDECTFT/AGEKKPEQLAQEEGE TPTSYTGPKGDHTTGVGYYMYIEASHM VYGQKARLLSRPLRGVSGKHCLTFFYH MYGGGTGLLSVYLKKEEDSEESLLWRR RGEQSISWLRALIEYSCERQHIFAIRG VSIRSIAIDDVKFQARPACGEMEDTPQQ SSGYSEDLNEIEY |
| 5328 | 13379 | A | 617 | 540 | 820 | KIGPQPGQHSKTL*TIKKKLARCGGTC LWSQLLGRRLRWEDCLSAGS*GCGEL*SY HCTPAWVTERDLVSKTQKNRAITGKLLL DVLSSLIR |
| 5329 | 13380 | A | 6170 | 2 | 392 | RNKKQGYPAFHVFFSTFFYPK*KSGGYQA VKRWTKGVNLFQEIIIVPIHRKVHWSL VQYLQDESKTKRNSDLNLEWTHHSM KPHEIPQQLNGSDCGMFTCKYADYISRD KPITFTQVSEDPLHPFTCY |
| 5330 | 13381 | A | 6171 | 2 | 386 | MNLLVERNKKQGYPALHVFSTFFYPKL KSGGYQAVKRWTKGVNLFQEIIIVPIH RKVHWSLVVIDLRKKCLKYLDMSGQKG HRICEMVLGYLQDESKTKRNSDLNLE WTHHSMKPHEIPQQLNGE |
| 5331 | 13382 | A | 6172 | 3 | 162 | |
| 5332 | 13383 | A | 6173 | 3 | 407 | TRRADPLRTWRWHNLLVSFAHSIVSGIW ALLCVWQTPDMLVEIETAWSGLLV CFSAGYFIHDTVIVASGQSASLLAEYL HHVMAMGAFFSGIFWSSFVGGVLTLL VEVSNIFLTIRMMMKISNAQDHL |
| 5333 | 13384 | A | 6174 | 13 | 367 | KYLFFFLKDHTKVGKRRMSIRLHQNLGR GRTKSCLKKLVAGANCRDQDDSPRNQ QPRSATFRPSNRCH*IPQ*PYSACPHPG SGGQFRSLRGLIVEYRSSERHISYRRYAG LCEY |

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| 5334 | 13385 | A | 6175 | 3 | 413 | AAIEELCGRQAARAEAVRGLRGRGLR/ WPLPWHAPPAPAHGAPLARPGARARRSE KPPSEKPRLLRSSPRAQEEGPGEPPPEL ALLPPPPPPPTPATPTSSASNLDLGEQRE RWETFQKRQKLTSGCRQAPARHL |
| 5335 | 13386 | A | 6176 | 2 | 445 | RPLPWHAPPAPAHGAPLARPGARARR/CE KPPSEKPRLLRSSPRAQEEGPGEPPPEL ALLPPPPPPPTPATPTSSASNLDLGEQRE RWETFQKRQKLTSEGAAKLLLDTFEYQ GLVKHTGGCHCGAVRFEVWASADLHIF DCKYRNYI |
| 5336 | 13387 | A | 6177 | 2 | 265 | FLMESRSVTRLECSSTITAHCNLCPLVSS DSAVSASQVAGTTGMRHHAQLIFVFLVE TGFHHVQDGLHLL/NIVHLPKPKVLG LQA |
| 5337 | 13388 | A | 6178 | 1 | 394 | WLVGFGFGFEIESRPVAQAGVQWRNL GSLQSPSKFKRFSFLNLPSSLDYRHTPPS LANFLYLVMGFHHVQDGLLELLTSDP PTLASQSAEITGVSHRTQPRSAILLQSQSS LLPLLRTFISSVPVTE |
| 5338 | 13389 | A | 6179 | 3 | 1306 | HEISLGAICAVLLVIMGLFATRCNREKKD TRSYNCRVAESTYQHHPKRPSQIHKGD ITLVPTINGTLPIRSHHRSSPSSPTLERGQ MGSRQSHNSHQSLNSLVTISSNHVPENFS LELTHATPAVEQVSQLLSMLHQGQYQPR PSFRGNKYRSRYALQMDKFSKDS GRGDSEAGSDYDLGRDSPIDRLLEGF SDLFLTDGRJPAAMRLCTEECRVLGHS QCWMPPLPSPSSDYRSNMFIPGEEFPTQP QQQHPHQSLEDDAQPADSGEKKKSFTF GKDSPKMRITLGDSTSTSLSEMSSVFQR LLPPLDITYSECSEVDRSNSLERRKGPLP AKTVGYPPQGVAAWAASTHFQNPNTNCG PPLGTHSSVQPSKWLPAMEEIPENYEED DFDNVLNHLNDGKHELMASELVAEIN KLLQDVRS |
| 5339 | 13390 | A | 618 | 45 | 364 | HHLHLFQRHKSQMRMTMNTGLFEILTMLL TTMNLVDIFHEKADVVDMAYNADFDEY LNCTDRMDIKYVVQLKEEQASHH*D TECENA*ARWAARMTHIFLPMDDYN |
| 5340 | 13391 | A | 6180 | 21 | 375 | GVSTVGIGRGRLELWAPPEKYTPPGRPS HPLWLWEGGGGSIRREIDTSSPHQVPV QSWFDDMGNTLLNLIPIFEELNGAKDV YTSL/GAAAGPLDCPAFKRRPFHYGTFFH CAFTI |
| 5341 | 13392 | A | 6181 | 3 | 471 | HASAHASAHQVYVLRPYVDEFLRGMG ELFECVLFTASLAKYADPVTDLDRRGV FRARLFRESCVFHQGCYVKDL SRLGRDL RKTILDNPSASYIFHPENAEVQSWFDD MAYTELLNLIPIFEELSGA*D VYTSL/GAA AGPLACPASKRRPSQ |
| 5342 | 13393 | A | 6182 | 1 | 1953 | |
| 5343 | 13394 | A | 6183 | 3 | 240 | |
| 5344 | 13395 | A | 6184 | 1 | 462 | |
| 5345 | 13396 | B | 6185 | 1 | 546 | MVKPLSLQMVPLHSSLGNRGSLSSENKNT GVWESAASCCMAGCGGPADGICSEPLG HDQDGRAQSLLLWAKLTRKDRFSSQPR SIPSFDFLKAKALAKQRETIWEKVFSPPQ AGVLSPPGSATLLSTLEQGAVGQKPPSV PCLMGLFVEHLTTWQLTSSVQASKSKRE DSPETVIAKQKAQSF* |

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| 5346 | 13397 | A | 6186 | 1 | 1846 | MWSVPCLEKVDVLAWTVLCLAVKIKM NKLRSFRRKKDVYVPEASRPHQWQTD EEGVRTGKCSFPVKNWQRLFIQSLAMR SLSASCCHQPAVYSSHGTAQVHAKGCL QAHHRACCPSCSPAAAAIFAAATPDG PLLPSRPLVNLIEKSQALVRETLTSQASA PNSGRAGQPVTVCLS/GANAAWRPALEA PVDTGLWPETQAVSQCLG*EHSACLER KQKREKECGVTATFDASRTTFTREGSFR VTATEQAEREEIMKQMDAKKAQTSV N*TAFPRGRTSTTSTGRLWLMGRPASLA RGMSVWMAAAGLSAVITSWTRPSRRTS VCGVGVTARPATPSQAPLTLMTSAEL*R MFVGNNTSMGTGPSRRPGPCQPAPSCI TSGVLRGT/SAPER/PPCPGPTSEPLVI/VA PASAGATAHGVTAAARSVAEVTSPAWCS APSTMRTPTTTCASASHGQLTGVPAlFTL ARRPSAGLLGWWRTWLCMGPQGCS/SP LGPCTRGLQSPPRMAGRQGHGHPAQP VEEAPSPAPCTASRLTGPASRRPWRLS VPGCLGSPLPFRPVTC SAVQPGARSPGES VLSVVALASGSGALLAGVKGVLC SIPQR APWKTGHL |
| 5347 | 13398 | A | 6187 | 1 | 1542 | |
| 5348 | 13399 | C | 6188 | 539 | 1039 | MPYPAPNPVVGITPSQMVANXFGTAG HPQAAHPHQSPSLVRQQTFFHYEASSAT TSPFFKPPAQLNGSAAFNGVDDGRLAS ADRHTEVPTGTCVPDPFEAQWAALENK SKQRTNPSPTNAFLHVTYRRRLKLNFKQ SLWLCILSIPDREQGVAVKGAKQTLCPD* |
| 5349 | 13400 | A | 6189 | 303 | 2235 | VKIKMNKLRSFRRKKDVYVPEASRPH QWQTD EEGVRTGKCSFPVKYLGHVEVD ESRGMHICEDAVKRLKATGKKAVKAVL WVSADGLRVVDEKTKDLIVDQTIKVSF CAPDRNFDRAFSYICRDGTTRRWICHCF MAVKDTGERLSHAVGCAFAACLERKQK REKECGVTATFDASRTTFTREGSFRVTT ATEQAEREEIMKQMDAKKAETDKIVV GSSVAPGNTAPSPSSPTSPTS DATT SLEM NNPHAIPRRHAPIEQLARQGSFRGFPALS QKMSPFKRQLSLRINELPSTMQRKTD FPI KNAVPEVEGEAESISLCSQITNAFSTPED PFSSAPMTKPVTVVAPQSPTFQANGTDS AFHVLA KPAHTALAPVAMPVRETNPWA HAPDAANKEIAATCSGTEWGQSSGAASP GLFQAGHRRTPSEADRWLEEVSKSVRA QQPQASAAPLPVLQPPPTAISQPASPF QGN AFLTSQVPVGVVPALQPAFVPAQS YPVANGMPYPAPNPVVGITPSQMVAN VFGTAGHPQAAHPHQSPSLVRQQTFFHY EASSATSPFFKPPAQLNGSAAFNGVD DGRLASADRHTEVPTGTCVPDPFEAQW AALENKSKQRTNPSPTNPFSSDLQKTFEI EL |
| 5350 | 13401 | A | 619 | 112 | 322 | NSLIAGYILVYVKTPRTQKEKSLKVLST YIKVAKYKV*ILKSITLFTTKEYSKINIK MPFTTPTFTPN |

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| 5351 | 13402 | A | 6190 | 795 | 2728 | GLSNFFRGRVPVQPLLQFKILIYIHRLEY WWASNPQTPHLGQAVKIKMNKLRQSF RKKD VYVPEASRPHQWQTDEECARTGK CSFPANDLGHAEFFESRGMHICEDAVKR LKATGKKAVKAVLWVSADGLRVVDEK TKDLIVDQTIKVSFCAPDRNFDRAFSY ICRDGTTASHGFCRCFMAVK/DTQGERV EHMQ*ICAFAALFRRARQKREKECGVT ATFDASRTTFTREGSFRVTTATEQAEREE IMKQMQDAKKAETDKIVVGSSVAPGNT APSPSSPTSPTS DATT SLEMMNPHAI HAPIEQARQGSFRGFPALSQKMSPFKR QLSLRINELPSTMQRKTDFPIKNAVPEVE GEAESISSLCSQITNAFSTPEDPFSSAPMT KPVTVVAPQSPTFQGTWVGQSSGAASPG LFQAGHRRTPSEADRWLEEVSKSVRAQ QPQASAAPLQPVLPQPPPTAISQPASPFQ GNAFLTSQPVVGVVPALQPAFVPAQSY PVANGMPYPAPNPVVGITPSQMVANV FGTAGHPQAAHPHQSPSLVRQQTFFHYE ASSATTSPFFKPPAQHLNGSAAFNGVDD GRLASADRHTEVPTGTCPVDPFEAQWA ALENKSQRTPNPSPTNPFSSDLQKTFEIE L |
| 5352 | 13403 | A | 6191 | 1 | 1825 | MNKLRSFRRKKDVVPEASRPHQWQT DEESVRTGKCSFPVKYLGHVEVDES MHICEDAVKRLKAQRKFFKGFFGKTGK KAVKAVLWVSADGLRVVDEKTKDLIVD QTIKVSFCAPDRNFDRAFSYICRDGTT RWICHCFMAVKDTGERLSHAVGCAFAA CLERKQKREKECGVTATFDASRTTFTRE RSFRVTTATEQAEREEIMKQMMDAKKA ETDKIVVGSSVAPGNTAPSPSSPTSPTS DATT SLEMMNPHAI RRHAPIEQARQGSF RGFPALSQKMSPFKRQLSLRINELP/SPT MQRKTDFPIKNAVPEVEGEAESISSLCSQ ITNALSPEDPFSSAPMTKPVTVLAPQS PTFQGNEWGHSSGAASPGLFQAGHRR TPSEADRWLEEVSKSVRAQPPQAPAPL QPVLPQPPPTAISQPASPIQGNAFLTSQPV PVGVVPAHMQPAFVPAQSYPVANGMP YPAPNPVVGITPSQMVANVFGTAGHPQ AAHPHQSPSLVRQQTFFHYEASSATTSPF FKPPAQHLNGSAAFNGVDDGRLASADR HTEVPTGTCPVVPFEAQWA ALENKSQRTPNPSPTNPFSSDLQKTFEIE L |
| 5353 | 13404 | A | 6192 | 164 | 282 | |
| 5354 | 13405 | A | 6193 | 193 | 274 | |
| 5355 | 13406 | A | 6194 | 3 | 247 | FFFFNRFIAALFKITKIWKQPRCPVSE WDKLWY/YTIEHNSALKRNLSCPKM RKLKSILLSKRRQSEKATYYITATM |
| 5356 | 13407 | A | 6196 | 57 | 361 | GLTMDTQKDVQPPKIQPMIYICGECH/ TPENEIKSRVDPIRCRECGYRIMYKKRTK RLGRFLMARWNAGEFQREWPSPYTLGF GSLPHFWIVCYSFSIFALQ |
| 5357 | 13408 | A | 6197 | 2432 | 3682 | NSLILLFFFFRQRSLTLECSGVISAHNL HLPSSSNS/P/ASAS*VAGITGMHRHAWPI CIFLVETGFRHVGQAGLELLTSGDPPAPT SQSM*ATTSGLILLSKILFPFHSTKVFK* SCPS*KILKEENCVINEWFNNESSYTSKE KNNLVPNAC*EINTM*VATNCDFT/SLL*R SENYPKLFHNNETTSQKIHLKIKISRPATS GQWULFSLVWWRARKG*GILMIHNGILY *TIC*IKLHRLP*GMDYPNQPD/MKSGWD KRMSHTL*F*GKEIVDFQNNQNKLSL YLSVQE**HEEFFFRDLKYNKPGSTIKSL VSF/HSLLTFFFFFEARSHSASQAGVQW GNIGSLQPAPPGLKRSSYLSLLSSWDYRR VPPHPANFCIFCR/GWGFGVSPCCPGSSG |

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| | | | | | | TPVLKWRAHLSLPNC |
| 5358 | 13409 | A | 6198 | 1 | 632 | KYRQDLTVPPGYCTGEQGAGGRPGETEP WLRPPALLPSWDFLLCASSSGAVLPVRTQ DPFLPYPPRACPQQQAASSATTSRPCPEV KEAGWGSPGHLARHALSHVPPPARVVL VLRERWHFCGDGRVLLGSRALRERHLG LMGYQLL/PGEWPWPWPWRILTPSLRVT CRPLLSQQLPFEELESQRG/LCPQLKSYLR QKLQALGLRWGPEGG |
| 5359 | 13410 | A | 6199 | 2 | 313 | EVRVYDLTQYEHCPDDVLVLGTDGLWD VTIDCEVAATVDRVLSAYEPNDHSRYT ALAQALVLGARGTPRDRGWRLPNKL GSGDDISVFNPPGRARQLLRG |
| 5360 | 13411 | A | 62 | 994 | 1108 | |
| 5361 | 13412 | B | 620 | 180 | 372 | MAKDAGLIEANGELKV FIDQNLSPGKGV VSLVAVHPSTVNPLGKQLLPKTFGQSNV NIAQQVVIX* |
| 5362 | 13413 | A | 6200 | 401 | 531 | |
| 5363 | 13414 | A | 6201 | 1 | 864 | |
| 5364 | 13415 | A | 6202 | 9 | 811 | YIVTTLRQLGTRGTPGRFIYTALNEPTID YGFQRLQKVIPRHPGDPERLPKEVILKRA ADLVEALYGMPHNNQEIILKRAADIAEA LYSVPRNHNQLPALANTSVHAGMMGV NSFSGQLAVNVSEASQATDQGFTRNSSS VSPHGYVPSTTPQQTNYNSVTSMNGY GSAAMSNLGGSPFTLNGSAANSPIAIVP SSPTMASSTSLPNSCSSSGIFSFSPANMV SAVKQKSAFAPVVRPQTSPPTCTSTNG NSLQAISGMIVPPM |
| 5365 | 13416 | A | 6203 | 299 | 826 | LEGHCHNLSSLQISASLGFKRFS/CLTSPS SWDSRNTPPCPANFC/EFLVENGFIHVG QAGLKLLTSSHPPSMASQSAGITGMSHQ AWPTFPVLINFNSLKMCRMCPMATHLG QCPSREYKIHSCSCAELEGQAHHEPDVG VTISIRKCPVPNALWWKELVPGAQGHGP HLEPEGLG |
| 5366 | 13417 | A | 6204 | 1161 | 2627 | RSDATNWGLSHLCFWFWFLRLSFLFS LPRLECNVTISAHCNLFCLLGSSNSPVSA SLVAGITGRHHAQL/LLYFFFFLVKTRF HHVDQADLELLTSGDPPTSASQSAGITG VSHCAR/LSHLCFLPPCLLFY/CYFIYVML LCY*WSLFLVAQVGQVQWHDLSLQPLPP GFK*FSCLSLSSWEYRRSPHPANFFFFF FLRR/RSRFVAQVGQVQWCNLDLQPPPPS FKHFSASACRVAGITVACHHAWLIF/FL YF**RQGFTILARLVLS*PRDPPPSASQS AEITGVSHHAWPILFIYLRQSL/DSVAQA GVQWYNLGLQPPPPGFKQFSLSS WDYRRVPPCPANFLCF**RQDFTMLARL VSIS*PHDLPASASQSAEITGVSHRAWPIF CIFI/CFFEMESRSVAQAGVQWRDLGSL QAPPPGFTPFSLSLPSSWDYRCPPRPA NFCIFSRDGVSPWSLSPDLVICLPRPPKV LGLQA |

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| 5367 | 13418 | A | 6205 | 24 | 617 | DPVSTKNTQISHMWWCTPVVPATQEAE AREFLENFLSPSTGFECSSLFFFFFFFLSQ GSHSVTQAGVQWCDHGSLOPQP\GRKP SSPLCLLSSWDNH/RPANFFYKTTVKSP E/FLQLAVVGCFACARVYSAFQTEKPQH SSSVGLHRSSFEISAFSHFPI*VFVPWSP LQYEEPTLSFPPSSSIPHCPSSTSPND |
| 5368 | 13419 | A | 6206 | 239 | 1789 | ATAPGQIFFFFFFLWLSLTLSPRLECSDAI MAHCNLKLLGSRNPPTSAS*VAKDYST HQQAWLISYFFFIETGFRHVAKAGLKL TSSDPPAPASQSAGIKRVRHHVWPSFSY VKNHLFSRGLRALS YKLK*QMQLFFNFL SILSHDFVAVPSCHD\HLRSPETCH**CSV THLEGLQVHF*L*DVIPVLIQGVSLNSSSS SFLEESQ*DNILSREWGSHSNLSYSKVI M*HLTATSSCDELASASV*VLS*PL*LR LSR*SF*TFLWLLFRDRIIHFCLFLKRWS L/DSVTQAGVQW/RNHGSLQPQTPGLGS DTESSFF*ARVSLCHPGLEVQWCNHGSL QASNS*AQVILPP*LPN*LRLQACTIMPG* FCF*ILVEMGLAMMPSLVSNS*AQ/CNH PVLASQSSGITGMRHCARLGRES*FDPLH *TVCPICNFFFLRRSFALVAQAGVQWR DLSSLQPLPLGFR*FSLCLLSSWDYGH SLRSANF/CVFLVEMGVSPCWTGWS*TP DLR |
| 5369 | 13420 | A | 6207 | 2 | 208 | LEHALRPSSKMLLKCSQGGTQPEPPNRI KRASSLNFLNKSVEDPTQHGGVQVFLSA ALSAPAPWTSFH |
| 5370 | 13421 | A | 6208 | 1 | 419 | SAFSVAVTKKLPTGAACP KFKTKILMNE GGHYNASSGKFRICGVLGIYYFHLWHITL GNKIDLAIGLGAQRPTASGPLMPNTGN HDVGSSTILALKQGDEVWLQIFYSEQN GLFYDPYWTDSLFTGFLIYADQDDPNEV |
| 5371 | 13422 | A | 6209 | 756 | 966 | |
| 5372 | 13423 | A | 621 | 39 | 460 | GVYLKLSINTVGKDKEKVRRHHHPITTQL QCGIQGHNLWVVTAAEISFHLSPSSRF RRFKSIFCHVTRSGKSMQMFTFPEKKN DFSGCPVRPRGRGRGEGAVRSAGRRG*A RAGAGPGGPGRGV PALGRVAPGLVPN |
| 5373 | 13424 | A | 6210 | 24 | 365 | PTEY/ENL/FPCIKEAF/VVEEWVKTAV L/WPAKQYPFVTPIEERILMEEGKAFFPSR STAKQLDGNPVSPTPVIGLSPTPNKEE KQPDWPLEPTGHLDGARDTAGPSWLH HRF |
| 5374 | 13425 | A | 6211 | 32 | 188 | KIFFFFFFLPPQFKILFKRPTGLRVPKGGR RALGGSPKGAKKAWPTRRLPSFNGLYLE GSSNGASTESPGNFVPGKTLQPPGVELG RGRWTAQQQPSRPVALGA*KL |
| 5375 | 13426 | A | 6212 | 122 | 339 | EKGFWFCAQGGKNLPGGNSLEPSASGL KEIFGLNLLNNWE*RGGPKTPGNFWIWK KGGV*PLWPGWG*NPGL |
| 5376 | 13427 | C | 6213 | 56 | 118 | MKALPSSQSCGPTSVNSPFH* |
| 5377 | 13428 | C | 6214 | 345 | 410 | |
| 5378 | 13429 | C | 6215 | 7 | 438 | |
| 5379 | 13430 | A | 6216 | 2 | 80 | |
| 5380 | 13431 | A | 6217 | 3743 | 4059 | GCAVFFFFFFFLWLSLLPRLE/CSGTVSA HCNLHLLGSSSSRAAASQVAGTTGMHH HARLIFVFLVEMGFHHVSNS*PQAIHPPQ RPKVLGIIGRDNRHLGLMEWSF |
| 5381 | 13432 | A | 6218 | 3 | 402 | DTMVHLTPVEKGAVTALWGKVNVDDEV GGEALGRLLVGYPWTQRFESFGDLSTP DAVMGNPKVKAHGKKVLGAFSDGLAH LDNLKGTATLSELHWDKLHVD*NFRL LG\NGLD*MLAHKFGKKISPNGKLG |

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| 5382 | 13433 | C | 6219 | 295 | 618 | MARKCSVAFSGGPGCTWDNLKGTFAHT EVSLHCDKAAPWPEELSGSWGNAWS CVLGPFTFGKRISTPPVAGLPNQENWLA WCWLNALGPTSNHLSLAFLAGPISN* |
| 5383 | 13434 | A | 622 | 138 | 320 | GFFQGAQKKRVHPKGPFGKSRF*KFFRA GPGGSIWNPHHLGGPGGPNCWPPGFQTP PNNPG |
| 5384 | 13435 | A | 6220 | 2 | 337 | IKKAL*HE*LREKKKSPIRTSQSSKAP*NL PRSSSSSESSNNYQLL*AHKLQVKEMG KLETPNLPLLSQKVAEPLNQPISSKIET LIKKPYHPEKSYGHDEVTAKFSRA |
| 5385 | 13436 | A | 6221 | 1 | 2349 | |
| 5386 | 13437 | A | 6222 | 2 | 1802 | |
| 5387 | 13438 | A | 6223 | 5175 | 5804 | IANNKDALRKTWNPKFTLRSHFDGIRAL AFHPIEPVLITASEDHTLKMWNLQKTAP AKK*EYSTLTLEFYFK*HLSILLYSI |
| 5388 | 13439 | A | 6224 | 3 | 115 | HETDYHKQPWQGEISGIVSTESQ*WGLG GGEVKVKWE |
| 5389 | 13440 | A | 6225 | 2 | 28 | TIADRELRYSEDEGGRRRGE*REEEGEA ARRKRVAKQVGKCRANEERKTEERWGD REGRRERRSEEMEVSGKERGHATSGREE KENTG*GPRAEI |
| 5390 | 13441 | A | 6226 | 1 | 236 | RTRGRTRGSTHAFVRQLMORNLDTGPI MAGHDNLQQLQKENSTPDSSLPETSNKEH ISPENMSLKTLRNSNP*DLYDEI |
| 5391 | 13442 | A | 6227 | 3 | 178 | LFGYLPK*VDNMSTKKPCTWIFTLALCIT ARTWKQPRCPLVGKWIRCSAEALGNRS LI |
| 5392 | 13443 | B | 6228 | 1 | 1050 | MVSISWPRDLPASASQSAGITGLIGALVL SVGIYAEVERQKYKTLES AFLAPAILILL GVVMFMVFIGVLASLRDNLVLLQAFM YILGICLIMELIGGVVALTFRNQQLLRQ QVLSHTLGCADLSDGPGSGPVKMFMGV PVIPAQPPELLASRLSRGYGLVLSWLEP RYEKMISGMYLGEIVRNILIDFTKKGFLF RGOISETLKTGRIFETKFLSQIESDRLALL QVRAILQQLGLNSTCDDSVLKVTCGVV SRRAAQLCGAGMAAVVDKIRENRGLDR LNVTVGVDGTLVYKLHPHFSRIMHQTVE LSPKCNVSFLLSEDGSGKGAALITAVGV RLRTEASS* |
| 5393 | 13444 | A | 6229 | 3 | 250 | SLCQPGWSAVADSRLTASSISQFTPFSC SFPSSWDYRRLPPRAIFLYF**RRGFTVL GWSRSPDLVIRLSRPPKVLGLQV |
| 5394 | 13445 | A | 623 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGT AQLSELHCDKLHVDPENFKLLGNVLT LAIHFGKEFTPEVQASWQKMTGVASA LSSRYH |
| 5395 | 13446 | A | 6230 | 135 | 466 | GIDTILTLNQ*SLKTRQ*FTLIIF/IFFFL RWSL/DSVAQAGVQWRDLGSLQAPPRG FTPFSCLSLPSSWDYRRLPRANFFYF** RRGFTMLARMVVIS*PRDLPAEFL |
| 5396 | 13447 | A | 6231 | 593 | 1030 | KCNSSSLNMNEFKFNPFCKMKNSSLIPL GLSAIKVSNKTNT*NMITI*ILWIIFFFFLI WSL/DSVAQAGAQWCHLGSQAPPEFT PFSCSLPSSWDYRHPRPA/NFFVFLVE RGFTVLARMVVIS*PRDLPALASQSLWII L |
| 5397 | 13448 | C | 6232 | 17 | 145 | MHRDLFFNIQFISSVYTSLYLLEKCILCKF SIKTLGLIHTMW* |
| 5398 | 13449 | A | 6233 | 82 | 377 | IPGLKRSLSLNLNSQSCATLPSYFFFFFF FFFFFLERRDLAMLPRLFSSSPGLK*SLH LGFPEHWDYSHEPPSWLLFFIFNNRRVF LLNVKFYHMY |

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| 5399 | 13450 | A | 6234 | 281 | 1102 | RMNIFPWGGWPLGHSQQATLTGPPGVC SPPNPRQNKGRPSLTWKSACGMFSICF FCSVTKTFLKLGPQRLKSSKTTYAT*DI LKRKVKLCECRPSFLPFFTAWKPLRICW GVAEEGLSSLKEGMLVDSLQPRKPRRC LPHNRLSTAPTFFDPESIPTDPVTLHPLCP KEQRDPPELPSLGEAPWR*SLPFLHSTPC SLKECETMKPHMCRSPCRGVLTPSATCA QWPDQGWGPVIPGAPFSDEVTVCSQLL LPEAPACSGNQCLSWFKK |
| 5400 | 13451 | A | 6235 | 2 | 260 | LSTQAGVQWCDHSSLQP*RLSNWDH MHAPSCLAIYFF*ETTSYIAQSYLKHLG SSNPPTSASQGTAITGISHWARLDTSQFG H |
| 5401 | 13452 | A | 6236 | 3 | 224 | KSCPGTTPGNGAGASLEDLWWSAGRW GGTSKPCPLSAGCPLAFGPPARLTGASM PPLSALNG*ERRKRQPL |
| 5402 | 13453 | A | 6237 | 3 | 307 | EAWRMSWGPP*ER*PLPSP*GVCSSC/AP PLPSVSAGLGEPRPPDVEDMSSSDSDSD WDGGSR/PFTISTPRPRLGCLLHAVLFL ARW/PSLPSV*PRTPHCEH |
| 5403 | 13454 | A | 6238 | 265 | 315 | |
| 5404 | 13455 | A | 6239 | 359 | 785 | GNPSWSFPKAMDSPSLRELQQPLLEGTE C/GDPCPEAW/PGMSWGPP*ER*PLPSP*G VCSSC/APPLPSVSAGLGEPRPPDVEDMS SSDSDSDWDGGSRLSPFLPHDHLGLAVF SMLCCFWPVGIAAFCLAQKVSCLCVGLG GDWA |
| 5405 | 13456 | A | 624 | 60 | 548 | APSPDAMGHFTEEDKATITSLWGKVNVE DAGGETLGRLLVVPWTQRFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGRCHK STWDDLKGTFAQLSELHCGQACMWDW ENFKLLGNVLVTVAIPFSGKEFHPWR LAGFPGQKDG*LGVASALVPSRYH |
| 5406 | 13457 | A | 6240 | 3 | 277 | |
| 5407 | 13458 | A | 6241 | 8 | 370 | RLGEEKAATGVVVHGLDCFFSPRAPTRP GSRLSQDPPGCEI*NPSWSFPKAMDSPSL RELQQPLLEGTECEDPCPEAWAGIELGSP FKRDSLRCRVPEGFCSSCSPPLPSVSAGLG GTKAP |
| 5408 | 13459 | A | 6242 | 1 | 351 | KTGSHSVAEAGVQWHHPSSL*QPPPGFK QSPHLRFPKCWDHRRTPPCPGNFFDLR* RWGSHHVAQAGLELLNSRDPPASTSQSA RITAMSHRARPVSTFLSTSTSCPVLSTFH RSLI |
| 5409 | 13460 | A | 6243 | 2 | 1036 | SHTLSYLVKELEVRMDLKAKMPDDHAR KILLSRINNYTIPEEEIGSFLFHANKPNAP JWLILNEAGLYWRAVGNSTFAIACLQRA LNLAPLQYQDVPLVNLANLLIHYGLHLD ATKLLLQALAINSEPLDLF*AGEMAYL ALKNISGALEAFRQALKLTTKCEPENS KLIRCMQIYPFLYNITSSVCSGNCREKTL DNSHDQKQYFDNSQSLDAAEEEPSEGT DEDPAFSVENSGRSDALRLESTVDES HGSDEMENSDETKMSEILALVDEFQQA WPLEGFGGALEMKGRRSRLTRNTGAEE RSPGWKWPETLAMETAEVKMMKQQNG LHSRSNV |
| 5410 | 13461 | A | 6244 | 31 | 372 | KRVRLGWVAHTYNPSTLGGQGRRIT*TO EALTSLDNIVRTHLYKKFYKLAQVWAC GQTCLEGGKEGYVNMNSNVHTGGQGDPC GLLGSLSLGRIFGCTWDSYRHAAIAMIFG KLK |
| 5411 | 13462 | A | 6245 | 816 | 929 | DRVLLYCPGWNAV*TWLTVASASSAQ AILLPQPCLA |
| 5412 | 13463 | A | 6246 | 3 | 119 | RRGLAVLPRVLNSWPQVIFLPHAPKVL GL*AQL |

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| 5413 | 13464 | A | 6247 | 2 | 285 | RSVLCECRNSVVSQIWGNRLYLVEMYPI MKVEKWAGCCGSCL*SQHFGRLRGVDR LRSGVQGPQGHDETPSLLKMQKWAGV WWWLPPVPACSL |
| 5414 | 13465 | A | 6248 | 3 | 437 | RPRRLFLLRWSFALVAQAGVQWHDLS PQPPPGFK*FLCLSLPSS*DYRNVPPHPA NFVFLVETGFCHVGQAGF*LPTSGDLSA WASQSAGITGVSHLARQAASDFNSRDRR GSQIPSNSQDANQNMEMLNKLKDFPIVT CNT |
| 5415 | 13466 | A | 6249 | 3 | 459 | VLITANLIPAKQCFDCNLFSTFSSVTTEAF VFLCLLVTCVTCMNFLLFIHVFHFSRRVV FFLPILGAPCKMGILFMIQTFLPSLNIFQF GSKCIQQYRILNFYAM*SVTLFLWPVYK YSFSTISRPTLYNRSTLLPRKDRWKGAR QQTPO |
| 5416 | 13467 | A | 625 | 32 | 452 | |
| 5417 | 13468 | A | 6250 | 2 | 342 | FKRQSLTLTPREYSGTHAHYNLKLCCSS NPPSSASQEAGTTGTYHDT*LIF*FFVETG SPYVAHAGLELPVSSNPPTSASQSGRIID MSHHIRKTALLSGKEWTRPPTHLL |
| 5418 | 13469 | A | 6251 | 2 | 207 | ARGDPESTVAEAFPTIPHCSMATLIGLPI KVKLLRSLPQSFKVSWS*APGVPRGIEGL LLRMGTGRA |
| 5419 | 13470 | A | 6252 | 1 | 90 | RWLIPISPAL*EAEAGRILLETRSLRPAWS T |
| 5420 | 13471 | A | 6253 | 3 | 290 | RQGFPLCNHKGTVTADLQPLPPGLK*ISH LSLLSSWNYRCTPPHPADF*FFVERRSHY VA*ACLELLCSSDLPALISQRVGITGMST TPGPICLL |
| 5421 | 13472 | A | 6254 | 2 | 378 | AGFTAHVILNHPGQ*SAGYAPVLDCHT AHIACKHAELNEQIDRRSAKKLEHGPNF LNSGDAIIDDMDTVKPMCVESFSHYSPF GRFADRDMRHTVAASVIMALDKKAAV AGKGSNSGQKAHKAK |
| 5422 | 13473 | A | 6255 | 3 | 735 | NASGTTLEALDCILPPTPTDKALRLPL QDVYKIGGIGTVPVGRVETGVLPKGMV VTFAPDNVTTEV*SV*LSHEALSREALPG DN/VGAFNVKNVSVKDVRRGNVAGDSK NDPPQEAAGFTAHHILNHPGQINAGYA PVLDCHTAHIACKYAELEKEIDRRSGKK LEDGPKFLKSGDAIIVDMVPGKPMCE SFSYDYPPLGRFAVRDMRQTVAVGVKAV DKKVAAGACKVTKSAQKAHKAK |
| 5423 | 13474 | A | 6256 | 328 | 621 | PVFLFCFVLFETESRSVAQAGVQWRDLG SLQALPPGSTPFSCLSLPGGWDYRCPPPC SANFFCIFSRRDRVSPC*PGWSQFPDLIR RARPLFLKNRKL |
| 5424 | 13475 | A | 6257 | 1 | 1245 | |
| 5425 | 13476 | A | 6258 | 1 | 248 | FPDQPIHIVYVPSHLHHMLFELFKV*YFTI IEILPFKKGLTSYIFISFIIRHKTEASISFPK NASSPPKRKKLYSQCLTKYM |
| 5426 | 13477 | A | 6259 | 1 | 1456 | |
| 5427 | 13478 | A | 626 | 3 | 570 | HSLSGTSEVINKLLVQTAMGHFTEEDKA TITSLWGVNVEDAGGETLGRLLVVYP WTQRFFDASFGNLSSASAIMGNPKVKAH GKKVLTSLGDAIKHLLDLKGTFACLSEL HCDKLHVDPENFKLLG/NMLLVTVLGN PIFGKEFHPWRLQASWQKQKMAEDGD CSWPVPCSSRLPLSLAHDGRVFGQ |
| 5428 | 13479 | C | 6260 | 63 | 302 | MIYKEKRESVSKEDLARATLVTTNNIGS VARMCAVNEKINRVFVGNFLRVNTLS MKLLGICTGLLVKRSTKSIVSXT* |

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| 5429 | 13480 | A | 6261 | 1 | 2063 | MGYGVTAFFIWAFSRVLSSCPASKKNEL MLTAMDICALSLRCATEDPGVAMGRRP ACCYRYCKNKYPKSRFCRGVPAKIRI FDLGRKKAKVDEFPLCGHMSDEYEQL SSEALEAARICANKYMKSCGKDGFIH VRLHSFHVIRINKMLSCAFRAHASKCFQ NFGNMIYKEKRESVSKEDLARATLVIT NNIGSVARMCVNEKINRVVFGNFLR VNTLSMKLLAYALDYWSKGQKALFLE HEVCVETVNDGQFHSVELVTNLQTLNL VVDKGTTPKSLGKLQKQAGGINSPLYLG AFPWFMDIGGTLVKLSYFEPIDITAE QEEVESLSIRKYLTNSVAYGSTGIRDVH LELKDLTLFGRRGNLHFIRFPTQDLPTFIQ MGRDKNFSTLQTVLCATGGGAYKFEKD FRTIGNLHLHLDELCLVKGLLYIDSVS FNGQAECCYFANASEPERCQKMPFNLD DPYPLL VVNIGSGVSILAVHSDNYKRV TGTSLLTGCESEFEEALEMASKGDSTQAD KLVRDIYGGDYERFGLPGWAVASSFGN MIYKEKRESVSKEDLARATLVITNNIGS VARMCVNEKINRVVFGNFLRVNTLS MKLLAYALDYWSKGQKALFLEHEFGY NIGVIS/SS*DSHTGLSQLHFEREVRRLSL* GFAHVPLALVCGHLPQW |
| 5430 | 13481 | A | 6262 | 2 | 527 | ILAVHSDNYKRVGTGSLGGGTFGLCS LLTGCESEFEEALEMASKGDSTQADKLVR DIYGGDYERFGLPGWAVASSFGNMIYKE KRESVSKEDLARATLVITNNIGSVARM CAVNE*INRVVFGNFLRVNTLSMKLLA YALDYWSKGQKALFLEHEGYFGAVGA LLGLPNFS |
| 5431 | 13482 | A | 6263 | 2 | 186 | RNGLRYROPI*CLIAENFPGLARDIDIWK LETQGVPNRNLKRSSQRQMIVKLSKV NREF |
| 5432 | 13483 | A | 6264 | 3 | 180 | EMGKGIDSLFNEIIAENFPGLARDIDIWK LETQGVPNRNLKRSSQRQMIVRLS*VKI |
| 5433 | 13484 | A | 6265 | 3 | 474 | GTDVGKVKAHALSHKKLCLKMTQVTT QWLEILQRLCLHDQLSVQHRGLVIAYNL LAADAELAKKLVESELLEILTVVGKQEP DEKKAEEVHTARECLIKCMDYGFIPVS *TATLRDAGSGPVLCRVLGWLSPGESG HLGIIAVTMKSQYKGT |
| 5434 | 13485 | A | 6266 | 2 | 651 | HSEGRQRKRVRQKTDTVREKGRERER QTGRERE*DRRQTQ*DRQGRERDKDR DRDREKERDRQTEKETQRRRQRTERN RQREGPSVAIQCLFFHFLFFSFFLSCIS VCMDCMYVCMYVCMYVCMYVCMYVCMYRI YLETGSHSVAQCSAVVRSGLHCSRLRP GSSHSPASRVAGVTGACPTAPDSISYF QVRDGGFTTLARAGLELLTSG |
| 5435 | 13486 | A | 6267 | 56 | 901 | EEIAVSILLPSALPAPATVGPVALVDGL GGWLCQCQAREQPAE*QPGVLVPPGGR ERQGGCSFRGQSLALLSSADFTGPGYK PHLSKENLVKIIQLDKKPQEGVFPTLGV SMRIKGRDCRLSSIRSPVLSPADRFSMC FPTVKDSVQRTSASAPSSLMIAAEEKC HSSE*PTASGSPQQHQTHTPGATGPAPLQ VETQYTRLSSGLAGPRTLSNESECSKPTL EPKAFWVYNKAKFCLCYLVVSPQLIPRHH GSDMGSHTFEIPLLARKGCPRAVW |
| 5436 | 13487 | A | 6268 | 132 | 378 | YHSQRCRRGVIIVLSKSKARSRRSRMKQ YKNETVKDKGYHKNVSMISLK*LEKP VRPLELYYYYYYYYYYYYYYQVLS |
| 5437 | 13488 | A | 6269 | 3 | 397 | QRDLTRHISLKSCTGVHLPENLNSARRI RNISGHRKSETEKESGL*PALRQILNASW RKVIWEQVIQLVS*TTRELRRG*LSVGID DVGVEVTVLVVFLCSSTIVALLCFSYV SCLCPCWCLLSLCSF |

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| 5438 | 13489 | A | 627 | 62 | 281 | SGVYFSFVQRLKTLTQHLILIFGFLP*EYP TLTTFEHEIISKHPFLTRKWDADVD RKHVWSKSDLCWVI |
| 5439 | 13490 | A | 6270 | 2 | 250 | KKARRSGVILAHCSLELPGSSGSLFSPA SSWDYRSAPPPSNIFLLF*GRVLTMLP RLASNSWAQAILLRWPPKVLGLQV |
| 5440 | 13491 | A | 6271 | 118 | 184 | QKEKL*KMGAVLKSLCNASILIRNANKC NNRRKSYQPFSSFMNIDAKVLNKI |
| 5441 | 13492 | A | 6272 | 798 | 1096 | KIMLEHLYSFEEAESRSVIQAGVQWRDL CSLQAPPPGFTPFSCSLQSSWDYRHLPP HPTNFFCIFSRDEVSPC*PGWSRSPDVVIC LPWPPKVLGLQA |
| 5442 | 13493 | A | 6273 | 3 | 163 | HASAHASGHASGGAEGKQAEVANQDST EDLPAENGEAKTDDSPASDEAGENDA*S DEAGENDA |
| 5443 | 13494 | A | 6274 | 3 | 330 | INIRFYLSQSIKASARSTQG*VSSCTKLQIF FFFFFEMESCSVTQAGVQWRNLSSLQPL PPGFKQFCSLSPSS*DYRCPPRPANFCI FSRDGVSPC*PGWSQTPDLR |
| 5444 | 13495 | A | 6275 | 167 | 362 | SPYGKSNLLEPSASRFKQFFCLGPLNNW DYRLFPPFGNFGVFKNRVFPFWSLV* TPDSRGIP |
| 5445 | 13496 | A | 6276 | 2 | 354 | |
| 5446 | 13497 | A | 6277 | 196 | 321 | EQTAKCPGAHEQVKN*NN*GHLLSPA HFSHLQLKQFDKMI |
| 5447 | 13498 | A | 6278 | 1 | 923 | MERWRDLALVTGASGGIGAARALV QQGLKVVCARTVGNIEELAAECKSAG YPGTLPYRCDLSNEEDILSMFAIRSQHS AVDICINNAGLARPDTLLSGSTSGWKDM FNVNVLALSICTREAYQVHEGSGMWTD GHIN*HQ*ACLATRVLPSTHVFYSATK YAVTALTEGLRQELREAQTHIRATWQLR REEAAAAGYQAAITVKLGFCGLHPLPSTS PRPGKAQPLRRPSLLAQCSIPGVVETQFA FKLHDKDPEKAAATYEQMKCLKPEDVA EAVIYVLSTPAHIQIGDIQMRPTEQVTY |
| 5448 | 13499 | A | 6279 | 28 | 311 | AGVQWCRLSSMQPPRRRLKLSFHLSPS SWDYGCTPPIARLIFVETGFHHVA*AGL KLLSLSNLPT*ASQSAGITGMNHQAQPMI SIFKSSSFG |
| 5449 | 13500 | A | 628 | 1 | 395 | |
| 5450 | 13501 | A | 6280 | 1 | 304 | |
| 5451 | 13502 | A | 6281 | 62 | 299 | LFFSPQTHPTQTAFLLSSVDLHHCYSQM MLPESVAIVCSPKFQE*V*RAWFWVFQ GSREESLRGKGLYSCGLVLCKIP |
| 5452 | 13503 | A | 6282 | 110 | 276 | QSETLSQKKKKKKKNW/YKCGGTHL/LI QATREAEALLQTGVRGCSEPLHHSPT AW |
| 5453 | 13504 | A | 6283 | 380 | 507 | SMNPGSPVCVMLITRIP/FCIAHAHLRCC MVL*LHHFHFRLSIC |
| 5454 | 13505 | A | 6284 | 14 | 235 | DRVSLCHPGGGGSELRSCHCNLAWVT EQNFVSKQKEKKR*LLYT*LVLPMSDGL HVAQDSFECSSTQICKLS |
| 5455 | 13506 | A | 6285 | 494 | 789 | DHRFAPSHLADFYFFCRDGVVQ*NDLDS WQA*PPGLKDHLPS*DRHFAPSHLAD YFFCRDGVVQAGLKLSSSNVPALASQS AGIIGVNHCTQPTLCLFKMMYLFNFCHH WVLHLPakeIPEPVFKLPRVFYTPFNCLS K |
| 5456 | 13507 | A | 6286 | 3 | 107 | HIQLCR*LIHTHTHTHTHTHTQFYLFK** HSAC |
| 5457 | 13508 | A | 6287 | 2 | 214 | VDFFFFFFKLDRVSQCCPSWKFSG*WL FTRTDHRTLPTQPGIKQSSCLSFPSRWDY KCVFQHVSSLSPS |
| 5458 | 13509 | A | 6288 | 3 | 213 | LLKQNKH*SRILYPTKLSFMNEREIKSFS DKHMLREFVTRPDLQEMQKGVNLNKT |

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| | | | | | | KGWHAPE*NLLKA |
| 5459 | 13510 | A | 6289 | 1120 | 1668 | SGDALFPLFFLFNFRVTKLRSSLWMHLG KQLPEPPNSRPTVETQKGSS*DT/PPR*SP *ACFHNSLFPRFG*PTLI*QEHLTTCLL/PG DFFFFFF*DRVLPYCYPGWEYSAKTMAHG SPNLLE*SSHLSLPSSWDHRRMPLCLAN* KKKKKKFQRHGLLMLPKLVLSWAQVIV LLWPPKVLGLQG |
| 5460 | 13511 | A | 629 | 27 | 121 | APTPDAMGHLTYED*ATITSLWCKVNVD DSG |
| 5461 | 13512 | A | 6290 | 186 | 297 | PNLG*LNPPPPRLKHFSCGLPSSWNKKA IACHGAK |
| 5462 | 13513 | A | 6291 | 59 | 132 | |
| 5463 | 13514 | A | 6292 | 1 | 335 | |
| 5464 | 13515 | A | 6293 | 1 | 457 | FETRAGSIAQAGVQWCHLGLLQPPPPGL KRSSCPQP*VTWDYRRTPSSPG*FLYFL* KTGCHHVAPGCKLVSSSDLPLASQSA GITDRHQPPCLGPKLWTLRKLGDIFLW FHDNLGYTLGRNTHFSTSRVITVFRS FKHSTPDFSG |
| 5465 | 13516 | A | 6294 | 76 | 343 | YTFSSFLYFFTFPLDNSKPKIFFFFFFFF FFFKETWIVLIGLNAGYM*TPQK*EALL GNTITHVTRLAKHSVLLT**IE*VHDSTF |
| 5466 | 13517 | A | 6295 | 362 | 561 | LEHNIFLSFETDSRSVAQAGLQWCNLSL QLLPPGFKRFSCISLVS*KAFCGPPQLLN FTPIVQY |
| 5467 | 13518 | A | 6296 | 3 | 349 | FFLETEPSCSVAQVGVQWPDLSLQPHL PRFK*FSCLSLLSSWDYRHAPPHSANLYI FSRDGVSPHWPGRSQTPDLRRPTLLSLPK RLDYSVSHRAQPWPYFRNKEEARPNPFF S |
| 5468 | 13519 | A | 6297 | 42 | 266 | |
| 5469 | 13520 | A | 6298 | 106 | 860 | RRRLPSVAIMIIYRDLISHDEMFSDIYKI REIADGLCWEVEGKMVSRTGNDDSL IGGNASAEVGAEGEGTEQHS*SLVVDHC HRTYHLAVKASFTKEAYKKYIKDYMT INQQGNLKQQRPERSKTFY*QGAVEQIK HILA*FQKTTQSFMEGNMNPDMVALL DYRED/GVVTPYMIFFKDLRNGKNVKN CGQLFWDLSPVIINWASAWSSTQHGLK TKWGLMVIFELHFILEDWGFILEVEAIVF |
| 5470 | 13521 | A | 6299 | 10 | 281 | SRSFFLSFFLFVEMECHSVAKSGMQWRN IGSLQPPPGFNQFSFLSLPNSWDYRCLP LHLANFCIISRDKVSPCWSAWFSRST*PT PDLK |
| 5471 | 13522 | A | 63 | 547 | 644 | IPGRPWRL*S*PVILRLQPQATSGG*MVR ASL |
| 5472 | 13523 | A | 630 | 128 | 379 | FNSRPSLRIGLFCITCSLWDCFWCCWIHA SLYSVIRSLLSFGTLVCFSLFCVAFLSFSF *VVLFFLLFISSGFFSFVFLVFLF |
| 5473 | 13524 | A | 6300 | 3 | 111 | FIKIHGLPMLPRLV*NSWPQAILLPWPPK VLGLQA |
| 5474 | 13525 | A | 6301 | 2530 | 4923 | TVPHH/AFILFFF/CFFERESYSAQTVQ WHNLGSLQPLPPGFK*FSCLSLPSCWDC GHGGVSL |
| 5475 | 13526 | A | 6302 | 2 | 300 | GSFALVAQAGVQWDLGSQQPPPPGPK QFSCLSLLSSWDYRRALPWLANFVFLVE TGLHHVGQAGL*LLTSSDPPALASQSAGI TGVGLLASTYFIEVI |
| 5476 | 13527 | A | 6303 | 1 | 453 | |
| 5477 | 13528 | A | 6304 | 305 | 432 | FLHFK*MMNNMGGDEVDLPEVDGAD DVSLKILFSVYFHTIK |
| 5478 | 13529 | A | 6305 | 3 | 306 | |
| 5479 | 13530 | A | 6306 | 1 | 122 | TRPEFPGRTPSQKG*GKKEEPET*KER TGPSEKGETKA |

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| 5480 | 13531 | A | 6307 | 2 | 392 | CSCSAEAASSGGAAPVRCFTFCFTDIVI MPKGKSPENTEGKDGSKVTKQEPTRRS ARLSAKPAPPKPEPKPRKTSKAKKEPGAK ISRGAKGKKEEKQEAGKEGTA\PS\EHGE TKA\EEA\QKTESVDNEGE |
| 5481 | 13532 | A | 6308 | 3 | 426 | AGNSSIQGHGGWTLRHSLSFLSLLPFSR GPQCMGAVQPLVLKQPRDASLRGCLLG YDSTATGLY*ILCNLRRHPGVMPSCGAR VLRDHNPEIDIEWLCSCLLEVLSGSLST PGLTLADQAGHSGGIMPLEGSLRSDCC |
| 5482 | 13533 | A | 6309 | 3 | 372 | HAGLGAHPLHHPVIQEQEFLPAPRGFGY RSEVD*IRIPAESTGQNSQCQLRK*KDDDS YFHCGYFCGCVCTCRGRLQSSTSHQCQA AL*LLLVPCLTMLRCISSLIYT*NLKTVHS VRLNFIYN |
| 5483 | 13534 | A | 631 | 1 | 371 | RQGPQGGRAAPRPPMPGPPLSSARHALP LGSWESWCCCLIPADRPWDRGQHWQL EMADTRSVHETMMQASRKEIQSLPKNG SFPSTNEMRLRYSSYNQASE*P*KLSRP GLWDPIGRAKWD |
| 5484 | 13535 | A | 6310 | 1 | 230 | SGRPFLFFQGKERVYFIPVVVLFYTVVV Q*LRKNVVRWQKTMEPPRSWLMQLGH TEEGPGYPLLGETETKLFRTA |
| 5485 | 13536 | A | 6311 | 2 | 100 | RRPFFFFFFFASCI*NLISPNVQLSNFTCILR N |
| 5486 | 13537 | A | 6312 | 2 | 192 | |
| 5487 | 13538 | A | 6313 | 1 | 451 | |
| 5488 | 13539 | A | 6314 | 231 | 1335 | |
| 5489 | 13540 | A | 6315 | 636 | 852 | FRGSGPRDKTPNCLISLLFSWQPHYFLQR FLYAKLLGLLAELRSINEAYGYIYQHIQG LSAMMLLL*EICS |
| 5490 | 13541 | A | 6316 | 1 | 690 | |
| 5491 | 13542 | A | 6317 | 3 | 302 | GFRGCKPOALAASTWC*LCSCTEVKN*G LGTSTWISEVRKHLVDVQAEVCCKGGA LVDNLCOGSTEGKCGVRAPTQSPQWGT AWWSYQKRATILQIPEW |
| 5492 | 13543 | A | 6318 | 1919 | 2245 | PMQRSP*RT*WS*KPWQENYVMRAQDS VADSINWKKG*QRLKJK*MK*SKKRSLE KKE*KEMNKASKKYGT*MDQIYVGLV YLKVTGRMEPSWKTLCRILSRRTSPT |
| 5493 | 13544 | C | 6319 | 395 | 1096 | |
| 5494 | 13545 | A | 632 | 323 | 585 | SQHFGRTKPEDSLRPGI*DQTGQPRETLF LQNLKKKLAGHGACLSQQLGRLRWE DRLISGV*GCSDT*LYHCTPAWVTEQDP VSE |
| 5495 | 13546 | A | 6320 | 304 | 475 | PRQTGSGVDLRQTPTDLQLRV*LLGKI TNRKGHLHQNPICTSPPSKTKGKDQIYV |
| 5496 | 13547 | A | 6321 | 224 | 1767 | HCLSNVSAGLHPFTSYCLLHEKKFKAAV LSLGECCDGDGADGGDGSMAKSGP LAAGLLEFAGGPLQTLFAWVSAEAAE QPILLNSKCCCLIVPLEASSWRGTRPCEVI VSEAGASIYSVSPEANKEMPGLDPNLRS AVSIARRVQDPLAELVKIEPKHIGVGMV QHDVSQTLKATLDSVVEECVSFVGVDI NICSEVLLRHIAGLNANRAKNIIHREKN GPFINREQLKKVKGLGPKSFQCCWAFI RNQPGLYPNVLQSANLKLQAKFQGVAV TSSADVEVTNEKQGGKSKTAVNVLLK PNPLDQTCIHPESYDIAMRFLSSIGGTLYE VGKPEMQKINSFLEKEGMEKIAERLQT TVHTLQVHHRWVFSQPEGDFRDTF**T WIFKEEGIVCLEDLQIGTVLTGKVENATL FGIFVDIGVGKSLPIRNVTEAKLSKTKK RRSLGLGPGERVEVQVLNIDIPRSRITLD LIQGVMSIPRRPDADFISFPQIDKDKSVV CKL |

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| 5497 | 13548 | A | 6322 | 2 | 64 | AFRFSSSVRIHERSHTGEKPYECKQCGK AFISSSHFRLEHRTMGEKV*EYKQHSE AFGCSSSF*HKRVYTGQKLCEYKHCSK ALD*SSFF*ARKNSHW*ETL |
| 5498 | 13549 | A | 6323 | 168 | 499 | VCSSAKQ*QTCFSLVSPM*NLKEFLNN IKFPQQDGTSQLVSGENVDRKIVGVS GVGSYLGSKIFRLGAVAHTCNPSTLGGR GGQITRSGDGDHPGQQGETPSLLKI |
| 5499 | 13550 | A | 6324 | 165 | 548 | SPSQHSLVPSTPLPGSVLWIGGCLPCAA EGSRSSQGDGWLRRSSVDLAVGDGEGK EVPRLALGCDLARDGSRTLSPLGPCPKP LGQRWES*ELRKVPGLAPDLSVESAPRS WEAPECOQMLQLSP |
| 5500 | 13551 | A | 6325 | 18 | 225 | TLGLK*SSHLSLLSSWDYRCMPPHLAN* NFCLFVF*RWGLAVLPRLLNSWPSAILP PWPLKVLELQV |
| 5501 | 13552 | A | 6326 | 724 | 900 | MTSFSDKFQSFQNRGSTIVTIAHFWSRKY LSDKECS*NACVVFIHSI*KWANTKTFIG D |
| 5502 | 13553 | A | 6327 | 15 | 185 | VPFENPWVDPRVRPRVRFSTGTFRCCA H*IS*LLQSGSSQASLCRYNEESQKHAAL SLSKEHNPTQYEERMRIQKAGGNVR*PR QACVIMRRVKNMQP |
| 5503 | 13554 | A | 6328 | 199 | 544 | PARLGLEEGRYLITGRGWVWVLTVPVIPA FWAEAVARSQGGQKIETILANMVKPHLY* KYKKKLAGGGGGYL*S*LLGRLRQENG VNLGGGACSEPRSCHCTPAWATEQDSV SKNKK |
| 5504 | 13555 | A | 6329 | 837 | 1096 | |
| 5505 | 13556 | A | 633 | 1 | 231 | |
| 5506 | 13557 | A | 6330 | 454 | 526 | |
| 5507 | 13558 | A | 6331 | 258 | 488 | NTVSTRKYKKLARRSGGCL*SQLLGRLR QENDVNPGGGACSEPRSRHCTPAWATE RDSVSKKKKKKCFQSSILK |
| 5508 | 13559 | A | 6332 | 3001 | 3080 | |
| 5509 | 13560 | A | 6333 | 6181 | 6292 | |
| 5510 | 13561 | A | 6334 | 3 | 222 | ASVTACRLNCQGCSPCQPFPCPHLAAPL P*VPNPQLETFFP*ARTQRIPLPSG*PGTIPS PKPTNHIPLTDPL |
| 5511 | 13562 | A | 6335 | 2 | 227 | FFETESRSLTQAGMQWPNLGSLOPPRPG FKQFSLSLPSRWDHRHMPSGLANFCIFS RDGVSPY*SGWS*TPDLR |
| 5512 | 13563 | A | 6336 | 2 | 218 | TWRLAVAQAGVQWRNLSSLQPLPPGFK *SSCLSLPSSWEYRLLPPRPANFYIFSRDR VSPCWPGWSQTPDLR |
| 5513 | 13564 | A | 6337 | 31 | 165 | GSHTVTQAGMQ*SNHGSLLQLYPLSLRRF SYLNLPSWDQRSNKEG |
| 5514 | 13565 | A | 6338 | 122 | 376 | KMGPLSSSSLPEAECDPRAATLGMNKM LHSHWVSSIAVPDPGMG*KAASGPDFET GQAEARLSPPSLQESSVWPGDFPHQIC |
| 5515 | 13566 | A | 6339 | 3 | 268 | GRVAVRKEKGSFWLVVFNWLSDLNWPL PPLPGELA*TLKSSLRPAAPRPPPPQT PSPTPRSLAVSSEGWRLLSMTLESDDL DL |
| 5516 | 13567 | A | 634 | 1 | 686 | ARAGLGFSCGFGVPDSGIGGAMSSFEGQ MAEYPTISIDRFDRNLRARAYFLSHCH KDHMKGLRAPTLKRRLECSLKVYLY*SP VTKEVLLTSPKYRFWKKRIISIEIETPTQIS LVDEASGEKEIVTLLPAGHCPSVMF LFQGNNGTVLYTGDFRLAQGEARMEL LHSGGRVKDIQSVYLDTTFCDFRFYQIPS REECLSGVLELVPKLDHSEVPCCVAEL Q |
| 5517 | 13568 | A | 6340 | 2 | 218 | IYTHIH*IDPMFSL*GHMEGEVWGLATHP YLPICATVSDDKTLRIWDLSPSHCMLAV RKLKKGKRLSHLNVD |

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| 5518 | 13569 | A | 6341 | 1 | 5748 | MPLKLQNCALHPERVLVATGQVGKEP YICWDSYTVQTSVLKDVHTHGIACLAFL DLDGQCSVKAVIDNARNNECGYIPVKLY LQKHSFSLICLPFYSLDFLDINQRLVSVG LDSKNAVCVWDWKRGKMLSMAPGHTD RFWSLCGNALTPKRGVFGKTGDLQTILC LACARDELTYSGALNGDIYVWKGINLIR TIQGAHAAGIFSMNACEEGFATGGRDGC IRLWDLTFKPITVIDLRETDQGYKGLSVR SV |
| 5519 | 13570 | A | 6342 | 2 | 252 | PPE*LGPNCGQGPPTPLPKFW*ILSKKNG GSPPIIGPGPILKPP*PLRWIPPCPLSPKCL RLPGHKPSAPQPEN |
| 5520 | 13571 | A | 6343 | 289 | 395 | SRICPHRDTRKEYNSYTI AFLINLLKFAEL DCIVYFRLNDN*M*IFRCSTIFYNPALAF HILRKPTTSFF*GRFLLSEMP*MLLLII*I PNYLIQIIKRSI |
| 5521 | 13572 | A | 6344 | 262 | 389 | PQVTFSIASRYATILL*FF*PCLVFYSLPN QFYVQGKLANA |
| 5522 | 13573 | A | 6345 | 1 | 103 | QSFTYCFESF*NLSVFLYCLIYRITN*VYY LYVE |
| 5523 | 13574 | A | 6346 | 7 | 156 | LFSFHVSGTMAHTCNPSTLTG*GRIT*GL EFKTSLGNTVRSHRYRKKKIA |
| 5524 | 13575 | A | 6347 | 94 | 469 | NCTYVIKVNLRHMYTPITAIKIISTRFKI YWYSLIFS*ICIHIFETRSLTPIAQAGVWC HDHSSLQPLPPGLR*SSYLSLSSSWDYRH TPPCSANLCVCVCRDRRVSPPYCWLLN ILNVCII |
| 5525 | 13576 | A | 6348 | 1 | 226 | FFEMESHSVTQAGVQWPDLSLQPLPPG FK*FFCLSPSSWDYRHTPPHAYFCIFSR NGVSPCWPGWPRTPDPR |
| 5526 | 13577 | A | 6349 | 3 | 308 | KDEKGEEDGKEDKNGNEKGEDAKEND DGKEKGDKKEGKDVKVEDEKEREDG KEDEGGNEEEAGKEKEDLKEEEEGKEED EIKEDDGKKEEPQSIV*NCPM |
| 5527 | 13578 | A | 635 | 52 | 264 | GLLVGVGAAAVMPGIVELPTLEELKVDE VNISAALKDACHDYGDEWDKPNVDIM L**LEQLHPSMGQAL |
| 5528 | 13579 | A | 6350 | 1 | 239 | MDGGTEKPFACPV*CTKRYKNVNGIK YHAKNGHRTQIRVRKPFKCRGKSYKT AQGLRHHTINFHPPVSAEIRKMQQ |
| 5529 | 13580 | A | 6351 | 219 | 688 | RRMHAYVSLDPLERPPFFFFLFFFFFFF LRRSFALVAQAGVHWRDLGSPQPPPRF K*FSCLSLPSSWNYRHAPPRANFVFLVE TGLQLPTSGDLPASASQSVGITGVSHCA WPGNWLLKETRCGSSVGRQITGPITPDA WVDPGIPDRYLQA |
| 5530 | 13581 | A | 6352 | 3251 | 3700 | KWPYWLKEESSKLLHHQETS*HSNLGN* ASGLRTLPRAEQKE*GMQTSGR*TR* KEALFSITTDQRRPAVGSSSLPAGHLCS QORRAFTDLRGEDVLADWSMGYGP RRGPRIPTLVGRGAHSMATTTTDPHRVL PAYHQCSPCI |
| 5531 | 13582 | A | 6353 | 3 | 347 | DAWEQTQDTELVETRPAGDGTQKWAA VVVPSGEEQRYTCHVQHEGLPQPLILRW EQSPQPTPIVIGIVAGLVVLGAVVTGAVV AAVMWRKKSSDRNRGSYSQAAV*DSFL VWD |
| 5532 | 13583 | A | 6354 | 3 | 174 | |

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| 5533 | 13584 | B | 6355 | 10 | 720 | MAPRTLVLGALALTQTWAGSQSMR YFSTSVSRPGRGEPRFIAVGYVDDTQFV RFDSDAASQRMPEPRAPWIEQEGPEYWD GETRKVKAHSTQDRENLRALRYYNQSE AGSHTLQMMFGCDVGS DGRFLRGYHQ YAYDGKDYIALKEDLRSWTAADMAAQI TKRKWEAAHVAEQRAYLEGTCVDGL RRYLENGKETLQRTDPPKTHMTHHPISD HEATLRCWALGFYPCGDHT* |
| 5534 | 13585 | A | 6356 | 3 | 223 | |
| 5535 | 13586 | A | 6357 | 1 | 179 | RSQVIRHQRIPTGQKSYKCHKC/GQGFSL RSLLAEHQKIH*DN*CTGNEYSKPSSIN CH |
| 5536 | 13587 | A | 6358 | 38 | 294 | LHLMQNRRLHTGDKLHKYDDCAGKAFT SHSHLIRHQRIHTGQKSYKCHQCGKVFS LRSLLAEQKIYF*DNSSECNEYSKPSSIN |
| 5537 | 13588 | A | 6359 | 2 | 244 | |
| 5538 | 13589 | A | 636 | 1 | 380 | KHSVCGRARASCSSFASVLFISKMVRE QYTTATEGICIERPENQYVYKIGYGRK RCLYLVLGMLLVNLTITWILNVTW VSSTSTAPHRV*H*NSLCAETQLQLRLPK RGRHVNFEVPY |
| 5539 | 13590 | A | 6360 | 339 | 1079 | ILSLPLLAGGTDIISCFMGHNSLPVYK GEIQARNLGMAVEAWNEE*KAGWGEGS ELACTKPIPCQPHFWNDENGKNKYRKA YFSKFPSIWAHGDY*RINPKTGGIVMLGR SDGTLNPNVGRFSGSEIYNIVESFQEVED SLCVPQYNKYREERVILFLKMASGHAFQ PDLVKRIRDAJRMGLSARHVPISLILETKG IPYTLNGKKVEVAVKQIIAGKAVEQGGGA FSNPETLDLYRDIPELQGF |
| 5540 | 13591 | A | 6361 | 1 | 1047 | MVSISWPRDLPASASQSAGITGLIGALVL SVGIYAEVER/HEI*NP*KCLPGSSHHPH PGRRHVHGLLHWCAGVPP*QPELLASL RLSRGYGLVLSWLEPRYEKMISGMYLG EIVRNILIDFTKKGFLFRGQISETLKTRGIF ETKFLSQIESDRLALLQVRAILQQLGLNS TCDDSLVKTVCGVVSRRAAQLCGAGM AAVVDKIRENRGLDRLNVTGVGDGTLY KLHPHFSRIMHQTVKELSPKCNVSFLLSE DGSGKGAALITAVGVRLRTEASS |
| 5541 | 13592 | A | 6362 | 2 | 55 | FFLRRSFTLVAQAGVQWRDLGSLQPPPL RFR*FSCSLPSSWDYRCLPPLANFLHF QQRFSFTILARLLVSN*PRDLPASASQS AGITGMSHHACPI*FFFETEFHSCCPGW SAVA |
| 5542 | 13593 | A | 6363 | 167 | 293 | VVKLLGILLNQMKTKMNFDFLTVM QKMSEKDTKEEILKSSQFHHHQA*KLF DDDETGKISGFL |
| 5543 | 13594 | A | 6364 | 3 | 226 | FLR*SLAVNQAGVQGRHLRSLQPLPPRF KLFSLLYLPSSWDYSHAPLPANFCIFSR NDVSPCWPGRSQTPDLK |
| 5544 | 13595 | A | 6365 | 1 | 648 | |
| 5545 | 13596 | A | 6366 | 26 | 612 | VGAGGRGWRFAAAVRRAAGGGLRPGP APGPRAGGGGPRGAHLALLRRAGALRA GKEYGKADARWVYFDPTTVSVEILAV DVSLALFLIYAIVKEKYRHFQITLCVC ELYGCWMTFLPEWAHPEAPNLQQPATG WLYWLGFLLFFF*RCVGLIPRNWLLWA VHGPTSRKWHQKGNQFQWKEVFSGTF QNP |
| 5546 | 13597 | A | 6367 | 3 | 292 | TPWLRDFHDPIVEVEVSVPFGEPLLSAP GLPEPRAGHSVPSGLSVVAPPSFSDNVP GSLEHLLVLHFPBGDVSLRLPLPI*ETP MIPLSRLRCPCSRVSFSPSQHACLGL VILSPVASVWLLFHRFLTMSQVPWSIFL FSISPGATCPSCALCAFLSRSEELRSHLCH R |

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| 5547 | 13598 | A | 6368 | 237 | 1202 | |
| 5548 | 13599 | A | 6369 | 2 | 58 | PRVRCFIYTGKAPNLDKMADDLLAAAD KVR*EGSKPRQNG |
| 5549 | 13600 | A | 637 | 23 | 360 | LCQSQATLLSIFSQEYQKHIKRTTHAKHHT SEAIESYYQRYLNGVVKNGAAPVLLDLA NEVDYAPSLMARLILERFLQEHEETSPFK GIINMMLRYPSQIPDGALAY*VYHGK |
| 5550 | 13601 | A | 6370 | 1 | 1136 | MSSGPVAESWCYTQVVHFLFNCFLFFYQ QIKVVKFSYMWTTNNFSFCREEMGEVIK SSTFSSGANDKLKWCLRVNPKGLDEESK DYLSTLYLLVSCPKSEVRKFKFSILNAK GEETKAMESQRYAYRFVQGGDWGFKKFI RRDFLLDEANGLLPDDKLTLCFVSVVQ DSVNISGQNTMNMVKVPECRLADELGG LSENSRFTDCCLCVAGQEFQAHKAILAA RSPVFSAMFEHEMEESKKNRVEINDVEP EVFKEMMCFIYTGKAPNLDKMANDLL AADKYALERLKVMCEDALCSNLSVEN AAEILILADLHSADQLKTQAVDFINYHAS DVLETSGWKSMMVVSHPHLVDEAYRSLA SAQCPFLGPFRKRLKQS |
| 5551 | 13602 | A | 6371 | 21 | 358 | GCRHSASCAAPRALGPAPARQR*PKAGR VFPERTS*T*G*PAPGRRHPGRIGRRR RSGCSRVRSSVRDC/PSSRSKASNPPLSL SSSTGCDGARPPCSV*RWSRFPGAR |
| 5552 | 13603 | A | 6372 | 1 | 1458 | SLPRNLPVTIISQDFGDASPRNGQEADD SSTSESPEDSKYFLPYHPPQRRMNLKGI QLQRAKSPISLKRSTDFQAKGHEEETD ASPSSCGSLPITNSFTKMPPRSRSSIMSITA EPPGNDISVRRYKEDAPHRSTVEEDNDS GGFDALDLDELAAGETVAQSPPGVPCQP PLFQGSPLCQLRLPTDETKDEWSSLMG KHQRYQVLKRDDSHERYSFGPSIHSSSS SHQSEGLDAYDLEQVNLMPKFSLERCR NRGPQRKGLAKAMQHGRGKEVGPRYP AVPIHDTVEPDPSGLRSPWGTGCAQGP RCSTRR*MATASPPSSPCWGATREGASC TRSSLALWPRKPASVRATSCC*KAASE ARGRVSRWTHAPKRKPTGPSRGAAAPS RCTKGQPRSPAENPWACRI*CGQHLQSP ELRSSTALQVWNSRERKFIPAGVPEAGE GHGGRPDHIGGLVLHPAEPEHLQAPGRL HHVPEV |
| 5553 | 13604 | A | 6373 | 103 | 226 | CCFEILKLMKILISEMHLMLFFL*QLRKS A*IPYVPELFLS |
| 5554 | 13605 | A | 6374 | 112 | 303 | |
| 5555 | 13606 | A | 6375 | 3 | 109 | AWKFFFYFILLFFFLEKHHFYVQ*NISL A*KKKK |
| 5556 | 13607 | A | 6376 | 22 | 175 | THDHVSVYFFFLGLKSTEQCDIKMQIFL FI*VENHLPVSIYILKYFLWIL |
| 5557 | 13608 | A | 6377 | 1596 | 1878 | TMSDTTFKALR*QLPVTRTKIDWNKILSY KIGKEMQNA |
| 5558 | 13609 | A | 6378 | 394 | 626 | SDSVNPQLRVFKILN*SLGILKTHIQIKLF FFFFSALTFALGTLVVCVSIYLYGLPRQD TTSIQQGETASKERVIGV |
| 5559 | 13610 | A | 6379 | 2 | 101 | KTLVPLILPIITLANPCKKD*YPYVVKISI AC |
| 5560 | 13611 | A | 638 | 1 | 77 | |
| 5561 | 13612 | A | 6380 | 1 | 297 | SRFKRFFCLSLPSSWDYRHAPTHALANF VFLIETGFLHVGQAGLKLLT*GDLPALAS QSAGITGGNHCTRQVQCFFRCWGYTRES GQKLDPARVMFENK |
| 5562 | 13613 | A | 6381 | 1 | 394 | TGTHHFYLLLVLLFLEMGPQSITQADV QGHNHSSLQPQTPGLKQSSRLSL*NSWD YRHTPPHPANFFRIL*RQGSYVAQG*SQ TPGLKQFSRLGFPKRWGYRHESPHMAR DRYSYCPHPDEETGDPER |

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| 5563 | 13614 | A | 6382 | 3 | 160 | QL*WSHLLKMLQRYSSCNV**KRRGLIR TYGLDMCSQSLCQYAKDIGFIKLD |
| 5564 | 13615 | A | 6383 | 1 | 1240 | |
| 5565 | 13616 | A | 6384 | 3 | 3129 | KLGSMEPAPARSPRPQQDPARPQEPTMP PPETPSEGRQSPSPSPTERAPASEEEFQF LRCQQCQAEAKCPKLLPCLHTLCSGCLE ASGMQCPICQAPWPLGADTPALDNVFFE SLQRRLSVYRQIVDAQAVCTRCKESADF WCFECEQLLCAKCFEAHQWFLKHEARP LAELRNQSVREFLDGTRKTNNIFCSNP HRTPTLTSIYCRGCSKPLCCSCALLDSSH SELKCDISAEIQRQEELDAMTQALQEQ D |
| 5566 | 13617 | A | 6385 | 2 | 416 | ACCLLYRGDMVPKDVNAAIIVTIKTKRRI QFVD*CPTGFMDGINYPSTVVPVENLD KVQRAVCMLSNNTTAAIEAWARLDHKFD LMYAKRAVHWYMGAEEMEEGEFS DAR EDMAALDKDYEEVDADSVQR*GDEDGQ EY |
| 5567 | 13618 | B | 6386 | 95 | 412 | TNRSIQFGDWCPGFKVGINYPPTAVP AGDLANVQRAVCMLSNNTTAAIEAWARL DHKFDLMYAKRAVHWYVGEEMEEGD FSKAREDMAALEKDYEEVCVDSVE* |
| 5568 | 13619 | A | 6387 | 2 | 614 | |
| 5569 | 13620 | A | 6388 | 151 | 1605 | RGKTLRGLWRFKGIPTHSRENMRCEISIH VGQAGVQIGNACWELCYCLEHGIQPDGQ MPSDKTIGGGDDSFNTFFSETGAGKHVP RAVFDLEPTVIDEVRTGTyrQLFHPEQ LITGKEDAANNYARGHYTIGKEIDLVL RIRKLADQCTRLOQFLVFHSFGGTGSG FTSLLMERLSVDYGGKSKLEFSIYPAPQV STAVVEPYNSILTHHTLEHSDCAFMVD NEAIYDICRRNLDIERPTYTNLNLIGQIV SSITASLRFDGALNVDLTFQTNLVPYPR IHFPLATYAPIVISAEEKAYHDQLSVAEIT NACFEPANQMVKCDPRHGKKMACCLL YRGDVVPKECHMLAILPPSKTKRTYPCF VDWVRPSGFHRCGISTIQPPTLLVPGGD TGARYQRSCVHC*ANTTAIAEAWARLD HKFDLMYAKRAVHWYVGEEMEEGE FSEAREDMAALEKDYEEVGVD\SVVEGEG EEEGEEY |
| 5570 | 13621 | A | 6389 | 1 | 251 | CLKEISFLNGSLTPGAAVKSWLTATSACS FKGFSLSLSSSWNYRCAPPRPTNFCIFS KDRVSLFLLFSLFLPLLARLVNLN*PQV IHLPWTPKVLGL*AAVKSWLTATSACSF KGFSLSLSSSWNYRCAPPRPTNFCIFSK DRVSLFLLFSLFLPLLARLVNLN |
| 5571 | 13622 | A | 639 | 34 | 421 | |
| 5572 | 13623 | A | 6390 | 3 | 445 | RLFFFFFFVFLVEMGFCHVGOAGLKLVT CDPPTSASQSAGIAGVSHRA*PNTSLK*K LTDKSPGICFFVCFEIES |
| 5573 | 13624 | A | 6391 | 2 | 176 | CKFAHGNAELHEWEERRDALGMKLNK ARKDHLIGPNDNDFGKYRFLFKDLN*YA GFYV |
| 5574 | 13625 | A | 6392 | 186 | 374 | |
| 5575 | 13626 | A | 6393 | 872 | 1122 | LRPWKPLCSSVERLWLPVAVELLPPPPAG VLPQPSAQYGERRTFGLTCQGGPGTRAG PSMGCTGYT*RVISQVASGPFHHWPL |
| 5576 | 13627 | A | 6394 | 3 | 415 | ERLWLPSELLPPPPAGVLPQPSAQYGE RRTFGLTCQGGPGTRAGPSMGCTGYT*R VSISQVASGPSPLASRMVQRGWLGPVVR LLPAAALGDMCAHLASSPCSPLLTVPR ASQVPPKELDPISPCSLRPRKVS GP |

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| 5577 | 13628 | A | 6395 | 3 | 349 | VSVVEFLCSKRFAQWSHLAQHLLHTG EKFPFPCLECGRCFRQRWSLAVHKCSPKA PNCSPRSAIGGSSQRGNH*KGKDCLRSF HFMEGPRKGKEEPQVIQGRVRTKPGSPA AQ |
| 5578 | 13629 | A | 6396 | 2 | 352 | EGAAPSSGGPLRDFWGFPRNTNKPCSGT G*SLQRICWMASLAPPGPAPRGQAPHTH RPLGRPSRGAQVQPAAGQATSKQSP GPGFWSQLPQDLTTASVSPSVNGASKAC LECKS |
| 5579 | 13630 | A | 6397 | 2 | 361 | GGEDPPALCRKPTAQTQTGKKHSGTAA VRSRERHKEVRAGHLSALDSPSLLPGI LSPVHQCDVTRVDPISLLTALLWPSAP K*RSEPHKPGVGDVWSAPPTSGEDLILL ATSAH |
| 5580 | 13631 | A | 6398 | 11 | 967 | GSWSGLGARPPGGWNYTGSKKLSPGGE AL*MKRSKELITKNHSQEETSILRCWKCR KCIASSGCFMEYLENQVIKDDSDVDAQ NICHVWHMNVEALPEWISCLIQAQWT VGKLNCPFCGARLGGFNFVSTPKCSCGQ LAAVHLSKSRDYQPTQAGRLMRPSVK YLSHPIVQSGCDKEALLTGGGSENRNHR LLNMARNNDPGRLEALCLEVRPTYFE MKNEKLLSKASEPKYQLFVPLVTGRC ATRAFHRSKSHSLDLNISEKLTLLPTLYEI HSKTTAYSRLNETQPIDLSGLPLQSSKNS YSFQNPSSFGS |
| 5581 | 13632 | A | 6399 | 105 | 465 | SRAYCSLTLDFFGLKQSSHLSPQVAGPT GACYHAWPIF*ILAQMRSHYVARAGLEL LSSRDPPASASQSAGVTGISHHAWPVLL LYLAGTQSPHEFIYDGLDNVSSCLHANF SSLSYST |
| 5582 | 13633 | A | 64 | 647 | 885 | TGNLQNGRKFSQPHLTGK*YPESTMNS NKFTRKKQTPSKSSSPQRTRHQRPW GSSQPLPAHSASPGRGSCSQHHF |
| 5583 | 13634 | A | 640 | 3 | 345 | DAWAWPLNRGFFRMMMDIGAAGVMQ GGDSVELLDIPLKLPDGSIDIPLPILLGRL GFHPLKNTVCIYGHLDVQPAALDGDW SEPFTLVERDGTLHGRGSTDD*VPLAGW INA |
| 5584 | 13635 | A | 6400 | 1 | 462 | HKSDGSTVSVPMMAQTINKFNYTEFTTP DGHYYDILELPYHGDITLSMFIAAPYEKE VPLSALTNILSAQLISHWKGNMTRLPRLL VLPKFSLETEVDLRKPLENLGMTDMFRQ FQADFTSLSDQEPLHVAQALQKVKEVN ESGTVAISSSTAVI |
| 5585 | 13636 | A | 6401 | 3 | 569 | NQASLSFLHLRPYSGHLIRGTPGRGWGK VGAASQRGRLEQLAICRFSLETEVDL RKPLENLGMTDMFRQFQADFTSLSDQEP LHGPQAL*KVKIEVNESGTVAISSSTGESG SGEAPRVSPSPFRITGPQTRKGPRSPLGT EQLCLCSAITHSPVSPQPKRAWDHGT FPRLMAPKFPDCEKAS |
| 5586 | 13637 | A | 6402 | 3 | 194 | FFFFTCTQMFITALFITAPNWKQPRCPSIG Q*TNLFNEAVLSREESIKTKTRDRCYHM DRISK |
| 5587 | 13638 | A | 6403 | 2 | 223 | EMESCSITQAGVQW*DLSSLQPPPPGFQR VSCLSFSPSSWDYRYLPPRLANFCIFSRDG VSPC*PGWSRTPDLR |
| 5588 | 13639 | A | 6404 | 2 | 247 | RLFFFF/CFEMESHSVTQAVVQWRDLG SLRPPPPGFKQFSCSLSSWDYRHTPPH PANFCIFSRDGVSPCWPG*SRTPDLR |
| 5589 | 13640 | C | 6405 | 65 | 211 | MSPNWRWGPPCLATPQGVTPSDTQPCQ ALGLGPHPRNVQPPHISGTG* |
| 5590 | 13641 | A | 6406 | 1 | 112 | GGRGCNQS*SRHCTPAWVTQGPISDIDI LIRPPLTI |
| 5591 | 13642 | A | 6407 | 259 | 380 | GCVQQGVNVQHCAGQQHL*ENGGPGSS DCGWHRGHPLCRL |

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| 5592 | 13643 | C | 6408 | 5 | 160 | MGFEGGPKILNWFKKVVXQSXSCLXKG QXESIFLNTXKVIRAGDTXKSVLG* |
| 5593 | 13644 | A | 6409 | 117 | 207 | KKTMFRQKLFYKRKQLQKGPRP*GAGF KV |
| 5594 | 13645 | A | 641 | 1 | 1254 | |
| 5595 | 13646 | C | 6410 | 155 | 394 | MLKWIYRIFVNLFLVFVRFFNCSFLCAEC ISLPGQECGGAEVSSFSRTFPQHLLSLYL MXXXXXXXXFLQALGLCYPIQ* |
| 5596 | 13647 | A | 6411 | 68 | 547 | LDNRCERCLTEGGWLTSHAPRGKGTW GQKKEPASWGPWGQW*RGAWPTGC KQGRGGSPSPQLGSGGRHEPGQAKATK ASPSQEGDGKGRPRQQGPSWRKSSPRPI SDPPTPGDGKGPSSTSLRL*TRLEPDLVS LGISAGPTRWTLSSAVQLQ |
| 5597 | 13648 | A | 6412 | 11 | 321 | KNFYLFF*DGVSIVAQAVQWRDLGSPQ PPPPGLKLLSCLSLPSSWDYGHVPTMPG* FCTFSRDGVSPCWSSWSRNSRISDASACL GLPKCWEFTRRDNSAPRS |
| 5598 | 13649 | A | 6413 | 17 | 237 | YVAQAGLNLASSQSSCLSLPKHWDYE CEPLCLAFFFL*ROGLAMLPRILPKISI SIRWRNGQKKMHQVL |
| 5599 | 13650 | A | 6414 | 806 | 1680 | AMGIHCITTRTERTSMPTTSAAVLPGPM RQWQLQLPPCIITQSRPCPSCHKSRIPW PVTSPPLSIPTIDTCRPPQELLQLLQ QPLLLLQLPLHITGGIGAPCVALQPQSP LLERATVTGMRVSCPQLQPRGILCTTW PGMSGSSMPIGRVTATNAKARCRHAAD TALPAASASCVTGTTAACWAAAWASAT TGPSCACCFMPPASCSTSLCCWALHCRP CCEPTRPSTWLPSSCFPGSC/CRDHHCRL LGRCVGFGNYRPFCLL/SSCRR/PSCSTS LCCWALHCRPCCEPTRPSTWLPSSCFPGS CCSQPHCPITLWSTLTPLSHGRLWLQSQ TLSSPWALWKSRSVSGSLH |
| 5600 | 13651 | B | 6415 | 61 | 516 | MTTLKKNLADDDAVSCLVLGTENKELL VLDPEAFITLAKMSLPSPVPFLEVSGQFD VEFRLAAACRNGNIYILRRDSKHPKYCIE LSAQPVGLIRVHKVLVVGSTQDSLHGFT HKGKKLWTVQMPAAILTMNLEQHSG LQAVMAGLANGE* |
| 5601 | 13652 | A | 6416 | 360 | 861 | RCGSFLQLLPMPKPADTALPAASASC GTTTAACWAAAWASATTGPSCACCFMP PASCSTSLCCWALHCRPCCEPTRPSTWL PSSCFPGSCCSQAECLWHSPLWPS*RTA WRVRCCAGLGCSSMGCCCGARPHGSG LGASTPMTWVPATTTCRQPWAPARRLGP |
| 5602 | 13653 | A | 6417 | 2 | 263 | NPRDGPTTAACWAAAWASATTGPSCAC CFMPPASCSTSLCCWALHCRPCCEPTRPS TWLPSSCFPGSCCSQP*SPLSSCKPLKPPV F |
| 5603 | 13654 | A | 6418 | 18 | 211 | NEPRASTLTSSKAGQRQAPWTLFPNSYP L*EYPPANPFQGGPHDCRAQTKDMGAQ APRVPEAGP |
| 5604 | 13655 | A | 6419 | 2 | 548 | NGFRGAHSQCPCVLPQGAMSTGGGRQ LPHPCMNPPSPGDSMDAVIKGAAVDLG GTWKGAAPLGLWHCGG*PIENRAGAGE T*SLHI*TPVRSFGFLGTSPMGSPGALKN HGSCARPLLSPLPYPPKERPLPPWHLQS EDLPPRGPEALMPQELGLERC*YPLPQV PRFRGTGAGLVQA |
| 5605 | 13656 | B | 642 | 52 | 554 | MGKEKTHINIVVIGHVDSGKSTTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFYA WVLDKLLKAERERGITIDISLWKFETSKY YVTHIDAPGHRDFIKNMILNHPGQISAGY APVLDCHTAHIAKFAELKEKIDRRSGK KLEDGPKFLKSGDAAIVDMVPGKPI* |

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| 5606 | 13657 | A | 6420 | 368 | 623 | LVCVFFFFF*ERESCSVTQAGVQWCDLGS SLQPPPPRSKQFSCLVLPSSWDYRHTPPC LANLCLIFKSRNPXYFIFPPNCEYWD |
| 5607 | 13658 | A | 6421 | 42 | 179 | |
| 5608 | 13659 | C | 6422 | 28 | 219 | MQILLKSKPKGSTKXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXFRCHD* |
| 5609 | 13660 | A | 6423 | 2 | 161 | KNLH*MESYSVAQAGVQWHDLSVQPL PPGFKRFSCFSLSSWDSRLYFRCHD |
| 5610 | 13661 | A | 6424 | 363 | 750 | REQDPACAWSSS/APNSSWSLHGEAVSH RECLSSPVLPGPDSSKALSSAAALSMSS GRGGGSLVPFSGPVSGVARWIASCVAGE SCLA*AGTRTRCTAPSEAT*SSTRGLSRG AASLAASVHHGSRMSL |
| 5611 | 13662 | A | 6425 | 890 | 1879 | LWGLVTSSCLSFSRRNFTTEIFQEDLMLS DPLNLLSLVMWLCTLWTSALAALSMSSG RGGGSLVPFSGPVSGVARWIASCVAGES CLA*AGTRTRCTAPSEAT*SSTRGLSRGA ASLAASVHPGSRMSL*VAGKPKGPGPTE AAPSCRSSITCTPLTLSSHSTADRAL KASPGLSLRGPGSSGGELCARLSPSSSGM DTFPCLSPTSSWRRFNLSLLALARPRA ASAKPTALSTRW*ITCRSCSEL*TAKPCP VTVMGVLGGGFPWPVLPPLVSLQA QQOHLASLPEFPMRMVRGAQAPSCR RLPRARGETPPRLPSGR |
| 5612 | 13663 | A | 6426 | 8 | 363 | AEVQWRNLSSLQPPPGFK*FLCLSLPRS *DYRLAPPCSANFCMVKTEFHHVGVQVG LELLASSDPPALASASQSAGITGVSHHA WPRASLLSLVIALKQASFFCSHAKPQVS QHFTN |
| 5613 | 13664 | C | 6427 | 87 | 287 | MIFFSFCVNTWCHSPFCATVTEYHSLIXX XXXXXXXXXXXXXXXXXXXXXXXXXWGLF CCIITQRKVEG* |
| 5614 | 13665 | C | 6428 | 11 | 328 | MHMYGXXXXXXXXXXXXXXXXXXXXXRI SEHILCIFRSNYRMIFFSFCVNTWCHSPFC ATVTEYPRLIXXXXXXXXXXXXXXXXXX XXXXXXWGLFCCIITQRKVEG* |
| 5615 | 13666 | C | 6429 | 76 | 276 | MIFFSFCVNTWCHSPFCATVTEYHRLIXX XXXXXXXXXXXXXXXXXXXXXXXXXWGLF CCIITQRKVEG* |
| 5616 | 13667 | A | 643 | 36 | 695 | |
| 5617 | 13668 | C | 6430 | 7 | 324 | MHMYGXXXXXXXXXXXXXXXXXXXXXRI SEHILCIFRSNYRMIFFSFCVNTWCHSPFC APVTEYHRLIXXXXXXXXXXXXXXXXXX XXXXXXWGLFCCIITQRKVEG* |
| 5618 | 13669 | A | 6431 | 1 | 336 | FFFFFRQSLVAQAGVQWCDLCSL*SPP PTLSTPLASASQVAGTTGAHH*TGIIFFVF VETVFCHVAQAGLELLGSSDPPASASQS AGITATVPSLL*LFIKQKQKNRTY |
| 5619 | 13670 | A | 6432 | 3 | 1105 | |
| 5620 | 13671 | B | 6433 | 52 | 936 | MAYLKIQKYEEAEKDDCTQAILLDGYSYK AFARRGTARTFLGKLNEAKQDFETVLLL EPGNKQAVTELSKIKKELIEKGHWDDVF LDSTQRQNVVKPIDNPPHPGSTKPLKKVI IEETGNLIQTNDVPDSTTAAAPENNPINL ANVIAATGTTSSKNSSQDDLFPSTDP AKVLKIEEVSSTSLQPQASLKQDVCQS YSEKMPIEIEQKPAQFATTVLPPIPANSFQ LESDFRQLKSSPDMLYQYKWLSSHQ DNTRAQRLEKAGWQLAFLRYYYHLLDV QKITVCMWQKAF* |
| 5621 | 13672 | A | 6434 | 1 | 309 | LPPIPADSFQLESDFRQLKRSMDLYHD* KQIEPSLYPKLFQKNLDPDVFNQIVKILH DFYH*GKKSPLIFEILQRLSELKRFDMA VMFMSETEKKIARGII |

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| 5622 | 13673 | A | 6435 | 1 | 936 | |
| 5623 | 13674 | A | 6436 | 1 | 1023 | |
| 5624 | 13675 | A | 6437 | 602 | 744 | TPASLKIPVE**NTLLAKMVSIS*PRDLPA SASQSAGITGVSHRARC |
| 5625 | 13676 | A | 6438 | 1447 | 1931 | RKVFKWLSAPLDVSNCPSLCKD*W*RV* RFMPETFPAR*GAENPTLPCCHYSIN/HFT VFSFLF/IFFFWR*SLTLVPQAGVQWRDL GSLQPLPPGFKRFSCLSLPSSWDYRCLPP CLANFLYF**RQGFTVLARMVSIS*PHDL PASASQSAVFSYLIFFLPY |
| 5626 | 13677 | A | 6439 | 1 | 74 | FWRPVRQSEYKQVNKGQDSTFPI*CLQ TNTDYRFRVCA*RRCLDTSQELSGAFSPS AGFVLQRSEVMLTGDMSGSLHDSKMNS MMPTEQIAAIIALGFATLAILFGFI*QSE YKQVNKGQDSTFPI |
| 5627 | 13678 | A | 644 | 62 | 1548 | PLKAKMGKEKTHNIVVIGHVDTGKST TTGHLIYKCGGNDKRTIEKFEKVEAAEM GKGSFKYA*VLDKLAERERGITIDISL WKFEDQQVLMWTHDCPRDTETFIQKHD LQGTSQGLAWFGGPPFWGGSPLIVCCW CLVEFESWYSSKHWGRPREHALLGFTYT GVWKQTKLFGVNKNWIST*GHPTAQKK ILKEIVKGKSALTLRKIGYNPDTSSILCPIS GLNGDHMPGAQMPNLPWFKEWKITRK DGNASGTTLEALDCILPPTRPTDKPLGL PLQDVYKIGGIGTVPVGRVETGVLPKGM VVTFGPVNVTTEVKSVMHHEALGEAL PGDNVGFNVKNVSKDVRRGNVAGDS KNDPPMEAAGFPAQVILNHPGQISAGY APVLDCHTAHACKFAELKEKIDRRSGK KLEDGPKFLKSGDAAIJDMVPGKPMCV ESFSDYPLGCFVAVRDMRQTVAVGVKA VDKKAAGAGKVTKSAQKAQKAK |
| 5628 | 13679 | A | 6440 | 2 | 174 | FFFFFLLLENLF*PSNFGSYKPVHCCVFF CCCCFFLAVFFFVCFCCFFSFSFLFF |
| 5629 | 13680 | A | 6441 | 1 | 271 | PPRFPEFFYSQPPKPPFKTPVFLGVKPG VSSSPPYQKKPTNFGPKMGAL*RIPLFET PIWVFPIKGFHKKKPPVLN*PPTRKPPD KI |
| 5630 | 13681 | A | 6442 | 3 | 128 | FFNKKPPFGRGWFLVPATLRF*G*KIFP PPPPPEVRFP |
| 5631 | 13682 | A | 6443 | 1 | 154 | LVWS*EASKIPGGAEAAHPPTTF |
| 5632 | 13683 | A | 6444 | 2 | 230 | FFESGSRSVTQAGVQ*HSLGSLQPLPPR FK*FSCLSLPSSWDYTHVPTRPANFCIFS GDGVSSCWPGWSRTPNLR |
| 5633 | 13684 | A | 6445 | 70 | 550 | NQVIWESFQAGRHHGHPAPSLAPSASSF LSSFCPSGKAETLESI*SSGKPGVGEGAT SLFPSIS*MFWEGPENGTOEPAGMPIHT PPSCSNPAIHSPGGTGAPGRREEALHCPP *HIPSHPPSRPPWLAPLSLRFPTMAVN DQDRSHVCFPLGLI |
| 5634 | 13685 | A | 6446 | 77 | 485 | NLVYVSSICFTWTFHFERKKFYVSHIVLY KVASPIMKCLYCHSGHTQVVQYLNGEA ARLGQGLLC*NVIIFICLLSLSLFFSFFG PMLKM*NFVFK*CFYNFIRKPKFVFFVTL DFNSLYIGTSNVITVLNKFH |
| 5635 | 13686 | A | 6447 | 3 | 349 | KVEDPSPVWRNSIFWKVITFKVYFFCLF VFLETESLSVVQAGVQWHSLSLQPLPP GFKQFSCSLSS*DYRCTPPRPADFCIFG RDGVSPYWSG*S*TPDLMLCPAWLPKVL |
| 5636 | 13687 | A | 6448 | 1 | 189 | FFF*IGPHSVAQAGVRWCDLGSCSLNLP GSSDPASASQVAGTTGVHYTYQLIFKFF IEMRAP |
| 5637 | 13688 | A | 6449 | 2 | 304 | LDTPLGAAPAAFFLPSLNQCLIYNPMPVR PLKAWRLKTGILTEPRVKGEALGAGMM PTGVSTASSPSYPLAPLGPRLPLQDCMH QALS*APLSDALCIAL |

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| 5638 | 13689 | A | 645 | 2281 | 2431 | KLFFLKNVLLNFFLPLLPSPVLVCYCCF SFFFLYLCLFFTIVLGSARNK*KLFFLKN VLLNFFLPLLPSPVLVCYCCFSFFFLYLC LFFTIVLGSARNK |
| 5639 | 13690 | A | 6450 | 21 | 359 | SLLQPSPAFFSPAFCGLL*PSVQVQSPAFS SLL*PSPAFSSLL*PSLLWPSFSGLL*PSLT FSNLL*SSLLPSTEETPAGQRQELQLFPV GGAADAYFFPKCFKILSSECLK |
| 5640 | 13691 | A | 6451 | 2 | 170 | LSLLSS*DYR*APSQLANFSIFL*RWGLA VLPRLVSDSWPQMILLPPVPDVLLEKA |
| 5641 | 13692 | A | 6452 | 3 | 112 | |
| 5642 | 13693 | A | 6453 | 4041 | 4215 | |
| 5643 | 13694 | A | 6454 | 3 | 309 | PPPPK*IL*RAPNPPLSSSSFNPTWGPGP QPPPSKFSKFARFPFLPPFPFKKEPPSSSL FFPTKEGTVI*KNPPFSGFQSPDSIK*GRV EPPGGTKRG |
| 5644 | 13695 | A | 6455 | 2 | 439 | RTSAREKRDLNRLKKLGDSSKNSDC*SV SSNTDADATQEKNNATSNRKSSVGKK NSKSRTLTRQMSRIPASSNSTSSKLTHIN NSRVPKKLLKPAKPLLSKIKLRNHCKRL EHKNASRKLEMGNLVLKEPKVVLNKL PHKKR |
| 5645 | 13696 | A | 6456 | 1 | 146 | |
| 5646 | 13697 | A | 6457 | 59 | 431 | PTAMAEEGIAAGGVMDVNTALQEVLT ALIHDLGLARGIREAAKALDKYVYQSQC GFLQPEQNCHPREEGMEFMVLAQKF*M ASVLPET*EK/RQAHLCLVLANCDEPMY VKLVEALCAEHQINLIKVDDNKKLGEW VGLL*ILWVLATGTLKPPKGRRHGVHGV SAKVLNGIRPTGNLKGAKPIFVCLHPT VMSLCMSSWWRPFVLNTKST |
| 5647 | 13698 | A | 6458 | 242 | 431 | |
| 5648 | 13699 | A | 6459 | 65 | 473 | PTAMVEEGIAAGGVMDVNTALQEVLT ALIHDLGLARGIREAAKALDKRQAHLCLV AFNCDEPMYVKLVEALCAEHQINLIKVD DNKKLGEWVGLCKIDREGKPRKVVGCS CVVVKDYGKESQAKDVIEEYFKCKK |
| 5649 | 13700 | A | 646 | 203 | 371 | HTDYIPNGPRTNEPTAHELIG*H**PSHFR T*VEQYNINADLKS*YQHSMRMLSG |
| 5650 | 13701 | A | 6460 | 32 | 485 | HLVLASLLACLASIFLPSVGLGQCDLVGS QKTIPRNEGLPRKQTFLSDLLPSCLWFP YSPRLAIKTTIPLHQKPAKPKNITLTF FLSV*NWAIGKLFGLPSGL*GQEGPPFQR ESCAI*GRKECCAKRPRILDRPRWVPH SVYQH |
| 5651 | 13702 | A | 6461 | 3 | 336 | FFFFDIGSCFFA*AGVQWHDHGSLOPP GLK*HDIPPTAS*VAGTTGAHHHA*LIF* LSVKMGSSPLVAPGWSMKSWTQANPSL LQPPQSAWDYRCEPPCLVRNTFEYV |
| 5652 | 13703 | A | 6462 | 2 | 280 | VLGIWRVPGGSGKMEKRESEKQILPRPIG CIWERGKSPGEAPSALPMPWSNPPPGTC TPSCPTYRCTPLPR*TDAPSRHHLAPRN GETIFA |
| 5653 | 13704 | A | 6463 | 1 | 171 | MWGWKEKIKINTFVYCWWEFKLVQNF WSTTWQHILKF*MSFDALLGIYPKYILT NT |
| 5654 | 13705 | A | 6464 | 21 | 402 | |
| 5655 | 13706 | A | 6465 | 42 | 266 | |
| 5656 | 13707 | A | 6466 | 60 | 656 | RRRRLPSVAIMJIYRDLISHDEMFSDIYKI REIADGLCLEVEGKMVSRTEGNIIDSLIG GNASAEGPEGEGTESTVITGVDIVMNH LQETCFTKEAYKKYIKDYMKSIGKLEE QRPERVKPFMTGAAEQIKHILANFKNY QFFIGENMNPDMVALDYREDGVTPY MIFFKDGLEMEKCVSTRKWVKINNVKK TF |

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| 5657 | 13708 | A | 6467 | 176 | 552 | MRSSKQMKPNFPRCSSITVLSVRGMVLF LTLACPRFKMSSRTDFRFGNPQVT*GSTI CSIFRLPSILSMRTTK/DQGMFIWQFQGM RFHF*SETHLVTFLLPPGIM*E*FQSLKPE PFSFLLSCYCH |
| 5658 | 13709 | A | 6468 | 98 | 507 | RATEKWKGRKNHELWSKCFPLKIFFRRS LAMVLCTSKLRPSVLSMRTTKARECLSG SSNA*GFTSSRLRHLSRFCARNHVGMI PVA*T*ALFLSSAPSLPKMPALPGWLCGL DKPSSFSGDFLEPKGFFALAPP |
| 5659 | 13710 | A | 6469 | 204 | 401 | WHEFTGAENHCKTLPKENF*WCLCKSH PSEPKNAAYNRTLCDLGISKSEVSLGTSE EMWTSQQQE |
| 5660 | 13711 | A | 647 | 12 | 355 | LFSSLSGGMQSLSLGQTGISGLN*LTSM APGNLWHMRNNFLFGSRCWMTRFSAEN IFKSVSFRLFGVKCHNTDSEPLKNEDLLK NLLTMGVDIDMARKRQPGVFHRMITNE QD |
| 5661 | 13712 | A | 6470 | 249 | 906 | RIHFPRVSGPSQSNPKFAVASRGFFSLSL SAQPDPLPPPLGEALALSLHPVPRSTET VAGDSSELQLGLRSPQQPLAGLAFLARL FLLFPPP*RCKSKPN*NDRRSSVDSQIHL VGRESAHLPLAGLRVCVSLPLARCFGQV LQGVPLWIPSPGGS/AGVSGRRREERH MGVVVMRVRVEARVSS*ESK/SRALR*S THLGLPKCWDYRREPPCPAH |
| 5662 | 13713 | A | 6471 | 401 | 659 | LIDLRFIYLFYLR*GLRLVP*AGVHWCN LGSLQSLPPGFKRFSCLSLSSSWDYRHAP PHPAHFCIFSRDAVSPCWSG*SQTPDLR |
| 5663 | 13714 | A | 6472 | 1271 | 1538 | |
| 5664 | 13715 | A | 6473 | 1 | 369 | ACSSCFHAGLEHVRVRGSGHSGVAAAR RSEAPDLFC*PPSLPVPSTPFPSPAPAMN QATSDPTHTCPTLPTCPNAA*AGPTAD TPS*GIPDLPAVVLKTPQHLDLPVCSLCG PPLGPTET |
| 5665 | 13716 | A | 6474 | 3 | 340 | ETRSYSVTQAGAEWHDHRS*P*PPGLR *SSHFSLSNWDYRCVPPHSANFLVIFVEI VFHHVAQAGLELLGSSDLPT*ASQSTGIT GVNHCPAEKEVLPREKAMQRGGSQA |
| 5666 | 13717 | A | 6475 | 21 | 273 | GMNERGNITKEIKKIWEY*LGTSQLD TLD*TNSQKDTNYQNQLTKYRKYGLEPI TSDYISNFKRLPKKSPGLDGFTGEFI |
| 5667 | 13718 | A | 6476 | 2 | 3204 | FGEPTSEQTGTAAGKTIAQTAPVSWKP QDSSEQPQEKLCNPCAMFAAGEIKTPT GEGLLDSPSKTMSIKERLALLKKSSEED WRNRLSRRQEGGKAPASSLHTQEAGRS LIKRVTESRESQMTIEERKQLITVREEA WKTRGRGAANDSTQFTVAGRMVKKGL ASPTAITPVASAICGKTRGTPVSKPLEDI EARPDMQLESCLKDRLETFLRRLNNKV GGMHETVLTVTGKSVKEVMKPDDDET AKFY |
| 5668 | 13719 | A | 6477 | 250 | 5816 | |
| 5669 | 13720 | A | 6478 | 553 | 7399 | NFNKKNLSFLGFPRQRKVSSFQKEFSLED KEQLANHERGIDAQLLVALPKVAELRQI FEPKKKEFLEMKRKERIARRLEGIENDTQ PILLQSGTGLVTHRLEEDTPRYMRASDP ASPHIGRSNEEEETSDSSEKQTRSKYCT ETSGVHGDSFYGSGTMDTHSLESKAERI ARYKAERRRQLAEKYGLTLDPEADSEYL SRYTKSRKEPDAVEKRGKSDKQEESSR DASSLYPGTETMGLRTCAGESKDYALH |

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| 5670 | 13721 | A | 6479 | 380 | 999 | AGAKGGPGGRGMKKTNSLTPLLSAYR LLPVELSKGWGILGFSVCPFAPGLMAKG VSPCDTAVKRDNIH*VGGGVSKCP*RSS *WSGPVPALTALFLVDNHHEVYLWQGW WPIENKITGSARIRWASDRKSAMETVLQ YCKGEAPSNMPAARNRWGSPSGMRSQE TPFPFCACQPASIHKAQVVDENPIFSPL KPFEDVIKFLD |
| 5671 | 13722 | A | 648 | 1134 | 1633 | PNPTGTLMMLARKWCPDGLQSLPPDVLGS *GEHLLSCLCQERACSSNSRRRQAWTG SQGSRVINFFFAKVGTC HQGPNHQA KAPGTPPTPSYPTSPRQLLWQVWQPRP ALPASSPCSRHQLYLPRQAMSWLLSPAP SVPLDFSGASPVWATLCFPHRPLPHR |
| 5672 | 13723 | A | 6480 | 78 | 200 | KKGSPFFPKVGGQGGNLGLLEPLPKLK KFFCFKPKRGDYSSSSSSPDSSSSKKK GVSPFWPGGV*TPKEGGL |
| 5673 | 13724 | A | 6481 | 179 | 384 | FNSYYMYVYVYVHICVFLYVCICIYRI YLCIAVITCLMNEW**FKCKGNDARGYE KKLPSKYEIEKE |
| 5674 | 13725 | A | 6482 | 76 | 205 | RKKPEPEKTCFDNITGNTYPCSTYEHDS D*YYVNRT*LCAER |
| 5675 | 13726 | A | 6483 | 2 | 774 | HSYSHSHGHCGSPAGDTEQGYKPVWPV CSLFPDGSHPGV*QPIHEPA/QGRGGLPP WGAA*TPRAWRLA*RPRG*AALPWA*T SPGRPASAPLAHTGSGCPSRPTAPGSP/ IPIQNIKRYPYGEAFVPSRAGPTVGVTRS FHLAPSLPPFPSS*LSPSLPRTTTSCTRAI LTPSS*QKLLYPPSRPVVLLVRRARPPAA APTSEEPERSPWETPHAAPSQLHELHET HSAQKSDLLPAPEAM*PGSVSSRFLLY |
| 5676 | 13727 | A | 6484 | 2 | 732 | GRRRPGPKPPRAPGRDRDRCNF*PCCPP GAKSSAACCCDIRRAARAIPLGNSPCSP LSAP*AP*NPLCRTVMGRSPMTLSLGSRT PTSLPAPFPWSPRFG*PTHPRARSLGTL WPMPTTP*QAATPWRR*PPATQASTP HSLRGSSSSQPRLAPLRPTSSRACMAGP TTPAAGALGPVTLGVLTTPQAWASLRTP GRLTSLSPRQPLQQRQWQQQQPQLQPQ PRPLWQPCRRHRTI |
| 5677 | 13728 | A | 6485 | 2 | 338 | CTTAIPTPEEMTRLRSMNRQLQINVDCA LTEVDLLQSRGNFDPKAMNNFYDNI*PG PDVPPKPSKKGPTDSEPKTSSGPCSNGC LLSCKFFHACSRFQNPICIHQSTLAA |
| 5678 | 13729 | A | 6486 | 84 | 300 | RVGARGKMTALASGQLGPLMCQFGLPA *AVEAANKGDVEAFAMQNIKPEQI* GDTKDKTD*KEDLSLD |
| 5679 | 13730 | A | 6487 | 91 | 668 | SRAQVVLHCVLREWAGGRRSPAPPSPW PVLHVDPQSWQLSSVALGCSPGWSSAL AWLFLQALGMFSAALASGQLGPLMCQF GLPAEAVEAANKGGKVAAPGTPRPEPG AGSIPVPLDLQKWG*GGKGHSALDPI ALIPSFGARVRHHLVSLTCSVDVEAFKA MQNNAKPEQKEGDTKDKKDEEDMSL D |
| 5680 | 13731 | A | 6488 | 1 | 414 | LQPGPAGAQQVDLA/SVV*PPEIMAPILA NADVQERLLPYLPSGEISLPQTADENQNT LTLAPSSQALGMFSAALASGQVGF MCQFGLPAEAVEAANKGDVEAFKA MQNNAKPEQKEGDTKDKKDEEDMSL D |
| 5681 | 13732 | A | 6489 | 205 | 553 | LSRPRHHKASTTGAQMQRTRSMRQEP EKAILTLRGSRPTPRAPQLVPSVPSSWL FLSLHSIAQTPLPHTHSTHTPRSQALPSQ APVVPVQHPHPPE*ALSPDNLFMILKSP |

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| 5682 | 13733 | A | 649 | 1 | 370 | QRLAEMSNAJERKHATKMTYQPTNGTL TSGYVADRRVKHHS GGEEFFQAQKQEP HPGTSRQ*QTRVNLHSLPDPHEMQTYF RGMRYRLGGWKAGPEGTFYDIPRYVTA YTFAHTRPADIRAM |
| 5683 | 13734 | A | 6490 | 3 | 347 | SFFFVLRRSLAVAQAEVQ*RNGLSLQPPP PEFKRFSCFSLPSGWDYRRPPRPANFLY F**RGVSTMWGQGWSTPDLRGDLAHL GSPKVLGMTGREPPCLGPLNGLTFLPEIS |
| 5684 | 13735 | A | 6491 | 280 | 406 | FFVFLGETGFHRVSQDGLNLLTL*SARLS LPRCWDYRREPPH |
| 5685 | 13736 | A | 6492 | 1665 | 1787 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 5686 | 13737 | A | 6493 | 1431 | 1553 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 5687 | 13738 | A | 6494 | 1740 | 1862 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 5688 | 13739 | A | 6495 | 1173 | 1295 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 5689 | 13740 | A | 6496 | 1027 | 1149 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 5690 | 13741 | A | 6497 | 631 | 744 | VIEHLVSQDGLDFLT*SARLGLPKCWD YRREPPRPVH |
| 5691 | 13742 | A | 6498 | 166 | 352 | IFFVFLVETGFHHVSQDGLDLLTS*STRL GLPKCWDYRREPPRPAPSSPIFHTVAPIQ YTHP |
| 5692 | 13743 | A | 6499 | 2250 | 2372 | FFVLLVETGFHRVSQDGLDLLTS*SAHL GLPKCWDYRHEPP |
| 5693 | 13744 | A | 65 | 1586 | 1775 | |
| 5694 | 13745 | A | 650 | 1 | 222 | |
| 5695 | 13746 | A | 6500 | 150 | 368 | EKELAFFPQGE MQGNG* LKPPPLR*R DFSCALPRGGNGRGAPPSPTNFGFLGG NGVYPSGGGFETPDLK |
| 5696 | 13747 | B | 6501 | 174 | 350 | MDEKTKAEEMALS LTRAVAGGDEQV AMKCAIWLAEQRVPLSVQLKPEVSPTQD IRFLM* |
| 5697 | 13748 | A | 6502 | 1 | 498 | EFRAPGGLPRTRRPARRVAGSGGPG*GV TIFPAPPPSPAPLPGPLSLPPLPLR TGASREERGLCLETDRDARGAPASGGPPG LGTPRLGGVRASFRRFPRLVPFPAP ADLSRRPLPSHRPTQDPLVIGQCDASRL PRGQRGTHRAWAAPEATRPG |
| 5698 | 13749 | A | 6503 | 919 | 1761 | RAFSFNREEPTADEQGLPTSVAGRPVIA AVPSWHARGTERRAPGRD*HHPHLG AQPSAALLPGLP*HCGHISAGGRREAGNI PGRKIIYPPPGFYGSNNGQHQA YIKLSD ARSLTR*IQSSMTSCRVL R*GPSLPSAGS SPGLGMSCLTSGTSCGYMTSSWPPTDA DLLCSRDCVVS RAGSPGL*L*HGLGPPV /SPRSLRTPMRH*SAEQETFLSFHPNL LGRPLNSKLGRQPLLSKTL SWHQPSR GLIWCCSGSGDFCGLKIEQKMS |
| 5699 | 13750 | A | 6504 | 131 | 575 | VFALKPGTPGALPQVGVLRLERPGWV VSGRPPFASHLGLVPFPAPKCGTLR PLPSHRPTQDPLVTGQL*CFPTAAGTAT AHTGLGPRRKPHRPWLSCSWSPRLFPD PEVSIFPRKARSPPGEWGTATPDGREDQE SRGNGP |
| 5700 | 13751 | A | 6505 | 2 | 291 | HEPQLNSNNVALHGAVIPGPPFLGACIN LMNFMVALFIPEYKIARGVQKHTYKHN GSLTNT*RGSEDEIEPLLRDSTIWELFSF EPPGNQCP |
| 5701 | 13752 | A | 6506 | 1 | 267 | PRFKLFPCLSLSS*DYR*VPAITPG*FLY FF*VKTGFHHVGTGLELLTSGDPPTSAS QSAGITGMSHCTWPISFLYLWHTGGKKK EC |

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| 5702 | 13753 | A | 6507 | 1 | 216 | HEWMGTRVGEWMDEWKEGWKMDGK VDK*MNGWMEGCLYQWLNTEILCQELI PYTCLCLFSGWIYIFKQSILD |
| 5703 | 13754 | A | 6508 | 74 | 356 | |
| 5704 | 13755 | A | 6509 | 2 | 375 | RHEVKPQWTPG*DTDHLPNLSVALGPTR QPGRQRPEGTQVPSIPASSIPASQSOPQ SQPPNPSLLHPRTPTPSLPIPASLPASPKT QTL*IPASEVGTVSNPTPWTRKLGPGEAN RLSLMV |
| 5705 | 13756 | A | 651 | 3 | 556 | LPTEVAAISFSLAIGKHSATVFSWPAGKP PSRILPHLGPLLPQKASWPLRLPVKPKF VKKRPKKFIRHQSDRYVVKIRNWRKPR GIDNRVRRRFKGQILMPNIGYGSNKYTK HMLPSGFRKFLVHNVKEQGLEVLMLCN KSYCAEIAHNVSSKNRKAIVERAAQLAI RVTPNPANRLRSEENE |
| 5706 | 13757 | A | 6510 | 3 | 148 | HERREVTVIRRGKGKHLRLVPTRWAGK GLLG*SICFWSFSLGHHWSVC |
| 5707 | 13758 | A | 6511 | 50 | 255 | LSMVSTVLVTIMKLCY*K*QIQSWLPC LTHTKTHTHTHTHTHKVLHTLTCKQ YYAIIIGNVLSFY |
| 5708 | 13759 | A | 6512 | 268 | 355 | |
| 5709 | 13760 | A | 6513 | 2 | 206 | |
| 5710 | 13761 | A | 6514 | 1 | 317 | FFFFFPLFRQCLTSPRLEYSGTISAHCS LSQPGSSDPPTSALRVAETTGRHHAWLI FVF*VETGLHHVVLAGLELMGSRNQPTS ASQSAGITGVNHRAWLTW |
| 5711 | 13762 | A | 6515 | 2 | 210 | KEKIFSPGFKHPPPPF*KTPLKGKRIFFS PPRKNWPPQRIFKKAPPSSSSSSSSSSSA QI*SFNSP |
| 5712 | 13763 | A | 6516 | 674 | 985 | WFFFWLCHPGWSAVAWWHDLSLQPPP PRLM*FSCSLLSNWDYRAPPFLASFVF LVDTAFRHLGQAGLELLTSSDPPTLASQS AGITGVSHRTQLRSSFDS |
| 5713 | 13764 | A | 6517 | 2 | 336 | |
| 5714 | 13765 | A | 6518 | 3 | 260 | CLGLLVIFVCNFSIRDYRRPPLH*LIFV FLVEMGFYVVG*AGLELLTS*SARLLAS LRAGITGVSHRARPRSFVFGFGWQDHG |
| 5715 | 13766 | C | 6519 | 38 | 478 | |
| 5716 | 13767 | A | 652 | 2 | 395 | |
| 5717 | 13768 | C | 6520 | 33 | 317 | MLTNHLHHWPFKNXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXTRCPRIITFFLRG* |
| 5718 | 13769 | A | 6521 | 1 | 253 | RRLFFFFLRWSFALVAQAREQWCNLG*L QPPSPGFKQFFCFSLLNSWDYRRAPSCPA NFVFLVEMGLYIFKEWDNDGRMICEAF |
| 5719 | 13770 | A | 6522 | 2 | 411 | GVLRLSSACPAQCPSTSTGP*AALAGFT TTGSLCWAWTPSSSFVSGSSREAPSGT ATTSWTRNVATATSATTANRMAMCTSR TARLLLAPTNCSPRSKLTLPIDPCSGGC RLTCKDNTPRLTGTGQGRRQGTG |
| 5720 | 13771 | A | 6523 | 2 | 222 | THIGLPKC*DYKCEPPVHRQFL*F*VETR FHHISQAGFKLTTSQDPPALASQSGRITG VTTRTQPLNGFYKVM |
| 5721 | 13772 | A | 6524 | 2 | 261 | VVVVSQYAAERPSVVAHACNPSTLGGR GRWLT*GQQVETSLASGYLPTLASPKCW DYRREPLRLACFNFFVETRNLTLVLPISV QQ |
| 5722 | 13773 | C | 6525 | 203 | 355 | MVALSTRGQVHLSGAVVPSSFLIFLIAPS GEQEVDIAMVAGYAVTSVVLL* |

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| 5723 | 13774 | A | 6526 | 2 | 671 | GVGGVGRGMLPPAPPAPAGFPSTILW PSPPLL*LPPPGLGTGFLPFGHGCPPLSQS PWILFPWGGAQAQPL*P*PRHPCPPHPR QSYGRQLPTFWLAPPSFCLSLVFSSLSLIL SLSSVSRSVLLP*HPPPHISFHPLGFLS*AS PISGVGGIKAFLPLRFQPPF*PLIPTTPLSL PKMGALWGRL*HSTPAQAMGSRAPFSG LAQASTYLLQPPGVVGS |
| 5724 | 13775 | A | 6527 | 3 | 477 | AGKFPLRSGHFPCFLTVESVCSPGPKPSV IPLSPCGASAPSPRFLSPSPGLVRAVLHC TLLVAS*APPPASPPGVAVFSPVSIWHPS RLPGSYGLCGQHRLDPTKPRSRTHFRA VPPLVSCSLPSPNLPLMTSGVQRPPKGLE NSLLQLADLNK |
| 5725 | 13776 | A | 6528 | 1 | 381 | |
| 5726 | 13777 | A | 6529 | 1 | 2654 | MSFFSTLKTALSKEKLAATGVLVLICAL VGAGFAWERHQLKQAJEKGSLDQAVK ERDKSIMDLNQTETMNAEQHFHSQEV KNESEQAKYADRQMERKAEVQKQLVA AGNVRQRIADTQRLRESISEFNADAD KGIFMSDKVTVKQTINKATSIYKIEQITV GKPGSEQYRRAFELADQLGLKHPDCIEH VFPTYADEQCTHVLTEEDFFSTEEREGV DRCIGVICSSVDELFPNVPEYGGIGYQF LYEGDELKCYEHDIESKAKELTVNSNNT VQPVALMRLGVFVPKPSKSGESKEIDA TKAFSQLEIAKAEYDDIKITGPRLDMDT DFKTWIGVIYAFSKYGLSSNTIQLSFQEF AKACGFPSKRLDAKLRLTIHESLGRLRN KGIAFKRGKDAKGGYQTGLLKSWRADS KLWELFQLDYRVLLQHHALRALPKKEA AQAIYTFIESLPQNPLPLSFARIRERLALQ SAVGEQNRIKKAIEQLKTIGYLDCSIEKK GRESFVIHTYLIPAIPPQHIIQDFPLSHIL DFYSPSSTHRSCRASRSHQLIESEAWLPIE AGNHQNDSGYNLNVEEIRVLYAWRMPK HVVTHLAKDQLHKVAQRANRMLNVL EQVQLQKDELHANEFYQVYAKAALAKL PLLTRANVDYANIIDIYEHGVPKYRDR YSERGVSKTVSTVSLAHAMRAHPHLLM EDLRILVIDLDPQSSATMFLSHKHSIGIVN ATSAQAMLQNVSRLEELFEFVPSVVP VDVMPASIDDAFIASDWRELCNEHLPQ NIHAVLKENVIDKLKSDYDFILVDSGPHL DAFLKNALASANILFTPLPATVDFHSSL KYVARLPELV/KLISDEGCECQLATNIEK QTNNWANP |
| 5727 | 13778 | A | 653 | 1 | 1055 | TDCRVDPRVRPRVRVEHSIVGTRLVSCQ LQPSQPNADQGKLTMMRIAVICFLLGIT CAIPVKQAESGSSEKQLYNKYPAIVA TWLNPDPS/QVRQNLGPTGFPFSKVQR KGHGPHGMIWDGWKVDDDDPC/VDSQDS IGLGTTLDDVDDTDVSHQSDSHHSDS DELVPDFPTDLPATEVFTPVVPTVDTYD GRGDSVVYGLRSKSKKFRFPDIQYPDAT DEDITSHMESEELNGAYKAIPVAQDLNA PSDWDSRGKDSYETSQLDDQSAETHSH KQSRLYKRKANDESNEHSDVIDSQELSK VSREFHSHEFHSHEDMLVVDPKSKEEDK HLKFRISHELDSASSEVN |
| 5728 | 13779 | A | 6530 | 1 | 945 | |

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| 5729 | 13780 | A | 6531 | 146 | 4368 | LGFLRLSEMPRKQGDYRT/SDMEIRGR VEQRVGYTIEQINMRDVFGRRLRAED VFPPVIGVAAHKGGVYKTSVSVHLAQD LALKGLRVLLVEGNPDQGTASMYHGW VPDLHIHAEDTLLPFYLGEKDDVITYAIKP TCWPGLDIIPSCALHRIETELMGKFDEG KLPTDPHMLRLAIETVAHDYDVIVIDSA PNLGIGTINVCAADVLIPTPAELFDYT SALQFFDMLRDLLKNVDLKGFEPPDDLAI LF |
| 5730 | 13781 | A | 6532 | 820 | 2011 | TTTLVRLPCRSKRRRIKALRSQRLGLPM MRVPSFRLRVTSPTFMKSLTWQVHLLVL MLLVMFWTCNPSVCTASYVAAMCWW QAPMAPAKPQPSRWKTSKARMYQSOK VAKTSTLTVLSLLITVPAAYFTRLLMLL LPLMRVPSFRLRVTSPTSMKSLTWQVHL LVLMLLVMFWTCNPSVCTASYVAAMC WWQAPMAPAKPQPSRWKTSKARMYQS EKVAITSTLTVLSLLITVPAAYFTRLLM LLLPLMRVPSFRLRVTSPTSMKSLTWQV HLLVLMMLVMFWTCNPSVCTASYVAA MCWWQAPMAPAKPQPSRWKTSKARM YQSEKVALTSTLTVLSLLITVPAAYFTR LLMLLVSKSL/CTCSLNYNIGQIALSFSKA PDKGTEIAIERGANGDVLDMQSVGVYSQ LRRRYVLVASSDGTSTATFKMEDFEGQ NVPIRKGRNTIYVSRIKSVVDNGSGSLH SFTNAAGEQITVTCSLNYNIGQIALSFSK APDKGTEIAIERATDDACTFIPVTRDQSDI YEVFNVAGSSFSGSYAAGDVLDMQSVGV YSQLRRRYVLVASSDGTSTATFKMEDF EGQNVPIPKGRKNYVNRKSVVDNGSG SLLHSFTNAAATADACTFIPVTRDQSDIY EVFNVAGSSFSGSYAAGDVLDMQSVGVY SQLRRRYVLVASSDGTSTATFKMEDFE GQNVPIRKGRNTIYVNRKSVVDNGSGS LLHSFTNAAATADACTFIPVTRDQSDIYE VFNVAGSSFSGSYAAGDVLDMQSVGVYS QLRRRYVLVASSDGTSTATFKMEDFEG QNVPIRKGRNTIYVNRKSVVDNGSGSLL HSFTNAAGEQITVTCSLNYNIGQIALSFS KAPDKGTEIAIERGSSST |
| 5731 | 13782 | A | 6533 | 1 | 3039 | MLNVLTEQVQLQKDELHANEFYQVYAK AALAKPLLTRANVDYAVSEMEEKGYV FDKRPAGSSMKYAMSIQNIIDIYEHRGVP KYRDRYSEAYVIFISNLKGGVSKTVSTVS LAHAMRAHPHLLMEDLRILVIDLDPQSS ATMFLSHKHSIGIVNATSAQAMLQNVSR EELLEEFIVPSVVPGVDMVPASIDDAFI ASDWK/ELCNEHLPVLKLISDEGCECQL ATNIGFMSKLSNKADHKYCHSLAKEVF GG |
| 5732 | 13783 | A | 6534 | 1 | 2607 | |
| 5733 | 13784 | A | 6535 | 1 | 4557 | |
| 5734 | 13785 | A | 6536 | 3 | 2847 | ELHAYAMSIQNIIDIYEHRGVPKYRDRIL AHAMRAHPHLLMEDLRILVIDLDPQSSA TMFLSHKHSIGIVNATSAQAMLQNVSR ELLEEFIVPSVVPGVDMVPASIDDAFIAS DWRELCNEHLPQGNHVLKENVIDKLK SDYDFILVDSGPHLDAFLKNALASANILF TPLPATVDFHSSLKYVARLHELVLKLSN EGCECQLATTIGFMSKLSNKADHKYCHS LAKEVFGGDMLDVFLPRLDGFPERCGES |
| 5735 | 13786 | A | 6537 | 1 | 4236 | |
| 5736 | 13787 | A | 6538 | 65 | 316 | |
| 5737 | 13788 | A | 6539 | 54 | 265 | |

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|------|-------|---|------|------|------|---|
| 5738 | 13789 | A | 654 | 2 | 1103 | PGRPTRPPTRPGGGRAQHRLYQTLQSAS CSLLSQTPTRGKLTMMRIAIVICFLLGITC AIPFKQADSGSSEKHFVYNKYPDVAT WLKP*PIFRRQNLGPTWLCPLKETNGL *TRRTLKLRNSNGKAMDHMDDMG*WK VDGWTMWDSQDSIDSNDSDDDVDDTD DSHQSDSHHSDESDELVTGFSTDLPAT EVFTPVVPTVDYDGRGDSVVYGLRSKS KFRRPDIKYPDATDEDITSHMESEELN GAYKAIPVAQDLNAPSDWDSRGKDSYE TSQLDDQSAETHSHKQSRLYKRKANDES NEHSDVIDSQELSKVSREFHSHEFHSHED MLVVDPKSKEEDKHLKFRISHELDSASS EVN |
| 5739 | 13790 | A | 6540 | 2034 | 2174 | EMPGHARCYADQQRYPFLPGSEVLP/ASI NVAWRPVDNLNTCSTRSPE |
| 5740 | 13791 | A | 6541 | 33 | 285 | |
| 5741 | 13792 | A | 6542 | 1 | 2448 | |
| 5742 | 13793 | A | 6543 | 1 | 2979 | |
| 5743 | 13794 | A | 6544 | 1 | 3276 | |
| 5744 | 13795 | A | 6545 | 1 | 67 | MTKCSHLCNNYLFWSLRDNGILIATGER RNVKQKEYISRGYFTLKETVIDTSNGSRI SFTTRITGKGQQWLMKRLLDADVVRTTS IVMLAKVTLSCITMSDFTFSGYELACFV THSGLSRSAGHILSQCANLAATTSEYFIH KPHRLITAETGYSQSTVVRAFREA VNK ILSVEIVIGDHRERRANLYRFTPSFLAFAQ QAKNALIESKLKISSAATKVAVLAKTL ALFNFLSTPPCQNDTPSPCQDDVAIKNK KSQVKKTKRSVSGGAGTTSLLKLT SWIA KAKAKADNLRLSKKRTQKHEFKQKVEA AARKYAYLKNRSPDIGGINSFNDLPHC MTVNEALNAVLAKNKDNEQWGAVAGA YIADITDGEDRARHFGMSACFGVGSV YMQTRYRGKLVSGFVVQMILTPRAD GTFITSTDSETVHYHYGPKDLVTILFYIFI TILHAVVQEYILDKISKRLHLSKVHHSK FNESGQLVVFHFTSVIWCIFYVVVTPQA LTRVLNCLLALGSNAAVMGECCGFAQLQ QTWASALADYAAAHKSMRPEILASCH QTLNCLIESTRNSMDATNK/ADAGICRS RDDRFR*RCYASAFIPRDDPACSVGGSY R*CVITEF |
| 5745 | 13796 | A | 6546 | 1 | 3435 | |
| 5746 | 13797 | B | 6547 | 9377 | 1600 | MSDWSRV TGMKVHASAVAAPN*TGRII ARNKGRRITPSETLIISAATDSSIALLVAS MLLRVDSLIAISVPLSGALENDRAI |
| 5747 | 13798 | A | 6548 | 3 | 127 | LFHPCQDSQQHH*CVCCRLTGHGAA*V HGPCQAVQTYRASH |
| 5748 | 13799 | A | 6549 | 2 | 323 | |
| 5749 | 13800 | A | 655 | 3 | 267 | TINPKLLKNHARGTPEVPNQKHHWSPKQ KPLLTKNPKNNLPRWPVPIPPFPEEKPR KFP*TPKRRIP*TKIGPLPSNPGYPTKPPF |
| 5750 | 13801 | A | 6550 | 2 | 94 | |
| 5751 | 13802 | A | 6551 | 171 | 632 | |
| 5752 | 13803 | A | 6552 | 3 | 325 | |
| 5753 | 13804 | A | 6553 | 2 | 171 | |

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| 5754 | 13805 | B | 6554 | 104 | 1164 | MCDEDETTALVCDNGSGLVKAGFAGDD APRAVFPSIVGRPRHQGVMMGQKDS YVGDEAQSKRGILTLKYPIEHGIITNWDD MEKIWHHTFYNELRVAPEEHPTLLTEAP LNPKANREKMTQIMFETFNVPAMYVAI QAVLSLYASGRTTGIVLDSGDGVTHNVP IYEGYALPHAIMRLDLAGRDLTDYLMKI LTERGYSFVTTAEREIVRDIKEKLCYVAL DFENEMATGRHPSILPWKRATSCQTGGQV ITIGNERFRCPETFFQPSFIGMEVGGHFR PPYNSIMKCDIDIQEGPCMPTNVMFGGH PRLYPWEFADPHARKRFTGAGTPGTHEE SKDKDSFAPRRSGKILG* |
| 5755 | 13806 | A | 6555 | 1 | 308 | LRPWC/GHLRT*AQYHTLRAARLDPNFA IA*MEAKATDGPPFFE/VRGFPTIYFSPA NNRLHPTSEGGRLDLSDFISYLHVEATNP PVIOEV*PKKKKKAQEDL |
| 5756 | 13807 | A | 6556 | 2 | 589 | AIRTAKEKFVMQEEFSRDGKALERFLQ DYFDGNLKRILKSEPIPESNDGPVKVVV AENFDEIVNNENKDVLEFYAPWCGHCK NLEPKYKELGEKLSKDPNIVIAKMDAT ANNVHSPYEVGRFVPSHILLSKPNKKLNP KKYEGGRELR*FLLAIYQREATKPPPIQ V*FIPKYRRRRHQEDLLKPVAQTPTL |
| 5757 | 13808 | A | 6557 | 1 | 129 | |
| 5758 | 13809 | A | 6558 | 23 | 115 | |
| 5759 | 13810 | A | 6559 | 1 | 1582 | GRGWRAVLGWSRRRSGLPATVGSMA LLFLLPLVMHGVSRRAEMGTADLGPSSVP TPTNVTIESYNMNPVYWEYQIMPQVPV FTVEVKNYGVKNSEWIDACINISHHCNI SDHVGDPNSLWVRVKARVGQKESAYA KSEEFVAVCRDGKIGPPKLDIRKEEKQIMI DIFHPSVFNVDGEQEVYDYPETTCYIRV YNVYVRMNGSEIQYKILTQKEDDCDEIQ CQLAIPVSSLNSQYCVSAEGVLHVWGV TEKSKEVCITIFNSSIKGSLWIPVVAALL FLVLSLVFICFYIKKINPLKEKSILPKSLIS VVRSATLETKPESKYVSLITSYQPFSLK EVLCEPLSPATVPGMHTEDNPGKVEHT EELSSITEVVTTEENIPDVVPGSVHLTPIER ESSSPLSSNQSEPGSIALNSYHSRNCSESD HSRNGFDTDSSCLESSESLDSEFPNNK GEIKTEGQELITVIKSPPSFCYDKPAHVL VDLLVDDSGKESLUGYRPTEDSQRFH EISLSCTQL |
| 5760 | 13811 | B | 656 | 197 | 404 | EQQLQAQHLSHGHGPPVPLTPHPSGLQ PPGIPPLGGSAGLLALSSALSGQSHLAIK DDKKHHDAEHRX* |
| 5761 | 13812 | A | 6560 | 69 | 523 | PLGCASSQISASRNTLCTTASSCCPQVL AHSKAAEYMTWKVQQMPHSQDRAL QSVFCAPFHS**LVALPTGHR*MTPAQFS ECFQATSGGSD*DPFLAPSFLVPLPVAP GLLLPLGPVHSRATMEEGQATHEELTVFI GLRPGVRGS |
| 5762 | 13813 | A | 6561 | 101 | 1469 | RTHPTFPHPGTGPTSAPPSGALEGTAGTI TSNEWSSPTSPEGSTASGGSQALDKPIDN DGEVWSPDIEQSFQALAIYPPCGRRKI ILSDEGKMYGRNELIARYIKLRTGKTRTR KQVSSHQVLARRKAREIQAKLKDQAAK DKALQSMAMSSAQIISATAFHSSMRLA RGPGRPAVSGFWQALPGQAETSHDVK PFSQQTAYAVQPLPLPGFESPAGPAPSPS APPAPPWQGRISVASSKLWMLEFSAFLE QQQDPDTYNKHLFVHIGQSSPSYLRPYL EAVDIRQIYDKFPEKKGGLKDLFERGPS NAFFLVKFWADLNTNIEDEGSSFYGVSS QYESPENMIITCSTKVCSEFGKQVVEKVVET EYARYENGHYSYRIHRSPLCEYMINFIHK LKHLPEKYYMNSVLENFTILQVVVTRD |

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| | | | | | QETLLCIAVVEVSASEHGAQHIIYRLV KE |
| 5763 | 13814 | A | 6562 | 1 | 1290 |
| 5764 | 13815 | A | 6563 | 604 | 1047 |
| | | | | | SNNRTDNPTSVAYLSKETDVVAKGWPH CLWVVVAVAILVLEAIKIIQKDFTVWT SHDVNGILGAKGNSWLSKRLRLRYQAL LLEGVVLQIHTCVALNPAIFLPEDGEPIKH DYQQIVAQTYVT*EDLLEVPLANPDNLN YTNSSSFV |
| 5765 | 13816 | A | 6564 | 1 | 1410 |
| 5766 | 13817 | A | 6565 | 510 | 755 |
| 5767 | 13818 | A | 6566 | 59 | 411 |
| | | | | | SWPSDKQTLVVQRGQKMEQANHPDPTD HMSQLMWT/VLPQGFRDSPHLFGQALA QDLGHFSSPGTLVLQYVDDLLATSSEA SCQOATLALLNFLANQGYK/LSRSKAQL CLQQVKYLCL |
| 5768 | 13819 | A | 6567 | 1 | 565 |
| 5769 | 13820 | A | 6568 | 126 | 492 |
| | | | | | CNNSMTSLQVRLKVCPRPCRTSM/LPIRII *KLPQVCLDLL*IREGEWDMYPCWAKFP CPYSLKGT*PIAWGILWSFGDFAY/IPLM QQQKH*FSSQNTRRNEEGQI*WPLLMHS QKPAPLPVV |
| 5770 | 13821 | A | 6569 | 1 | 342 |
| 5771 | 13822 | A | 657 | 2 | 651 |
| | | | | | LSRVLEFEFQFLQAQYHSLKLECEILAS EKTEMHRHYVVMYYEMSYGLNIEMHKQ TEIAKRLNTICAQVIPFLSQEHQQQVAQA VERAIQVTMAELNAIIGVRGLPGLPPTQQ QLQAQHLSHGHGPPVPLTPYPSGLQPPG IPPLGGASAGLLALTSALDGQSHLAIKDD KKHHDA*HHRGDRPGKPD*DFVLILLQC CKVVCIAKESPNLYREQT |
| 5772 | 13823 | A | 6570 | 55 | 219 |
| | | | | | LGNKHLGSDPRGSWVTGEYIFLRPIIA A*GRQ*DFLPPELWWTSLNNSWAFS |
| 5773 | 13824 | A | 6571 | 339 | 1371 |
| | | | | | ASHPLRGLLCGSPSPNEPCPLLHGTSRHR PLKG*GVRAHSTGLAGSSTCRPLRDPLG EASWAPESAQGL*IHQSALCI*LKLKPAG QRAKLGDRLDIPDRRKSSITLGRAGDLQ PAMPEPPTLSVGSCAAQASPMNPAPCST APSPIDHSRAEECGRIARDWQAAPPAGP CGIHWVKPAGLLSLRDCKYTNRHSVSS SRFANTNQHPASSSGFVNAPIDTLYLANL VGTWRTFVASSGIVNAPITLSKQTTWL YQSAGCGKESTQASGAQTGGTSFKSLET TGSISEASSAKHCTELFSRFTTFNPDSVPS DGVVGDAGTVWPGVLKGEPCHLGTCY RCVLDPHPTPSESDTIQGIHVQVCYMSL HDADVCDTNDPVTHTNKKYISTEFTS NNPELRSEDETVFRALEKWKTSQTIGE MDFYICNDPHPDALYQNGLSKMQDTV SLSVFSPSVAA |
| 5774 | 13825 | A | 6572 | 749 | 1002 |
| | | | | | QLKKGTSNLLVSKSPVWIPTGTLTQIMG TGVANIC*PVF*KD*GELGKMNYAMMS TITQKKEENPAFLKWLWEALRKYTPLSP |
| 5775 | 13826 | A | 6573 | 1 | 1632 |
| 5776 | 13827 | A | 6574 | 307 | 543 |

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| 5777 | 13828 | A | 6575 | 1 | 1149 | |
| 5778 | 13829 | A | 6576 | 119 | 409 | GDICHHLGLTPVGSHLLSCSR*QVA*VG AVTAATIGTGILLQQLAFLVCNWLLLSG SSENFPRSALICFKSEREKGTCIQVGNPSP PPTACKGHN |
| 5779 | 13830 | A | 6577 | 1 | 2433 | |
| 5780 | 13831 | B | 6578 | 97 | 1065 | MHAVHTSLLVERTILTTKERGSTLQYPL RPGAHKGLQDIVKRKAQALIRKCSSPC NTPILGVQKPNGQWRLVQDLRLINEAVI PLYVPVNPYNLLSQIPEEAEWFTVLDLK DAFFCIPLHSDSQFLAFEDPTDHTSOLT WTVLPPGFRDSPPLFGQALAQDLGHFSS PGTLVLQYVDDLLATSSEASCQATLD LLNFLANQGYKTHSRSDAPVGFTRHRL VATEKIPRGREPLSSLA VYTRGRPTRTGA RRTIVSRIRDRFRFFRYLAQREPLYQQ SLLIHLQLDSQPALS VVIGKVPNVVELTP NFGTAAQV* |
| 5781 | 13832 | A | 6579 | 1 | 2403 | |
| 5782 | 13833 | A | 658 | 455 | 1033 | GLYFGKVGEVIEQVKAFDELKALIAFFPL SSLSFLAPFVCLNLLFCFRLPLLSCLFSP GCRLHRHHCHHYLLLLLLFLSHHHHQ QQQLQAQHL SHGHGPPVPLTPHPSGLQP PGIPPLGGSAGLLALSSALSGQSHLAIKD DKKHDAEHHRGERPGKPD*DFVLILLQ CCKVVCIAKESPNLYREQTMR |
| 5783 | 13834 | A | 6580 | 1 | 2838 | |
| 5784 | 13835 | A | 6581 | 1908 | 4698 | SNDRTEDDCGKHPPMSSPPTEPWVCLII EGQEIDFLDTGTTFSVLIPCLGRLLSSRSV TIQGILGQPVTRYFSHLLSCNWETLLFSH AFLVMPESPTPLGRDILAKAGAIISMKT GNKLPICCPLEGINPEVWALEGQFGR KNAHPLQIRLKDPI SFYQRYPLRPEAH KGLQDIVKHLKAQDSVRKCSSPCNTPI GVQKLNSQWRLVQDLRLINEAVIPLYPV VRNPYTLSSQVPEEAEWFTVLDLKD |
| 5785 | 13836 | A | 6582 | 1529 | 2945 | |
| 5786 | 13837 | A | 6583 | 3 | 154 | |
| 5787 | 13838 | A | 6584 | 3 | 425 | |
| 5788 | 13839 | A | 6585 | 3 | 223 | |
| 5789 | 13840 | A | 6586 | 3 | 330 | |
| 5790 | 13841 | A | 6587 | 50 | 1740 | RSPHCCLTAHMTASAARLTMMWEEVT CPICLDPFVEPVSI ECGHSFCQECISQVGK GGGSVCACVRQRFLKNLRPNRQLANM VNNLKEISQEAREGTQGERCAVHGERLH LFCEKD GKALCWVCAQSRKHRDHAMV PLEEAAQEYQVRPKRHLEKLQVALGELR RKQELAEKLEVEIAIKRADWKKTVETQK SRIHAEFVQKNFLVEEEQRQLQELED EREQLRILGEKEAKLAQSQALQELISEL DRRCHSSALELLQEVIVLERSSESWNLKD LDITSPELRSVCHVPGLKKMLRTCAVHIT LDPDTANPWLILSEDRRQVRLGDTQQSIP GNEERFDSYPMVLGAQHFGHSGKHYWEV DVTGKEAWDLGVCRDSVRKKGHLLSS KSGFWTIWLWNKQKYEAGTYPQTPSHL QVLPCQVGIFLDYEAGMVSYFNITDVHGS LIYSFSECAFTGPLRPFFSPGINDGKNT APSNPLVPLNIGSQGSTDYWMAFSGTLP LSPHWAPASSATKPWPLFPHGTLEPLSS AEASRDPPQASFSREVTS PINIPADGVV |
| 5791 | 13842 | A | 6588 | 2 | 472 | |
| 5792 | 13843 | A | 6589 | 1 | 239 | QCCSGGTHGNPAIGDRMQKQILPWAPA QMKIRFMAPPERKYSVWIAAPILASLSTS SRMWISKQEYDESGPSIVHRKCF |
| 5793 | 13844 | C | 659 | 178 | 360 | MERPERKIXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX |

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| | | | | | | YYSFKNLI* |
| 5794 | 13845 | A | 6590 | 1 | 834 | |
| 5795 | 13846 | A | 6591 | 1 | 702 | |
| 5796 | 13847 | A | 6592 | 1 | 1623 | |
| 5797 | 13848 | A | 6593 | 1 | 1132 | MEEIEAALVIDNGSGMCKAGFAGDDAP RAVFPSIVGRPRHQGVMMVGMGQKDSYV GDEAQSKRGILTLKYPIEHGIVTNWDDM EKIWHHTFYNELRVAPEEHPVLLTEAPL NPKANREKMTQIMFETFTNPAMYVAIQ AVLSLYASGRTTGIVMDSGDGVTHTVPI YEGYALPHAILRLDLAGRDLTDYLMKIL TERGYSFTTTAEREIVRDIKEKLCYVALD FEQEMATAASSSSLEKSYELPDGQVITIG NERFRCPEALFQPSFLGMESCGIHETTFN SIMKCDVDIRKDLYANTVLSGGTTMYPG IADKMQKEITALGPSTMKIKIAPPERKY SVWIGGSILASLSTFQQMWISKQEYDES GPSIVHRKCF |
| 5798 | 13849 | B | 6594 | 635 | 646 | MCDEDETTALVCDNGSGLVKAGFAGDD APRAVFPSIVGRPRHQGVMMVGMGQKDS YVGDEAQSKRGILTLKYPIEHGIITNWDD MEKIWHHTFYNELRVAPEEHPVLLTEAP LNPKANREKMTQIMFETFTNPAMYVAIQ QAVLSLYASGRTTGIVLDSGDGVTHNVP IYEGYALPHAIMRLDLAGRDLTDYLMKI LTERGYSFVTTAEREIVRDIKEKLCYVAL DFENEMATAASSSSLEKSYELPDGAGHH HRQRALPLPGDPSFIGMEVGGHFTRPY NSIMKCDIDIQEGPFMPTTFMSGGTHDVP WESLTACRKEITRAGTPAPMEDQDSFAP AGAQNTRVWIGGSILASLSTFQQMWITK QEYDEAGPSIVQPQMLDLHLQARDFS RTTNLLNCGGG* |
| 5799 | 13850 | A | 6595 | 1 | 1284 | MGDTPRQFGGARPRSGGALRGCRSRGG GNRRGLCLSRALANGDRRLTMDDDIAA LVVDNGSGMCKAGFAGDDAPRAVFPSI VGRPRHQGVMMVGMGQKDSYVGDKIAQ SKRGILTLKYRIEHGIVTNWEDMEEIWL HTFYSELHVAPEEHPLLLTEASLNPKAN HEKVNQIMFETFTNPAMYVAIQALLSLY ASGRTTGIVMDSGDGVTHTVPIYGGYA LPHTILHLDLAGPDLTDHLMKILTERGYS FTTAKREIVHDIEENLCYVALDFEQEM AMVASNPLEKS*ELPDGQVITIGNEWF RCPEALFQPSFLGMESCGIHETTFNSIM KICDVDIRKDLYANTVLSGRTPPCTLGIA DRMQKEITALAPSTMKMKIAPPERKYS VWIGGSILASLSTFQQIWISKQEYDESGP SIVHRKCF |
| 5800 | 13851 | A | 6596 | 1 | 370 | ETESRSVAQAGVQWHNLGSLQSPSPGFK RFSCSLSPSNWDYRHPPPCPANFCIFVET RFHHVQGAGLKLLTSGDPPTLAS*IAGIT GMSHCAWPSLHIWTLFFFACPRRWGTG QVLLAAIFSQ |
| 5801 | 13852 | A | 6597 | 2408 | 2810 | IHTHTHTHTHTIFFLKR SFALVAQARVQ WRDLCSLKPPPPEFKQFSCSLPSS*DYR CPPPCPANF/SFFFVFLVETGFHHVQAG LKLLTSSDSPTLASQNAAGVTGMSHCAWP QSNKYQNNFTMIQEQQQQKE |
| 5802 | 13853 | A | 66 | 275 | 577 | GGWITRSGVQDQSGQHSVDVSL/LKKYK KLTKYGGVLL*SQLS/RRLRQDNHMPG GRSCS*PRQHHCTPAWVTVRDSISKKKK KKNNKKKKEKKGKKALLEPG |
| 5803 | 13854 | A | 660 | 365 | 800 | INVNFLEFYMTDITCFLFSYSLTLMSPYIL DVLLLSLLLFLFHIAGMHILTFINHDI*VV HSFYLRH*HAMEITVYEFICLRIRYPFKAS KIFSMYNATVLFHI*CDR*LGS*IGILERS |

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| | | | | | | VGVC SVMCIVYIRYVISSVDAP |
| 5804 | 13855 | A | 6600 | 111 | 426 | RIYKDRAGSPAHSQCQRDPLRTSPRGPH SLPWGQAAQSDAETEATHMGAPSLGP AQLPLEPGGRGSHTTSVDSRHDSVEGFR DSRQTESPWNEN*NLLDYGSL |
| 5805 | 13856 | A | 6601 | 1 | 2219 | |
| 5806 | 13857 | A | 6602 | 1 | 221 | |
| 5807 | 13858 | A | 6603 | 2 | 217 | |
| 5808 | 13859 | A | 6604 | 101 | 456 | |
| 5809 | 13860 | A | 6605 | 62 | 558 | |
| 5810 | 13861 | A | 6606 | 2 | 178 | |
| 5811 | 13862 | A | 6607 | 1 | 194 | |
| 5812 | 13863 | A | 6608 | 59 | 132 | |
| 5813 | 13864 | A | 6609 | 3 | 104 | |
| 5814 | 13865 | A | 661 | 2 | 58 | |
| 5815 | 13866 | A | 6610 | 2 | 620 | GFRPGDPRVRETGVLPKPGMLVTFAPVN VTGGVKSVMHHEALSEALPGDNVGFN VKNVSVKDVRRGNVAGDSKNDPPMEA AGFTAQVILNHPGQISAGYAPVLDCHTA HIACKFAELKEKIDRRSGKKLEDGPKFL KSGDAAIVDMVPAARPMCVESFSDYPPL GRFAVRDMRQIVAVGVKAGDKKAAG AGKVTKSAQKAQKAK |
| 5816 | 13867 | A | 6611 | 293 | 384 | |
| 5817 | 13868 | A | 6612 | 39 | 543 | QVAMGNLSGLRLAAGSCFRLCERDVSSS QRLTRSSDWKGANGFCVTKPTGKVP GAP IPALTNRPVFNTPKPTDWQKKRPLIWSRS PSKMEDEIPQSLSPLEDALNACQRTKMP SERSSLSQWICPDGGMDCIFMVIEGQK\AA\QRHDDFTQA*TLEKKARLERGKQL |
| 5818 | 13869 | A | 6613 | 1 | 194 | |
| 5819 | 13870 | A | 6614 | 71 | 1145 | NLRREPTNSRTLTVGATAGSITMKRLVC VLLVCSSAVAQLHKDPTLDHHWHLWK KTYGKQYKEKNEEAVRRLIWEKNLKFV MLHNLEHSMGMHSYDLGMNHLGDMTS EEVMSLMSSLRVPSQWQRNITYKSNPNR ILPDSVDWREKGCVTGVKYQGSCGACW AFSAVGALEAQLKLTGKLVSLSAQNLV DCSTEKYGNKGCNGGFMITAFQYIIDNK GIDSDASYPYKAMDLCQYDSKYRAAT CSKYTELPGYGR*DLKEAVANKGPVSV VVDARQPSFLPLQESGVYDPSCTQNV NHGVLVVGYGDLNGK\EYWL*NSWGP WFGEEGYIR/LWARNKGNHCGIASFPSY PEI |
| 5820 | 13871 | A | 6615 | 2 | 289 | |
| 5821 | 13872 | A | 6616 | 2 | 125 | |
| 5822 | 13873 | A | 6617 | 9 | 106 | |
| 5823 | 13874 | A | 6618 | 2 | 505 | |
| 5824 | 13875 | A | 6619 | 1 | 104 | |
| 5825 | 13876 | A | 662 | 218 | 342 | |
| 5826 | 13877 | A | 6620 | 1 | 109 | |
| 5827 | 13878 | B | 6621 | 99 | 285 | MPRKIEIKDFLLTARRKDAKSVKIKKN KDNVFKVRCRSLYTLVITDKEKAEKL KQSLPXX* |
| 5828 | 13879 | A | 6622 | 239 | 449 | NCGNQRTSLRHRPTKMPNSCQDPRKIR TLVKFKVRCRSLYTLVITDKEKAEKLK QSLPPGLAVKELK |
| 5829 | 13880 | A | 6623 | 1 | 104 | |
| 5830 | 13881 | A | 6624 | 1 | 109 | |
| 5831 | 13882 | B | 6625 | 99 | 285 | MPRKIEIKDFLLTARRKDAKSVKIKKN KDNVFKVRCRSLYTLVITDKEKAEKL |

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| | | | | | | KQSLPXX* |
| 5832 | 13883 | A | 6626 | 239 | 449 | NCGNQRTSLRHRPTKMPNSCQDPRKIR TLVKFKVRCSTRYLTYLVTITDKEKAELK QSLPPGLAVKELK |
| 5833 | 13884 | A | 6627 | 2 | 129 | YGPTHASGAMLRSCAARLRTLALCLPP VGRRLPEASRDPS |
| 5834 | 13885 | A | 6628 | 1 | 289 | |
| 5835 | 13886 | A | 6629 | 6 | 418 | RRLMRDFKRLQEDPPVGVSGAPSENNIM QWNAVIFGVTFKL VIEFP EYPNKPTVRF LSKMFHPNVYADGSICLDILQNRWSPTY DVSPILTSIQSLLEPNPNPSPANSQAAQL YQENKREYEKRVSAIVEQSWNDS |
| 5836 | 13887 | A | 663 | 527 | 665 | |
| 5837 | 13888 | A | 6630 | 3 | 330 | ARRRLMRDFKRLQEDPPVGVSGAPSEN NIMQWNAVIFGVYADGSICLDILQNRWSP TYDVSSILTSIQSLLEPNPNPSPANSQAA QLYQENKREYEKRVSAIVEQSWNDS |
| 5838 | 13889 | A | 6631 | 51 | 418 | |
| 5839 | 13890 | A | 6632 | 3 | 141 | |
| 5840 | 13891 | A | 6633 | 1 | 581 | HSDSAAAPGGGGAARDFFFFQTDRRGSC GACSTPARRRLMRDFKRLQEDPPVGVSG APSENNIMQWNAVIFGPGVTPFEDGVT F*LIVIEFSEYYPNKPPVTRVFIPKMFSP NVYA*WVGICLDILQNRWESQHMDVS FLSLTFNSVSGWDEPNP*QSSPIAQAAQL YQENKREYEKRVSAIVEQSWNDS |
| 5841 | 13892 | A | 6634 | 2 | 266 | YCGPL*SVWVARNPFGAFVEFEDPRDA AGVV*ELDGRTLCPGPSWGHPR*DDYC RRGLPPRRRPPRRRLSCSRSLYSPWT LSL |
| 5842 | 13893 | A | 6635 | 3 | 164 | |
| 5843 | 13894 | A | 6636 | 1 | 947 | IFLVFFITEMHRDSCPLDCKVYVGNLGN NGNKTELEAFGYYGPLRSVWVARNP GFAFVEFEDPRDAA*V*YLCPLRTLGC RVRVELSNGEKSRNRGPPPSWGRRPRD DYRFPSMLFSLSLNLNQGSSHLDRPHI PGQSAQLFIYQMSSQQLQQPSANKKAG KIHNTPFANQLNPTATSGQNLFRQILGP SVRAGLTFTISSLLKPKTNLQEGEASLAA GAGPFLEIGEERDRCLGREITSRPDPSLGL VVDLGQMKGNRRQFAREVVRKLLHLT GVCTENFKFCLRLHKLGAFLRCFSCSNL FVS |
| 5844 | 13895 | A | 6637 | 1 | 282 | |
| 5845 | 13896 | A | 6638 | 116 | 561 | PLDLEMHRDSCPLDCKVYVGNLGNNG NKTLELAFGYYGPLRSVWVARNP LAFVEFEDPPRMQLDAVPRS*DGKNTNV ACPCKEWELVRMGEKRSRNRGPPPSL/ WGRRPDGFIRREGVPPTLFGSPRKGG RFLFAARSRLS |
| 5846 | 13897 | A | 6639 | 126 | 376 | VLLARLQANGANTVELSAEWTFPSGYV GSVLPQGHREPNA/CLSFSKFRVLGSAP FLINRRTASNCVNRYCRLAATWRAVLPL |
| 5847 | 13898 | A | 664 | 1233 | 1706 | CLVFWLLYYPLQLPFHLLPHSLGSGQQ SSEESAATPSLAEGRREAAFRCPAGLA RQAWRPHARLPGAAPLAAPSLAPLPTG RSGRWLPMCAASC*SPSPAMSVYPQRR LGQGAEDSEGGPVSRGCRAPGPQRPLA APGEQTAARTQAICLIW |
| 5848 | 13899 | A | 6640 | 464 | 781 | AFAFTKDRQLGSSKKRRMSSRFASSAAK CRAVRPLLRSRRFPVPMPPGPVVSSTK LGSRLGRHQASCRG*SQRAR*SGLTGPT HMEPNKVRSTGLKFLPAQQS |
| 5849 | 13900 | A | 6641 | 201 | 318 | EINLTNFI CFSSRSDVS*RESPFSRELHRIS SISLEPG |

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| 5850 | 13901 | A | 6642 | 1 | 1714 | |
| 5851 | 13902 | A | 6643 | 1 | 789 | |
| 5852 | 13903 | A | 6644 | 1 | 293 | SPEMESHPIQAGVQWHNSSLQPEIPGL KQSSHLSPSSWDHR*EPLPWPKNIFKM LIL*IGFSHVIGNNGTYLYQSINNVEGPLK RSQKDRSCGN |
| 5853 | 13904 | A | 6645 | 1 | 252 | |
| 5854 | 13905 | A | 6646 | 1 | 1974 | |
| 5855 | 13906 | A | 6647 | 3 | 320 | |
| 5856 | 13907 | C | 6648 | 238 | 324 | MADLPIFLVEFSCFIIYFNFSFMFSQKK* |
| 5857 | 13908 | A | 6649 | 1 | 1088 | |
| 5858 | 13909 | A | 665 | 598 | 1159 | CRQTGVKIYDVWFFWLLYYPGLQLPFHL LPHSLGSGQSSSEESAATPSLAEGRREAA FRCGPAGLARQAWRPHARLPGPAAPLA APSLAPLPTGRSGRWLPMCAASC*SPSP AMSVYPQRRLGQGGGAEDSEGGSVSRGC RAPGPQRPLAAPGEQTAARTQASVYLL PHSPPLLSALHHHLLPPS |
| 5859 | 13910 | A | 6650 | 1 | 368 | |
| 5860 | 13911 | A | 6651 | 3 | 243 | |
| 5861 | 13912 | A | 6652 | 24 | 288 | |
| 5862 | 13913 | A | 6653 | 2 | 272 | |
| 5863 | 13914 | A | 6654 | 965 | 2737 | AASPGVLVCPQARTYIQSLPPALDVQLTP LPTTGFPAAIDLLGRMLVLDSDQRVSA EALAHAYFSQYHDPEDPEAEPPGCGR HKLTLSLHLELTYQEVLSWDEAAGR PPPALPRLRPSPGSGPPAAAAASGFRRW AAPGPAMSSPPPARSGFYRQEVTKTAW VRAGACAGCPAFPLSGPPRSSAVDGR AKVAIKKLYRPFQSELFANPARVLCILN PMWPPQVIGHAEAGSVR*QRSGPSHSYL VMFPMGTDLGKLMKHEKLGALRGCAE ACHHAWEGGAQWPPFLCPHRS LGVP*N PPPQFFPQILDFGLARQADSEMTGYVVT RWSHPVPLTELTRASISVDIWSVGCIMA EMITGKTLCSGPGGSGGPDWPPSCVP DLGADLDQLKEIMKVADLGLGVGPSFPL PTQAKNYMKGLEWSVGPVWPDPAPS PAAVNLLKMLVLD AEQRTVAGEALAH PYFESLHDTEDPQVQKATTDGPSLPSDP HASPGLHGLGDVIAISSGATLTCGMAAV HTGPKVWAHRWPEDWGVAFALQTPRPP RLSPQVFLRPGRVGLGAALDPDPGWGA GRDL |
| 5864 | 13915 | A | 6655 | 3 | 229 | |
| 5865 | 13916 | A | 6656 | 27 | 142 | |
| 5866 | 13917 | A | 6657 | 3 | 308 | |
| 5867 | 13918 | A | 6658 | 192 | 310 | |
| 5868 | 13919 | A | 6659 | 88 | 1506 | ACGRFGFPEGPEGGRGRHVRAARGPVG PRAGEGPCAAWVGVP GSAPGTSLREG PGAGAPQRPAGGRASGRAARSRPEAR EGAPSPVVGAPPAGSAGWAAPGPAMSS PPPARSGFYRQEVTKTAW EVRAVYRDL QPVGSGAYGAVCSAVDGR TGAKVAIKK LYRPFQSELF AKRAYRELRLKHM VIGLLDVFTPDFTLDDFTDFYLVMPFMG TDLGKLMKHEKLGEDRIQFLVYQMLKG LRYIHAA GIIHRDLKPGNLAVNEDCELKI LDFGLARQADSEMTGYVVTRWYRAPEV ILNWMRYTQTVDIWSVGCIMAEMITGKT LFKGSDDLQKEIMKVTGTPPAEFVQR LQSDAEAKNNMKGLPELEKKDFASILTNA SPLAVNLLKMLVLD AEQRTVAGEALA HPYFESLHDTEDPQVQKYDDSFDDVDR TLDEWKRVITYKEVLSFKPPRQLGARVS KETPL |

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| 5869 | 13920 | A | 666 | 358 | 644 | RRSLALSPSPECSDVISAHCKLCLPGFTPF SCLSLSSWDYRCPPLANFFVFLVET GFHRVSQDGLDLLTS*SARLSLPKCWDY RCEPPRPA |
| 5870 | 13921 | A | 6660 | 71 | 921 | |
| 5871 | 13922 | A | 6661 | 2 | 310 | |
| 5872 | 13923 | A | 6662 | 5517 | 5831 | |
| 5873 | 13924 | A | 6663 | 1 | 625 | CKFIRVMAHTRLRLPLRRKKAHLMEIQ VNEGTVAEKLDWARERLEQQVPVNQVF GQDEMIDVIGVTGKGKGYKGVTSRWHTK KLPRKTHRGLRKVACKDGLIKNNAST DYDLSDKSINPLGGFVHYGEVTNDFVML KGCVVGTKKRVLTLRKSLLVQTKRRAL EKIDLKFDITTSKFGHGRFQTMEEKKAF MGPLKKDRIAKEEGA |
| 5874 | 13925 | A | 6664 | 1 | 1261 | MSHRKFSAPRHGSLGFLPRKRSSRHGK VKSFPKDDPSKPVHLTAFLGYKAGMTHI VREVDPRGSKVNKKEVVEAVTIVETPPM VVVGIVGYVETPRGLRTFKTVFAEHISDE CKRRFYKNWHKSKKKAFTKYCKKWQD EDGKKQLEKDFSSMKKYCQVIRVIAHTQ MRLPLRQNKAAHLM*IQVNGGHCGPRS WDWPPREGLKQGTVDPSVLGRNKMID VIGVTQGPKGKGGHPVVWHTQESCPR KD/HHPRACRKGHVLGAWHPARVAF SVARAGQKGVYHHRTEITKKD/IYKIGPG LSPLFRTAKVIKGTIASTDYDLF*QEASTP PGGFVHYGEVTNDFVMLKGCVVGTCK RVLTLRKSLLVQTKRRALEKIDLKFDIT SKFGHGRFQTMEEKKAFMGPLKKDRIA KEEGA |
| 5875 | 13926 | A | 6665 | 1 | 168 | |
| 5876 | 13927 | A | 6666 | 3 | 203 | |
| 5877 | 13928 | A | 6667 | 3 | 523 | LQFFRRSEVKMKNHLLFWGVLAVFIKA VHVKAQEDERIVLVDNKCKCARITSRIJR SSEDPNEDIVERNIRNIVPLNNRENISDPT SPLRTRFVYHLSDLCKKCDPTEVELAD NQIVTATQSNICGWMTPVQSTCYTLSTG NKCYTAVVPLAVYGGETKMVETALTPDA CYPD |
| 5878 | 13929 | A | 6668 | 3 | 276 | |
| 5879 | 13930 | A | 6669 | 2 | 152 | |
| 5880 | 13931 | A | 667 | 55 | 288 | PFKKGGFFNGNLPPTFGKLGNKKFPLNL FPGGPPLPHGGLKKGPGAPQVPPLFLKK PQTSP*GLREGPPPLKKFYLF |
| 5881 | 13932 | A | 6670 | 1 | 936 | |
| 5882 | 13933 | A | 6671 | 1 | 1023 | |
| 5883 | 13934 | A | 6672 | 106 | 125 | KYLEQCLKHGKSS*HSILOANFFASEND RAKMK*KPCFYKCF*AITFLREDWDYRR EPLRLAYPVYFLTCKIRIMYTHLKDYTG H |
| 5884 | 13935 | A | 6673 | 3 | 155 | |
| 5885 | 13936 | A | 6674 | 3 | 266 | |
| 5886 | 13937 | A | 6675 | 5 | 160 | RDLGSLQPPPGFK*FSCLRLPSPQVQRC CVPSPWLLEQMITAWGASIHRN |
| 5887 | 13938 | A | 6676 | 1586 | 2220 | |
| 5888 | 13939 | A | 6677 | 3 | 441 | |
| 5889 | 13940 | A | 6678 | 1 | 91 | |
| 5890 | 13941 | A | 6679 | 2 | 226 | |
| 5891 | 13942 | A | 668 | 2 | 385 | ARGEPTMELSHADTTNVKAAWGWVGA HAGE*GADVLVRMVLCLPTIWTYFPYFD LSHGCAQVNGHGKKVADALTNVAVHV DDMPNSLIGLSELHAH*LLVDPVNFLL NHCLLGTLADHLLDEFTPAV |
| 5892 | 13943 | A | 6680 | 3 | 187 | |
| 5893 | 13944 | A | 6681 | 2 | 209 | |

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|------|-------|---|------|------|------|--|
| 5894 | 13945 | A | 6682 | 2 | 702 | FVSVPSVLLGLQFWRSERD/TARLQSAR WRVERGRLKELLSRQRP RRREEVVGR EVCRTMEVRASLQKIVSNGDEQLEKA MEEILRDFEKRPSLLVDCQSSSEISDHSF GDIPASQTNKPSLQLLDPSNTEISTPRPSS PGGLPEEDSVLFNKLTYLGC MKVSSPRN EVEALRAMATMKSSSQYPPFTLYVPN VPEGSVRHLSLLGGGEDVIASSGVELTV NSHCRHAE |
| 5895 | 13946 | A | 6683 | 3 | 497 | |
| 5896 | 13947 | A | 6684 | 1 | 224 | |
| 5897 | 13948 | A | 6685 | 1 | 789 | |
| 5898 | 13949 | A | 6686 | 1 | 7500 | |
| 5899 | 13950 | A | 6687 | 1 | 8175 | |
| 5900 | 13951 | A | 6688 | 3 | 598 | QCGGIRATTMAMSFEPWPQYRFPFFFT LQPNVDTRQQLAAWCSLVLSFCRLHK QSSMTVMEAQESPLFNNVKLQRELPVE SIQIVLEELRKKGNLEWLDKSKSSFLIMW RRPEEWGKLIYQWVSRSGQNNSVFTLYE LTNGEDTEDEEFHGLAEKPLLRALQ/CP YSREHKAEIHHCSGDGRGVQVLLGRDLS PFTS |
| 5901 | 13952 | A | 6689 | 2 | 356 | |
| 5902 | 13953 | A | 669 | 787 | 896 | LLYNIYCGEKKREERKD*PGQHGETPSL QKIQLAG |
| 5903 | 13954 | A | 6690 | 2 | 123 | |
| 5904 | 13955 | A | 6691 | 161 | 464 | |
| 5905 | 13956 | A | 6692 | 3 | 86 | |
| 5906 | 13957 | A | 6693 | 3 | 85 | |
| 5907 | 13958 | A | 6694 | 2 | 201 | |
| 5908 | 13959 | A | 6695 | 1 | 119 | |
| 5909 | 13960 | A | 6696 | 1 | 3414 | MEPNDSTSTAVEEPDSLEVLVKTLDST RTFIVGAQMNVEKFEHIRASVSIPSEKQ RLIYQGRVLQDDKKLQEYNVGGKVIHL VERAPPQTHLPSGASSGTGSASATHGGG SPPGTRGPGASVHNRNANSYVMVGTFN LPSDGSADVHINMEQAPIQSEPRVRLV MAQHMIRDIQTLLSRMETLPYLQCRGGP QPQHSQPPQPPAVTPEPVALSSQTSEPV ESEAPPREPMEAEVEERAPAQNPETPG PA |
| 5910 | 13961 | A | 6697 | 1 | 441 | |
| 5911 | 13962 | A | 6698 | 2 | 180 | |
| 5912 | 13963 | A | 6699 | 1 | 143 | |
| 5913 | 13964 | A | 67 | 1016 | 1461 | VSHSHLSSQFNHSLNRRPTRIPLSPQPK* GPAYSRPPVWTPAEPEALRWGRHRGP*K ARGSRPSSAHSGWRPRGEAPHRTGTAQP PTAVPCRRHLGEDSTPGPPGALGGVGF PSASP/PVPTPT*TQTGRRPETQLRQQTPR GAPPA |
| 5914 | 13965 | A | 670 | 539 | 786 | SIGRLRRVGHLRSGVRDQPGQHGGTSL LKIQKFAGHGGAFLYSQVLGRLRQENRL NSRGGGCSSESGSQHYTPAWVTE*DSI |
| 5915 | 13966 | A | 6700 | 2 | 1069 | SLVERLKMAASQAVEEMRSRVVLGEFG VRNVHTTDFPGNYSYDDAWDQDRFEK NFRVDVVHMDENSLEFDMVGIDAAIAN AFRRILLA EVPTMAVEKVLVYNNTSIVQ DEILAHRLGLPIHADPRLFYRNQGDDEE GTEIDTLQFRLQVRCTRNPAAKDDSSDP NELYVNHKVYTRHMTWIPLGNQADLFP EGTIRPVHDDILIAQLRPGQEIDLLMHCV KGIGKDHAKFSPVATASYRLLPDITLLEP VEGEAAEELSRCSFGVIEVQEVQGGKV AQSCPTPRLDTFVSREIFRNEKLKVVRL ARVRDHYIFSVESTGVLPDVLVSEAIK VLMGKCRFLDELDAVQMD |

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| 5916 | 13967 | A | 6701 | 197 | 310 | WLCYIIYK*YDNWWHSMCFSKPLYPEIV SLNYILLKG |
| 5917 | 13968 | A | 6702 | 3 | 67 | |
| 5918 | 13969 | A | 6703 | 3 | 517 | |
| 5919 | 13970 | A | 6704 | 150 | 840 | GSLSPDMANKGPSYGMSREVQSKIEKK YDEELEERLVEWIIVQCGPDVGRPDGR LGFPVWLKNGVILDRL*TTFTPDASKPV KVPEKPPPCSSSKTEPLPHFLKAAEDY GVRPKSNIFQDL*TSLKGVDMGSSSRGP LMAFGQLWQVTKNDGHYRGDPNWFY ERKPQQHKREFHRRALQKKGKACPLAL PDGAANRRGPPQARH*QGYGTTLGQIHK LEAERAKP |
| 5920 | 13971 | A | 6705 | 3 | 842 | |
| 5921 | 13972 | A | 6706 | 1 | 570 | |
| 5922 | 13973 | A | 6707 | 1 | 1437 | |
| 5923 | 13974 | A | 6708 | 3 | 286 | |
| 5924 | 13975 | A | 6709 | 172 | 364 | FYLYLVMLCFIEPVKLLIVGAYIL*LLKT IHEFHNCQCFVDTKSLKGRHFKEYVFFTF NMFHR |
| 5925 | 13976 | A | 671 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGT AQLSELHCDKLHVDPENFKLLGNVLTV LAIHFGKEFTPEVQASWQKMTGVASA LSSRYH |
| 5926 | 13977 | A | 6710 | 1 | 683 | |
| 5927 | 13978 | A | 6711 | 18 | 292 | |
| 5928 | 13979 | A | 6712 | 1 | 687 | |
| 5929 | 13980 | A | 6713 | 1 | 119 | |
| 5930 | 13981 | A | 6714 | 1 | 339 | |
| 5931 | 13982 | A | 6715 | 3 | 470 | |
| 5932 | 13983 | A | 6716 | 2 | 2942 | TGAPAWPSRRLRDLPAAGMWRLRRAA VACEVCQSLVKHSSGIGKSLPLQKLHLV SRSIYHSHHPTLKLQRPQLRTSFQFSSL TNLPLRKLKFSPIKYGYQPRRNFWPAL ATRLLKRLYLILGSAVGGGYTAKKTFDQ WKDMIPDLSEYK WIVPDIVWEIDYIDFE KIRKALPNSEDLVKLAPDFDKIVESLSLL KDFFTSGSPEETAFRATDRGSESDKHFRK VSDKEKIDQLQEELLHTQLKYQRILERLE |
| 5933 | 13984 | A | 6717 | 38 | 359 | |
| 5934 | 13985 | A | 6718 | 122 | 282 | |
| 5935 | 13986 | A | 6719 | 2 | 1010 | |
| 5936 | 13987 | C | 672 | 336 | 728 | MGLPKTGHHQHFQPELESSSRIPHAGLS QVQVHFRLGQRCLRSSQVLLWHLPRK VSTFLPCALTLGVAHGWQRQRTGCQSC QRTSGSMGRQPGAFPGFLLQHLSTFLP HRLCDSSLVLLCEMTHGRLD* |
| 5937 | 13988 | A | 6720 | 326 | 513 | |
| 5938 | 13989 | A | 6721 | 1 | 1076 | |
| 5939 | 13990 | C | 6722 | 11 | 79 | MLPILRHTFLRVTLRGKKACLL* |
| 5940 | 13991 | A | 6723 | 3 | 198 | |
| 5941 | 13992 | A | 6724 | 1 | 432 | |
| 5942 | 13993 | A | 6725 | 123 | 336 | |
| 5943 | 13994 | A | 6726 | 1 | 227 | |
| 5944 | 13995 | A | 6727 | 1 | 131 | MPVLLTSDMHKSSVKAGFAKVDQQQA PKSVQLLTVKTRDSTSNRGNSSGPRSQAT DRICRTPYHFEDC*SGSTASPVSSASDS EDKRLNK |
| 5945 | 13996 | A | 6728 | 3 | 364 | |
| 5946 | 13997 | A | 6729 | 2 | 197 | |
| 5947 | 13998 | A | 673 | 1 | 1254 | |
| 5948 | 13999 | A | 6730 | 2 | 421 | |
| 5949 | 14000 | A | 6731 | 33 | 294 | |

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|------|-------|---|------|-----|------|---|
| 5950 | 14001 | A | 6732 | 2 | 670 | |
| 5951 | 14002 | A | 6733 | 1 | 171 | |
| 5952 | 14003 | A | 6734 | 1 | 789 | |
| 5953 | 14004 | A | 6735 | 3 | 363 | |
| 5954 | 14005 | A | 6736 | 2 | 379 | |
| 5955 | 14006 | A | 6737 | 116 | 373 | |
| 5956 | 14007 | A | 6738 | 1 | 164 | |
| 5957 | 14008 | A | 6739 | 3 | 122 | |
| 5958 | 14009 | A | 674 | 1 | 921 | |
| 5959 | 14010 | A | 6740 | 83 | 2455 | |
| 5960 | 14011 | A | 6741 | 83 | 2450 | IRIAALDDFRTSLTMSSTRSQNPGLKQI GLDQIWDDLRAIGIQVYTRQSMASRY MELYTHVYNYCTSVHQFVGLLEYKRLK EFLKNYLTNLLKDGEDLMDESVLKFYTQ QWEDYRFSSKVLNGICAYLNRHWVRE CDEGRKGIYEIYSLALVTWRDCLFRPLN KQVTNAVLKLIKERNGETINRLISGVV QSYVELGLNEDDAFAKGPTLTVYKESFE SQFLADTERFYTRETEFLQONPVTEYM KKAEARLLEEQRVQVYLHESTQDELA RKCEQVLEKHLEIFHTEFQNLDDADKNE DLGRMYNLVSRIQDGLGELKKLLETHIH NQGLAAIEKCGEALNDPKMYVQTVLD VHKKNALVMSAFNNDAGFVAALDKA CGRFINNAVTKMAQSSSKSPELLARYC DSLLKKSSKNPEEALEDTLNQVMVVK YIEDKDVQKFYAKMLAKRLVHQNSAS DDAEASMISKLKQACGFYTSKLQRMF QDIGVSKDLNEQFKKHLTNSEPLDLDFSI QVLSGSGWPFQSQCTFALPSELSYQRF TAFYASRHSGRKLTLWLYQLSKGELVTN CFKNRYTLQASTFQMAILQYNTEDAYT VQQLTDSTQIKMDILAQVLQILLKSKLLV LEDENANVDEVELKPDTLIKLYLGYNK KLRVNINVPMTQEQKQEQETTHKNIEED RKLLIQAAIVRIMKMRKVLKHQQLLGEV LTQLASSRFKPRVPVIKKCIDILIEKEYLAE RVADGEKDTYSYLAALTSGKGLDLCDPQ QIVHVGKE |
| 5961 | 14012 | A | 6742 | 3 | 318 | |
| 5962 | 14013 | A | 6743 | 17 | 174 | |
| 5963 | 14014 | A | 6744 | 3 | 711 | LSSCLCGSGKAFGMPTMRLLSFVVLALE AVTQAEEGARLLVSKSLNRYAVEGRD LTQYNIYNVGSSAALDVELSDSFPPED FGIVSGMLNVKWDRIAPASNVSHTVVLR PLKAGYFNFTSATITYLAQEDGPVVIGS TSAPGQGGMLVQREFDRRFSPHFLDW AAFGGHDPPFSGIPLLLWYSSKRKYDT PKTKKNLIWGFHKPSSPKKSKAPLPKKP QVLSQTPKGY |
| 5964 | 14015 | A | 6745 | 74 | 471 | |
| 5965 | 14016 | A | 6746 | 1 | 1371 | MAENDVDNELLDYEDDEVETAAGGDG AEAPAKKDVKGSYVSIHSSGFRDFLKP ELLRAIVDCGFEHPSEVQHECIPQAILGM DVLCAKSGMGKTAVFVLATLQQLPEP TGQVSVLVMCHTRELAFQISKEYERFSK YMPNVKVAVFFGGLSIKKDEEVLKKNC PHIVVGTGPRILALARNKSLNLKHIKHFIL DECCKMLEQLDMRRDVQEIFRMTPEHEK QVMMFSATLSKEIRPVCRFMQDPMEIF VDDETKLTLLHGLQYYVKLKDNEKNRK LFDLLDVLEFNQVVIFVKSQVQRCIALAQL LVEQNFFAIAIHRGMPQEERLSRYQQFK DFQRRILVATNLFGRGMDIERVNI AFNY DMPAEDSDTYLHRVARA'GRFGTKGLAI TFVSDENDAKILNDVQDRFEVNISELPD EIGHLLPTLEQDVEDSPILGMLTVCFSQ |

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|------|-------|---|------|-----|----------|
| | | | | | GGGTPGWG |
| 5966 | 14017 | A | 6747 | 2 | 139 |
| 5967 | 14018 | A | 6748 | 3 | 270 |
| 5968 | 14019 | A | 6749 | 21 | 301 |
| 5969 | 14020 | A | 675 | 659 | 1601 |
| 5970 | 14021 | A | 6750 | 4 | 366 |
| 5971 | 14022 | A | 6751 | 3 | 263 |
| 5972 | 14023 | C | 6752 | 54 | 161 |
| 5973 | 14024 | A | 6753 | 161 | 1122 |
| 5974 | 14025 | A | 6754 | 1 | 891 |
| 5975 | 14026 | A | 6755 | 2 | 104 |
| 5976 | 14027 | A | 6756 | 957 | 1285 |
| 5977 | 14028 | A | 6757 | 1 | 716 |
| 5978 | 14029 | A | 6758 | 2 | 835 |
| 5979 | 14030 | A | 6759 | 759 | 1022 |
| 5980 | 14031 | A | 676 | 1 | 1335 |
| 5981 | 14032 | A | 6760 | 2 | 689 |
| 5982 | 14033 | A | 6761 | 2 | 1011 |
| 5983 | 14034 | A | 6762 | 2 | 151 |

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|------|-------|---|------|------|------|--|
| 5984 | 14035 | A | 6763 | 3 | 740 | RPIGEFRSNADYQYQLLRNCVNDLLKHIQL GLTFMNEQGEYPPGTSTWQFNFKFNLTE DMYAQDSIELLTSTSGIQFKKHEEEGIETQ YFAELMTSGVVLCEGVKWLSEHSGYD FGYLIKILTNSNLPEEELDFEILRLFFPVI YDVKYLMKISCKNLKGGIAQEVAEQLAE LERIGP\QHQAGSDSLTGMMAFFKMREM FFEDHIDDAKYCGHLYGLGSGSSYVQN GHRGMHMEEGSQQSGSPWTWK |
| 5985 | 14036 | A | 6764 | 296 | 522 | IWVFHNLKGLFEIFCCILKYFLEELLILF* KTKL*KHASFLKNNPSIQDMESSTTVHRS GLGGSLCADVLSLQWL |
| 5986 | 14037 | A | 6765 | 3 | 333 | |
| 5987 | 14038 | A | 6766 | 1326 | 1980 | TSEASRQSERVDSAALSALSLLSRSSKCR PWGTARVARAGGCLTPLLRRFLETRPF TGPWDPGLGVTCWCCPPKRRLKSTPRPK FSVCVLGDQHCDEAKAVDATFEVCLG DQVLSNANGFLSLSAKKYDAFLASESLI KQIPRILGPGLNKAGKFPSSLREEGQAIC YSSTNLT*SSLPSSQVLCIAVAVGHVKM TDEELVYNHIAVNFLVSLK |
| 5988 | 14039 | A | 6767 | 11 | 713 | EAMSSKVSRTLYEAVREVLHGTQRKR RKFLAETVELQISLKNYDPQKDKRFSGT VRLKSHSPALSFSVCVLGD\ROH\CDVEA KA\VDIP\HMD\NEALEKTSTKNKKLVKK AGQRKYDAVFGPQSLLIKQIPRIPRAPGL NKAGK\FP\SLTHNENMVAKVDEVK\IS PIKF\QMKKVLCIAVAVGHVKMTDEEL VFNIHLA\VNFL\VSLK\KNWQKCSGAL YYQEAPMGQSPKRLY |
| 5989 | 14040 | A | 6768 | 2 | 277 | |
| 5990 | 14041 | A | 6769 | 1 | 336 | |
| 5991 | 14042 | A | 677 | 1 | 811 | |
| 5992 | 14043 | A | 6770 | 132 | 347 | |
| 5993 | 14044 | A | 6771 | 3 | 109 | |
| 5994 | 14045 | C | 6772 | 5 | 160 | MGFEGGPKILNWKFKKVXQXSCLXKG QXESIFLNTXKVIRAGDTXKSVLG* |
| 5995 | 14046 | A | 6773 | 52 | 310 | YIIRTQTQISHHPLHYILGSAKKKLCFGKS YFIRGSSFRKGQGEERGLKYKKKTGEG V**KRTKKQTKTKTKIKYKLSRCCGNV |
| 5996 | 14047 | A | 6774 | 149 | 333 | |
| 5997 | 14048 | A | 6775 | 1 | 1616 | LFFFFFFLESTRFY*FFFFFFFTIQTFKGG PLSPFFLLFFIKPLPQFFFIL |
| 5998 | 14049 | A | 6776 | 2 | 138 | ASGHREVQDSYEAYGQDDWNGTITSLK/ APPARPVKGAYREHPYGRY |
| 5999 | 14050 | A | 6777 | 1 | 1212 | |
| 6000 | 14051 | A | 6778 | 3 | 150 | |
| 6001 | 14052 | A | 6779 | 2 | 1622 | ASVATAPALPPPPTAARASVAAASLSRSL DRTSSQMQRDDPAARMSRSGRSGSM DPSGAHPSVRQTPSRQPPLPHRSRGGGG GSRGGARASPATQPPPLPPSATGPDATV GGPAPTLLPPSATASVKMEPENKYLPEL MAEKDSLDPSTHAMQLLTAEIEKIQKG DSKKDDEENYLDLFSHKNMKLKERVLP VKQYPKFNFVGKILGPQGNITIKRLQET GAKISVLGKGSMRDKAKEELRKGGDP KYAHLNMDLHVFIIEVFGPPCEAYALMA HAMEEVKKFLVPDMMDDICQEQFELS YLVNGVPEPSRGRGVVVRGGAAPPPPV PTGRGVGPPRGALVRGTPVRGAITRGAT VTRGVPPPPTVRGAFC*RARTAGVQRIP LPPPPAPETEEYGYEDTYAEQSYEGYE GYYSQSQGDSEYDYGHGEVQ\DSYEA LWPRTNWNTRPSLKAPLARPVKGAAY REPPYGRLLKTKHEGENISYEQSLLLDFL YLPGIPVALPTTDQGNWSKCFFFRGSFSP SPTLIPFL |

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|------|-------|---|------|------|------|--|
| 6002 | 14053 | A | 678 | 269 | 561 | LSFVGSLSRLFTAGFAECPRFRFRPAPNP RTPSTRNSAPDSQKGATWATAVQAAPR WT*ETGSNPWPTLAAPCSRSPRGPPASFS GGPSASCKLCLK |
| 6003 | 14054 | A | 6780 | 1 | 76 | |
| 6004 | 14055 | A | 6781 | 1 | 287 | CFL*DRVLLCHPGWSAVAHNHSSLP*T PGIKQFSCRL/SSS*DYRCTSPYLAIFFFF *FFCRKQSLATVPRTISNSWPQAILLSWS KHVEITGF |
| 6005 | 14056 | A | 6782 | 3 | 64 | |
| 6006 | 14057 | A | 6783 | 2 | 69 | |
| 6007 | 14058 | A | 6784 | 1576 | 3458 | |
| 6008 | 14059 | A | 6786 | 1 | 960 | |
| 6009 | 14060 | A | 6787 | 507 | 755 | NKRGYKQMEEHSMMLGRKNQYRKNGH TAQGNL*IQCHPHQATNDFLHRIGKNDP QVHMEPKKSPHRQVNPKEQSWRHHA T |
| 6010 | 14061 | A | 6788 | 274 | 882 | PDQVDRGGAHWQTDADDPWLADHLQH CQRCGEILRHYSGGIRGNVSAVKCAEHH VPAFARLRNPQCGDFQRLDYRLFDSPGV KRREL*TA YRFCHVAP*LMDLRSGWAA GAVYRYQSH*FTADRLRSVDMDEAGN HHSQQTSDQKIKQRTFSLISGS*TRTH GHREGNITHRGLSRPNTARILCASKAHL GLPLRSSLP |
| 6011 | 14062 | A | 6789 | 114 | 329 | |
| 6012 | 14063 | A | 679 | 415 | 1094 | SKSRMSAEVIHQVEEALDTDEKEMLLFL CRDVVAIDVVPNVRLDILTERGKLSV GDLAELLYRVRFDLLKRILKMDRKAVE THLLRNPHLVSDYRVLMAEIGEDLDKSD VSSLIFLMKDYMGGRGKISKEKSFLDLV ELEKLNLVAPDQLDLEKCLKNIHRIDLK TKIQKYKQSVQAGTSYRNVLQAAIQKS LKDPSNNFRMITPYAHCPDLKILGNCSM |
| 6013 | 14064 | C | 6790 | 1 | 1983 | MGDGTSDFDPIDGIRQSNYSCGGCPRI PYVWRVTGRAHGTQTIIVVMAKVYYG NVMRREKDSGGAWGNPWAGILLPPPST RNCTVHSSFSNENIFPQHTSSCVVHNQ YIGADFPWSNFSFVVEYNYVEDSCWTK HCKELNIPYMAFKVILPDTVLERSTLLDR FGGFLEIQIPYVFFASEGLLNTPDILQLL ESKDMDEAGNHHSEQTVTRTENQTLHV LTHR WELNNENTWTQDGEHHTPGPVVG WRELIIAPGVEATALIIRQIADHSLMTSKR DPHEWLDKSWLKVSPSEENRNQISTLSS QSSASDLDSVIEHNEYQYGLGETVQ EDKTTILNDNSSIMELKEISSFLPPVTSYN QTSYWKDSSCKSNIGQNTPFLINIESRRP AYNSFLNHSDSESDVFSGLTQMNCETI KSPTDTQKRVSVPFRINSQKRRTHEAK GFINKDVSDPISLEGTSPLHWNFKKNI WEQENHPFNLQYGAQQTACNKLYSQKG NLFTDQKCLSDSEGLTCESSKDETFW RELPSVPSLDLFRASDSNANQKEFNSLYF YQRAGKSLGQKRHHESFNSGDKESLTE EKTEAQEKMTTEDRGRGWGYATTNRR MPRIAGNHQEPGERRGTPPPSEAFEGSNP ANTLILDFPPPEL* |
| 6014 | 14065 | A | 6791 | 190 | 486 | FLLHFFLHD*YSSNKLQKVNKSIPPTGPS LCPCVLIVQLPLMSENMRCLVFCSCVSL LRMMVSSFIHVPLNFFNAFLLLNFRFCP LLSCHMIKKSSS |
| 6015 | 14066 | A | 6792 | 1 | 597 | |

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|------|-------|---|------|-----|------|---|
| 6016 | 14067 | A | 6793 | 1 | 721 | MTSYNEQNKKPVTDPNEMAIHEDSNQE FKIAVVNETQRSRSPSTEHLMTPLPT REQQPPLTVIFHYLPKSYKTAPPLSFPDS LFGLSQPAPRDMDEAGNHHSQQTKQEQ KTKHCFSLTSGS*TMRTGHREGTVIH RGLLGQFSQQLINKSEFSNTVCREKSGR VLQVNME SPL*MIQDALQDQTPKGPIT VFL*LFYLDHLLRSSHKVASYLSTESRSR GSITVLFIRCSEP |
| 6017 | 14068 | A | 6794 | 417 | 696 | DRNRKANTACFQHSQVGVEQ*EHMDTG KV*SI*YGNYEHTSTCERMEIQKATTEHL NL*S*SGSFLRFTWKMLQFSKISR SFYQV LKHQQKIM |
| 6018 | 14069 | A | 6795 | 325 | 1489 | RSPTLLMHVHYIKVISWRELLLIWLRAA NASINPGVEQSPSGDPKTVTGFPFLRLEA ADWVEEASVPKGVHIALSSQEQRAGDP RDLEAPSNLVISERTHRSFRVSWTPPSDS VDRYKVEYYPVSGGKRQEVVRTPGVDP LRLPAIPQAAWLLAHLPAAPSAPTELPT KHTEAQSORCWSLLCSVTEVAAPSQV VKEAPSPFHTGTENGYQGEESLFNKAYY GGGTNFRKESQKLQQSACKRDAELAN GALGHIENNDYTLKKVMKPLITSNTVTD EIERANVFKMNGKWYLFDSRSGSKMTI DENKIPRNPTYKGREGPLQGELOTTAQG NKRGYKQMEEHSMMLDRKNQYRENGL TAQAPQPPPSGI*GYTAPCFPWENLI |
| 6019 | 14070 | A | 6796 | 274 | 716 | QACYIYTEYYAAIKNDEF/TVLCRDM EAGNHHSQQTVTRTKNQTPHVLTHRWE LNNENTWTQEGEHHTPGPVMLDSAPPTL GHQTPGSSAFGLWDLHQRLRLPRPQTKG STVGFPGSEAFKLGGLGHYWLSFFPSLQT AYRGTLFPNH |
| 6020 | 14071 | A | 6797 | 1 | 870 | |
| 6021 | 14072 | B | 6798 | 328 | 2283 | MKLEAIIJSKLTQEQKNQTLHVLTHRWE LNNENTWTQGGGYHTLGPVDGFKKEE AAIGAILQPLLVIQTVLGVDLQQTADLQ QRGLLEKLTNRKKIAHTVRDHIQREHN SSPAREQNWMENFDELTVQVGFRRWVI NSSELKEHDLTQCKKGTWMMLETIFSK LTQEQKNQTLHVLTHKWELNNENTWTQ GGEHHTLGPVWRMFQYVVAERMLDKI PSLAFGLDLRQWFARGCWSFGHRLKA ARITAPRLAREQNWMENFDKLTVEVFR RWVITKSKLKEHALTQCKEDKNLEKKEL ATQQKMSSRTASEASSVFTATPHCYHYY LSSASYHISGSIRFPVLEKIRLHMGLNK CKVLLSGSSSQMYGDLEGGWNGKV VFPWSWAVQEPASPPTLGQISLTVCCST VNGLPASVDVFFCREALPRNLQKFAKD LGCILLQYIDNLLGYSTAVGCARRMDA LLRHLED CGYKVS KKAQICRQQTEGEQ TIRERWIKLSDGRIAPQLGA AVVLAV HKTIHLGOESLEKLLGQYFYISHLPALAK TVAQQCVTCQQRHAKQGPSVPPGIQAY RVASFENLQVDFTEMPKCGDQGLERGST VALVEGTPDHYPDHSHSYKGRRNPKLD SHSCVKPATAKT* |
| 6022 | 14073 | A | 6799 | 2 | 472 | |
| 6023 | 14074 | A | 68 | 241 | 492 | GGQIMRSGY*DHPG*/HGETRSLKIQKL AGHGGRLH*SQLLRRPRLNRLNLGGRG CSEPSSRHCTAAWATE*DSVSKKKKSRR |

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|------|-------|---|------|-----|------|---|
| 6024 | 14075 | A | 680 | 551 | 1706 | SKSRMSAEVIHQVEEALDTDEKEMLLFL CRDVAIDVVPNVRLDLDIFT/RERGVLS VGDLAELLYRVRFDLLKRILKMDRKA VETHLLRNPHLVSDYRVLMAEIGEDLDK SDVSSLIFLMKDYMGRGKISKEKSFLDL VVELEKLNLVAPDQLDLEKCLKNIHRI DLKTKIQKYKQSVQAGTSYRNVLQAAI QKSLKDPSNNFRLHNGRSKEQRLKEQLG AQQEPVKKSIQESAEFLPQSIPEERYKMK SKPLGICLIIDCIGNETELLRDFTSLGYE VQKFLHLSMHGISQILGQFACMPHRDY DSFVCLVLSRGGSSQSVYGVDDQTHSGLPL HHIRRMFMGDSCPYLAGKPKMFFIQNY VVSEGPAGEQQPLGGWMGQR |
| 6025 | 14076 | A | 6800 | 1 | 239 | QCCSGGTHGNPAIGDRMOKQILPWAPA QMKIRFMAPPERKYSVWIAAPILASLSTS SRMWISKQEYDESGPSIVHRKCF |
| 6026 | 14077 | A | 6801 | 2 | 440 | TGIVMDSSDGITHTMPYEGYTLPHAILP LDLAGQDLTDYFMKILKEGGYSFTTTAE REIMLDIKEKLCYITLDFEQEMATAASSS SLEKS*ELLNGQVITISNQWFHCP/EYLFQ PSFFTSIMKCDVDICKDLYANTVLSGGT TMY |
| 6027 | 14078 | A | 6802 | 2 | 212 | |
| 6028 | 14079 | A | 6803 | 3 | 443 | |
| 6029 | 14080 | A | 6804 | 1 | 1470 | MSTRPRRPPQLGRSTGRARLASRVAAAA GPPGARAPLAGDRAPAAGAPRRAGAGP CRPDPPPPAAGPTRGSPREGGKTGNRGK EREKGRRRAQSLAFADPPPVATRRQLTMD DDIAALVVDNGSGMCKAGFAGDDAPRA VFPSIVGRPRHQGMVGMGQKDSYVGD EAQSKRGILTLKYPIEHGIVTNWDDMEKI WHHTFYNELRVAPEEHPVLLTEAPLNPK ANREKMTQIMFETFNTPAMYVAIQAML SLYASGRTTGIVMDSGDGVTHTVPIYEG YALPHAILRLDLAGRDLTDYLMKILTER GYSFTTTAEREIVRDIKEKLCYVALDFEQ EMATAASSSSLEKSYELPDGQVITIGNEI RFRCPALFQPSFLGMESCGVHETTFNSI MKCDVDIRKDLANTVLSGVGTTMYPG IADRMQKEITALAPSTMKVIKIIAPS*RK YSVWIGGSILGLLSTFQQMWISKQEYD ESGPSIVHRKCF |
| 6030 | 14081 | A | 6805 | 171 | 393 | GKPKPKPKPLPKPKSREISHIP*GL*KAGP FRAPGRPGCKPCWLGPSIGPGR*GCP*K ASPEKVLGENLTLKNP |
| 6031 | 14082 | A | 6806 | 3 | 264 | SRRGSSPAQGSGLGRPQLLSAQYKWVG GGDRVSL*TMDFSLAPKTNRASQSKLD LQPA*APWP/PQLCGHPVPSASCPKSPF KPT |
| 6032 | 14083 | A | 6807 | 1 | 632 | |
| 6033 | 14084 | A | 6808 | 1 | 591 | |
| 6034 | 14085 | A | 6809 | 783 | 1516 | |
| 6035 | 14086 | A | 681 | 76 | 158 | |
| 6036 | 14087 | A | 6810 | 1 | 951 | |
| 6037 | 14088 | A | 6811 | 122 | 271 | |
| 6038 | 14089 | A | 6812 | 3 | 132 | |
| 6039 | 14090 | A | 6813 | 3 | 302 | |
| 6040 | 14091 | A | 6814 | 2 | 2158 | |
| 6041 | 14092 | A | 6815 | 2 | 186 | |

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|------|-------|---|------|-----|------|---|
| 6042 | 14093 | A | 6816 | 1 | 866 | MMEAIIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELAAMQKCLKGTEDELDKYSEALKDAQEKLELAEKKAADAEAEVASLNRRQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIERALKDEEKMELQEIQLKEAKHIAEEADRYEVARKLVIIEGDLERTEERAELAESKCELEEELKNVTNNLKSLEAQAQEKYSQKEDKYEEIKILTDKLKEATRAEFAERSVAKLEKTDDELELFAQKLKYKALSEELDHALNDMTSI |
| 6043 | 14094 | A | 6817 | 1 | 639 | |
| 6044 | 14095 | A | 6818 | 1 | 1710 | |
| 6045 | 14096 | A | 6819 | 764 | 1203 | FWLWVSFWVPCNTHITTSKSTSFSSPSTQATRFGVL/WFVIKASIIQGYCIARERKEFTHPVGRLSCLRQKLYNGTTETVTSWSSNHTERNPFKFPKLRTVWTHPESHRDWTAPTGLYWICGHRFAKLPDESAGIGGPKQG AIGIKE |
| 6046 | 14097 | A | 682 | 1 | 2313 | |
| 6047 | 14098 | A | 6820 | 24 | 225 | ARQAQAWFWAWRWAACLWFYFLVVS*NRY*VSNNKNNIRSLSSLNSSCKF/WS TRQQK*IPKMLS |
| 6048 | 14099 | A | 6821 | 1 | 1752 | |
| 6049 | 14100 | A | 6822 | 110 | 203 | |
| 6050 | 14101 | A | 6823 | 76 | 353 | |
| 6051 | 14102 | B | 6824 | 64 | 930 | MLRSVWNFLKRHKKKCIFLGTVLGGVYILGKYGQKKIREIQERAAEYIAQARRQYHFESNQRTCNMTVLSMLPTLREALMQQLNSESLTALLKNRPSNKLEIWEDLKHSFTRSTVAVYSTCMLVLLRVQLNIIGGYIYLDNAAVGKNGTTLAPPDVQQQYLSSIQHLLGDGLTELITVIKQAVQKVLGSVSLKHSLSLLDLEQKLKEIRNLVEQHKSSSWINKD GSKPLLCHYMMMPDEETPLAVQACGLSPRDITTIKLFHKTEDMLGSPDFRQFLNTCFKPRF* |
| 6052 | 14103 | A | 6825 | 385 | 666 | |
| 6053 | 14104 | A | 6826 | 701 | 930 | VAERQTGTGQGTVDITDRATSM*MRQRRGCCFATCC/FRHEGVVPWPQGRYHDHEGGFPRARLIHCTPDVLTYPYHVP |
| 6054 | 14105 | A | 6827 | 248 | 719 | TDEPSLLSHTFCPKGALLSACSGACPLSSGTQAGMPPSTEALQPCRGLTVPHQQDKGHRACC/VWKALAADWSVEWQKGRRGLGKALSVTSR/IRATSM*MRQRRGCCFATCC/FRHEGVVPWPWERYHDHEGGFPRARLIHCTPDVLTPAISPNVGNSTA |
| 6055 | 14106 | A | 6828 | 1 | 2489 | |
| 6056 | 14107 | A | 6829 | 227 | 547 | FHNKCPRRLES LRQISIFGMPENHLLKMQILRSAPDSLDFPCAGPLHLGEELLHRVEQVGAEVARVQQDFVL*GDMVEHLPRPGRQAESTPPTVPGNPPETLRRR |
| 6057 | 14108 | A | 683 | 788 | 926 | PSPPELPEGDFEGFFPQKLQ*SCLPTLQKKKNNNNNNNNNNNNNNNEK |
| 6058 | 14109 | A | 6830 | 3 | 433 | |
| 6059 | 14110 | A | 6831 | 37 | 360 | |
| 6060 | 14111 | A | 6832 | 280 | 1816 | |
| 6061 | 14112 | A | 6833 | 3 | 251 | GGALRLHQVPPALPLRGAVSGAAAVQGMSDCTPCCEVHLLQD*VPAGEARVQWHDGSLQPPPPRFKRFSCILPSSWDYRH |
| 6062 | 14113 | A | 6834 | 3 | 251 | GGALRLHQVPPALPLRGAVSGAAAVQGMSDCTPCCEVHLLQD*VPAGEARVQWHDGSLQPPPPRFKRFSCILPSSWDYRH |
| 6063 | 14114 | A | 6835 | 2 | 340 | |
| 6064 | 14115 | A | 6836 | 220 | 412 | |

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|------|-------|---|------|------|------|--|
| 6065 | 14116 | A | 6837 | 425 | 619 | |
| 6066 | 14117 | A | 6838 | 1 | 684 | MESQEPTESSQNGKQYIIEELISEGKWV KLEKTTYMDPTGKARTWESVKRTRKE QTRDGVAVIPVLQRTLHYECIVLVKQFR PPMGGYCIESPAIGLIDDGETPRKQLLSR ELEEEETGLQRGPLPEC/SLPAVCMGPQAC PNCTVHIVTV/TPINGDDAENARPKP/KSP GDGEFVEVISLPKNDLLQRLDALVAEE HPHSGTPRVYSYALALKHANAKPFEV PFLKF |
| 6067 | 14118 | A | 6839 | 3 | 194 | |
| 6068 | 14119 | A | 684 | 242 | 437 | KSCFFCLIRCYDSLPLPLLLNNFFFLGTES CSVAQAGVRWLNLSSSATSGLPGSINSP ASAS*AA |
| 6069 | 14120 | A | 6840 | 1 | 168 | |
| 6070 | 14121 | A | 6841 | 3 | 191 | |
| 6071 | 14122 | B | 6842 | 15 | 377 | MAALCRTRAVAAESHFLRVLFFRPFRG VGTESGSESGSSNAKEPKTRAGGFASAY GAARRSFYRRWSPYRKVEPRGSPKKC GILCIYAETILPLTTDGTTLQTTKLVHWTG SFIFVENDL* |
| 6072 | 14123 | A | 6843 | 2 | 205 | |
| 6073 | 14124 | A | 6844 | 1260 | 1628 | SFLCLVSCFSNFS*NCSRPFVSLSLKFDFV FVLFCDGVLCHPGWIAVAQSRLTTAST SRVSRFSCLTIRSSWDYRRPPPCPADFCIF SR/DRGFTMLARLVWNS*PQVICPPPPK VLGLQA |
| 6074 | 14125 | A | 6845 | 3 | 629 | |
| 6075 | 14126 | A | 6846 | 15 | 241 | |
| 6076 | 14127 | A | 6847 | 93 | 172 | |
| 6077 | 14128 | A | 6848 | 3 | 82 | |
| 6078 | 14129 | A | 6849 | 2 | 237 | |
| 6079 | 14130 | A | 685 | 1 | 1254 | |
| 6080 | 14131 | A | 6850 | 407 | 529 | |
| 6081 | 14132 | A | 6851 | 2 | 383 | |
| 6082 | 14133 | A | 6852 | 1 | 444 | |
| 6083 | 14134 | A | 6853 | 1 | 279 | |
| 6084 | 14135 | A | 6854 | 3 | 989 | |
| 6085 | 14136 | A | 6855 | 1 | 318 | |
| 6086 | 14137 | A | 6856 | 1 | 397 | |
| 6087 | 14138 | A | 6857 | 15 | 95 | |
| 6088 | 14139 | A | 6858 | 3 | 350 | |
| 6089 | 14140 | A | 6859 | 118 | 325 | |
| 6090 | 14141 | A | 686 | 73 | 1553 | PLKAKMGKEKTHINIVVIGHVDSGKST TTGHLIYKCGGNDKRTIEKFEKEAAEM GKGSFKYAWVLDKLAER/ERGITIDISL WKFETSKYYVTYPFDAP/ghrDFYPKT WITGDIFRLDWFGGPPFWGGSPLIVAAG/ VGEFEAGYLPRNGADPERHALLAYTLG CETTKLSGVNKNIGIPLEPTPTAQKKILKEI VKGKSALTLRKIGYNPDTSILCPISGWN GDNMLEPSANMPWFQGDGKVTBKDG NASGTTLEALDCILPPTPTDKPLGLPL QDVYKIGGIGTVPVGRVETGVLKPGMV VTFGPVNVTTTEVKSVMHHEALGEALP GDNVGFNVKNVSVKDVRRGNVAGDSK NDPPMEAAAGFPAQVILNHPGQISAGYAP VLDCHTAHIACKFAELKEKIDRRSGKKL EDGPKFLKSGDAAIVDMVPGKPMCVESF SDYPPLGCFVDRMRQTVAVGVIAVD KKAAGAGKVTKSAQKAQKAK |
| 6091 | 14142 | A | 6860 | 1 | 135 | |
| 6092 | 14143 | A | 6861 | 1009 | 1140 | |
| 6093 | 14144 | A | 6862 | 3 | 416 | |
| 6094 | 14145 | A | 6863 | 4 | 252 | |

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| 6095 | 14146 | A | 6864 | 3 | 130 | |
| 6096 | 14147 | A | 6865 | 1 | 1590 | |
| 6097 | 14148 | A | 6866 | 1 | 595 | GTRRLAPTAQRKRDENQSVKPEPGRGAS VRGGNLQTLPAAGDFLTCPASARDFRRVP AGQTQVPAAETA VEPVPAVVAGARGGR VMSEPQPRGAERDLYRDTWVRYLGYAN EVGEAFRSLVPAVVWLSYGVASSYVL ADAIDKGKE/ELERCPALEASRSARVTVA VVDTFVWQALASVAIPGFTINRVCAASL YVLGT |
| 6098 | 14149 | A | 6867 | 2 | 453 | |
| 6099 | 14150 | A | 6868 | 1 | 265 | |
| 6100 | 14151 | A | 6869 | 46 | 194 | |
| 6101 | 14152 | A | 687 | 67 | 408 | KAAGKRGDFKTEGAYQRQRTIFKNKRR ARREKTGRENLRGNYKNMGRGLKTPRG ALGGPYLDKKGPLRGKGPFGGTLSSS PKIKIQGT*IRRNYPYIRRYNRFKKRQ KNM |
| 6102 | 14153 | A | 6870 | 4 | 228 | |
| 6103 | 14154 | A | 6871 | 1 | 288 | |
| 6104 | 14155 | A | 6872 | 1 | 885 | |
| 6105 | 14156 | A | 6873 | 532 | 687 | |
| 6106 | 14157 | B | 6874 | 158 | 3331 | PRPPAAGEAQAAADMNHQQQQQQQKA GEQQLSEPEDMEMEAGDTPPRITQNP VINGNVALSDGHNTAEEDMEDDTSWRS EATFQFTVERFSRLSESLSPPCFVRNLP WKIMVMPRFYDPRPHQKSVGFLLQCNA ESDSTWSCHAQAVLKIINYRDDEKSFSSR RISHLFFHKENDWGFSNFMWSEVTDPE KGFIDDDKVTFEVFVQADAPHGVAWDS KKHTGYVGLKNQGATCYMNSLLQTLFF TNQLRKA |
| 6107 | 14158 | A | 6875 | 589 | 732 | |
| 6108 | 14159 | A | 6876 | 1 | 799 | |
| 6109 | 14160 | A | 6877 | 2 | 470 | |
| 6110 | 14161 | A | 6878 | 3 | 204 | |
| 6111 | 14162 | A | 6879 | 367 | 551 | EHSTLKLPHYHTQEAGAAPGPTGTDSEV DHLEGGAGKEAGPCA*SLGTMVAPVRS NSGSPE |
| 6112 | 14163 | A | 688 | 10 | 386 | AGAAAIGEPMA*RGEHPPWSVDERAD STNVNNWHWTERDASHWSTDKLKTLFL AMHVQNEERNGEATEVSKLDGEASINN RIGKLMFFYEWGVTLDTWTGAS*SGVPY KGHVEIPYLADENCVDE |
| 6113 | 14164 | A | 6880 | 24 | 547 | |
| 6114 | 14165 | A | 6881 | 1 | 828 | |
| 6115 | 14166 | A | 6882 | 2 | 270 | |
| 6116 | 14167 | A | 6883 | 2 | 114 | |
| 6117 | 14168 | B | 6884 | 75 | 293 | MPSIKLQSSDGEIFEVDVEIAKQSVTIKT MLEDLGMDDEGDDDPVPLPNVNAAILK KVIQWCTHHKDDPPSS* |
| 6118 | 14169 | A | 6885 | 446 | 639 | |

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|------|-------|---|------|-----|------|---|
| 6119 | 14170 | A | 6886 | 3 | 1503 | ARQRRSRAPTTHTHRALVRLFSGSQSAP PPPPRSPSPSAAMSTRSVSSSSYRRMFGG PGTASRPSSSRSYVTTSTRITYSLGSALRP STSRSLYASSPGGVYATRSSAVRLRSSVP GVRLLQDSVDFSLADAINTEFKNTRTNE KVELQELNDRFANYIDKVRFLEQQNKIL LAELEQLKGQKSRLGDLYEEMRELRR QVDQLTNDKARVEVERDNLAEDIMRLR EKLQEEMLQREEAENTLQSFQDQVDNAS LARLDLERKVESLQEEIAFLKKLHEEEIQ ELQAQIQEQHVQIDVDVSKPDLTASLRD VRQQYESVAANKLQEAEEWYKCQVC* PLLRASNRRNNEPLRQAKIQESITELPENR VQSLTCVEVDAL*RKPMSSLERQLREME ENFC/AVKAANYPRLLARLQDEIQNY* RREMASLTFVEYQ*PALNVKMAP*HLRF ATLQE/MLLGRRGERGFPLASFPNFSLP* TLRGNLIWDSLPSGLIPHSKRDT |
| 6120 | 14171 | A | 6887 | 3 | 232 | |
| 6121 | 14172 | A | 6888 | 252 | 384 | |
| 6122 | 14173 | A | 6889 | 3 | 196 | |
| 6123 | 14174 | A | 689 | 2 | 323 | REMDLQVHNAMDQLEQRVSEFFMNAK KNIPEWREEQMASIKKDYKALEDADE KVQLADQIYDL/RSLELDTPSQPVNNHH AHSHTPAEKRYNPTSHHTTTDHIPEK |
| 6124 | 14175 | A | 6890 | 1 | 2994 | |
| 6125 | 14176 | A | 6891 | 75 | 350 | TGIPVNSYRVKINWYTLOFVSLFRPFPGL VINQLADQSESEGPVQESAEPSQLVEP ATEEIKETDGSSQIKQEPDPTWETSFLG EISF |
| 6126 | 14177 | A | 6892 | 1 | 2935 | |
| 6127 | 14178 | A | 6893 | 214 | 301 | |
| 6128 | 14179 | A | 6894 | 1 | 2879 | MAQVAMSTLPVEDEESSESRMVVTFML SALESCKELAKSKAEVACIAVYETDVF VVGTERGRAFVNTRKDFQKDFVKYCVE EEEKAAEMHKMKSTTQANRMSVDAVEI ETLRKTVEDYFCFCYKALGKSTVVPVP YEKMLRDQSAVVVQGLPEGVAFKHPEN YDLATLKWIGENKGGISFIKRPFLEPKK HVGGRVMVTDADRSLSPGSGCGPIKVK TEPTEDSGISLEMAAVTVKEESEDPDYY QYNIQG |
| 6129 | 14180 | A | 6895 | 1 | 334 | |
| 6130 | 14181 | A | 6896 | 3 | 444 | |
| 6131 | 14182 | A | 6897 | 117 | 1009 | |
| 6132 | 14183 | A | 6898 | 5 | 808 | LPLPGRAVWCTHCCAPTSPGPVLPHSAA MSFLKSFPFPPGAEGLLRQQPDTEAVLN GKGLGTGLYIAESRLSWLDGSGLGFSL EYPTISLHALSRDRSDCLGEHLYVMVNA KFEEESKEPVADDEEDSDDDVEPITEFR FVPSDKSALEAMFTAMCEQALHPDPED EDSDDYDGEEDVEAHEQGGQDIPTFYT YEEGLSHLTAEGQATLERLEGMLSQSVS SQYNNMAGVRTVEDSIRDYEDGDGRDLT TPITVCLGQFEDADV |
| 6133 | 14184 | B | 6899 | 233 | 411 | XALNGLSAQDNWAKLQRDYPDALITNY YLWPAVQLANFYLVPLHYREDPASTTLV SDPT* |
| 6134 | 14185 | A | 69 | 709 | 941 | SQHFERSGDQHHPGQHGETLSLLKMQK LAGCGMRL*SQLGLRLRQENLLNPGG RGCSKPRSHHCTPAWVTQQDSIS |
| 6135 | 14186 | A | 690 | 2 | 495 | AKKNKPEWREEQMASIKKDYKALEDA VDEKVLNSNQIYDLVDRGGRKLDQELAK FKMELEADNAGITEILERRSLELDTPSQP VNNHHASHTPVEKRYNPTSHHTTTD HIPEKKFKSEALLSTLTVRCLLRENTLGC RNNNSTASSNNAYNVNSSLPLGSYN |

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| 6136 | 14187 | A | 6900 | 109 | 435 | |
| 6137 | 14188 | A | 6901 | 34 | 408 | RQWLQEEAYITKEQKYSFLHDSQTSFCF SDSIPTSSNMEETQQ/KSNLELLHISLLLN QSRLEPVRFLRSTFTNNLVYDNSDSDDY QLLKDLEGGIQMLMGRLEAATN*LGGP QANYNKFDKTRTT |
| 6138 | 14189 | B | 6902 | 80 | 495 | XPGSRTSLLAFALLCLPWLQEAGAVQT VPLSRLFDHAMLQAHRAHQLAIDTYQEF EETYIPKDQKYSFLHDSQTSFCFSDSIPT SNMEETQQKSNLELLRISLLIESWLEPV RFLRSMFATTWCMTPTAMTITS* |
| 6139 | 14190 | A | 6903 | 1 | 597 | |
| 6140 | 14191 | A | 6904 | 3 | 552 | |
| 6141 | 14192 | A | 6905 | 3 | 716 | |
| 6142 | 14193 | A | 6906 | 359 | 648 | WIPRPNSPNHSGSCGQAHLVAMAPGSRT VSLLLAFALLCLPWASRRLGAVPKPFRIS RLFDHAMLQAHRAHQLAIDTYQEFEE TYIPKDQKYSFLA*PQTSFCFSDSIPTPS NRRITQQKSNLELLRISLL/TESWLEPV RFPQEYCSANNLGVLTPRTAIDYHLLKD LEGGHPTV*WNICREVCFSCFSGRIRDD IEEEDDQEAIFYRYMAENPTAGVVQEEEE DNLEYDSDGNPIAPTCKIIDPLPIDHSEV DQHGLRPEGTHLTLKERTSWVESVADTL CTILTTLVMDPKAQLPEPLRVLWTGSPS GNGSRLPDVPCSWLLPCACPGQGGW VPCQNRSVYPGFFDHAIAPSPSRAPAGH CTPTRSLKKPHIPKDQKYSFLA |
| 6143 | 14194 | A | 6907 | 113 | 411 | |
| 6144 | 14195 | A | 6908 | 3 | 1162 | |
| 6145 | 14196 | A | 6909 | 2 | 265 | |
| 6146 | 14197 | A | 691 | 50 | 391 | GSQKIAPVFWSGFECDSEIRLTDLESWLY ILPATQPWSLTIFYFYQFSFILTLRYDKLF FFFTLYLYLNLYFFLYVFLFIV*ICIFYIY LVFIFKCVV*FFIFFVCFMLFFL |
| 6147 | 14198 | A | 6910 | 3 | 151 | |
| 6148 | 14199 | B | 6911 | 58 | 359 | SLAALQAYSHWLAQYCEVHRQNTQQF VTLISTTMDAITPLISTKVQDKLLLSACH LLVSLATTVRPVFLISIPAVQKVFNRITDA SALRLVDKRMSSSGP* |
| 6149 | 14200 | A | 6912 | 4 | 329 | |
| 6150 | 14201 | A | 6913 | 2 | 256 | |
| 6151 | 14202 | A | 6914 | 1 | 350 | |

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|------|-------|---|------|-----|------|---|
| 6152 | 14203 | A | 6915 | 257 | 2659 | VDCRMS/FSYIEKFTDFLRFLVSVHLRRIE SYSQFPVVEFLTLLFKYTFHQPTHEGYFS CLDIWTLFLDYLTSTIKSRLGDKEAVLN RYEDALVLLLTEVLNRIQFRYNQAQLEE LADDETLDDDDQTEWQRYLRQSLEVVA KVMELLPTAFSTLFPVLQDNLAEVYGL QQFIVTSGSGHRLNITAENDCRRHLCSLR DLSSLLQAVGRLAEYFIGDVFAARFND LTVVERLVKVTLYGSQIKLYNIETAVPSV LKPDLIDVHAQSLAGGCRLSAHWLAQY CSEIHRQNTQQFVTLISTTMDAITPLISTK VQDKLLSACHLLVSLATTVRPVFLISIP AVQKVENRITDASALRLVDKAQVLVCR ALSNILLPWPNLPENEQQWPVRSINHAS LISALSRDYRNKPSAGAPQRKMLDDT KLIHQTLQRLRKILWENISGESTKSSTDF AYQFGCRESVQVSLGLFPFVHQSDVT DEMLSFFLTFRGLRVQMGVPFTEQIIQ TFLNMFTRQLAESILHEGSTGCRVVEKF LKILQVVVQEPGQVFKPFLPSIALCMEQ VYPILAEPSPDVKAELFELLFRTLHHN WRYFFKSTVLASVQRGIAEEQ MENEPQ FSAIMQAFGQSFLQPDHILFKQNLFYLA TLNTKQKLYHKKVFRITAMLFQFVNVL LQVIVHKS HDLLQVEIGHRSYNMAS VDFADGFFAAFLPEFLTSCDGVADANQK SVLGRNFKMDRVRRERGRAKRAEWA RKPGTCAARRGHIEASGRGLCPPCSLAA AHEMPADLVL |
| 6153 | 14204 | A | 6916 | 1 | 321 | |
| 6154 | 14205 | A | 6917 | 1 | 259 | |
| 6155 | 14206 | B | 6918 | 1 | 3045 | MPDCTSKCRSLKHALDVLSVVTGSEN QIKAFLLSSH CYNAATIKDVFGRNALHLV SSCGKKGVLDWLIQKGVDLLVKDKESG WTALHRSIFYGHIDCVWSLLKHGVS LYI QDKEGLSALDLVMKDRPTHVVFKN TGC LLDPNGEKC VTAPRQVSALHHKDIALSL VAASDGATVCVTTRGDIYLLADYQCKK MASKQLNLKKVLVSGGHMEYKVDPEHL KENGGOQKICILAMDGAGRVFCWRSVNS SLKQCRWAY |
| 6156 | 14207 | A | 6919 | 1 | 1149 | |
| 6157 | 14208 | A | 692 | 3 | 546 | PAPPGRVFAAWPGSEEARVLVVLKGCA CRAGLFKMYPLLPMTVEVCTKSSTVTWF CFAAYESLFETPFAIGSVLVPSWGLTL ALS*VCFAAFA*LLASLFSQDPLVSPSAA MWASPACFCAEPSSAAIGVSSPSSSVFTQ QS**GSPLAGSASASAKN MARARSVAPP RNGRPGNTNADS |

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| 6158 | 14209 | A | 6920 | 426 | 2967 | HSAPPAVLRGGMSEAGGAGPGGCGAGA GAGAGPGALPPQPAALPPAPPQGS PAAAGGSGACGPATAVAAAGTAEGP GGGGSARIAVKKQAQLRSAPRAK KLEKLGVYSA CKAEESCKCNGWKNPNPSPTPPRADL QQIIVSLTESCRSCSHALAAHVSHLE NVSEE EMNRLLGIVLDVEYLFTCVHKEEDAD TKQVYFYLFKLLRKSILQRGKPVVEGS LEK KPPFEKPSIEQGVNNFVQYKFSLPA KER QTIVELAKMFLNRINYWHLEAPSQRRL RSPNDDISGYKENYTRWLCYCNPQFCDS LPRYETTQVFGRTLRSVFTVMRRQLLE QARQEKDKLPLEKRTLILTHFPKFLSMLE EEVYSQNSPIWDQDFLSASRTSQLGIQT VINPPPVAGTISYNSTSSSLEQPNAGSSSP ACKASSGLEANPGEKRKMTDSHVLEEA KKPRVMGDIPMELINEVMSTITDPAAML GPETNFLSAHSARDEAARLEERRGVIEFH VVGNSLNQKPNKKILMWLVGLQNVFSH QLPRMPKEYITRLVFDPKHKTLALIKDG RVIGGICFRMFPSQGFTEIVFCAVTSNEQ VKGYGTHLMNHLKEYHIKHDVLNFLT YADEYAIGYFKKQGYCKEIKIPITKYGGYI KDYEGATLMGCEALNPRNPYTEFSV IIKK AE/EGIIKKLIERKQAQIPKKFTLGLSCFK DGVROIPIESIPGIKKA/GWNP SGKEKSKE PRDPDQLYSTLKSILQVVKSHQSAWAF MEPVKRTEAPGYEYEVIRFMDLKTMSER LKNRYVVSKKLFMADLQRVFTNCKEYN AAESEYYKCANILEKFFFSKIKEAGLIDK |
| 6159 | 14210 | A | 6921 | 1 | 184 | |
| 6160 | 14211 | A | 6922 | 114 | 384 | |
| 6161 | 14212 | A | 6923 | 141 | 1741 | |
| 6162 | 14213 | A | 6924 | 1 | 153 | |
| 6163 | 14214 | A | 6925 | 1 | 200 | |
| 6164 | 14215 | A | 6926 | 2 | 242 | |
| 6165 | 14216 | A | 6927 | 132 | 251 | |
| 6166 | 14217 | A | 6928 | 132 | 251 | |
| 6167 | 14218 | A | 6929 | 2231 | 2578 | PLPPGSRTLHWMAPEEDFRIGN*TMNA IFFFLFLFFFFFLRQSFALVVQAGVQW HDLSSLQPPPPRFK*FSCLSLPSGWD*RH APPRPAIFVFLVEMGFHHVNQDGLDLIT W |
| 6168 | 14219 | A | 693 | 3 | 389 | DAWVDPRFRLIFLKTLTGKTM AVDLEPN DTIANAKA*IQDKEGIPPDQRLIFAGKQ LENGRTLDPDYIIHKESTLLVLR LKGGMQ IFVKTLTA*TISLQAEP SDTIHNV*EKIQD KESIPPDQHTVIL |
| 6169 | 14220 | A | 6930 | 2 | 94 | WRDLGSL*PPPPGFKRFS*LSLKSHPNVT S |
| 6170 | 14221 | A | 6931 | 130 | 295 | GIISNADFVSFFFF*DGVFALVAQAGVQ WRGLGSLQPLPPGFKRFSCLSLPSTW |
| 6171 | 14222 | A | 6932 | 3 | 403 | TYKILDFIVNSIRHRRGT PRFPGHTEVTS MTLDFIGAG*/SNLQ*PAST*PGDQY*I*L LQST*NYVLHKFQLPTWKG RSEISEQAV SAKEKT*KS/T*LALVK*ARTLESN WPG/L *ILILISLSMIWTNDSNLF |
| 6172 | 14223 | C | 6933 | 78 | 335 | MWSPLTKEIFSCPTPQT CGAFKGLKRA PXXXXXXXXXVKIGXXXXXXXXXXXXX XVSPRPLSARVLAPCLGCDFFVS FNRTTV WK* |
| 6173 | 14224 | A | 6934 | 1 | 143 | |
| 6174 | 14225 | A | 6935 | 1 | 1676 | |
| 6175 | 14226 | A | 6936 | 1 | 161 | |
| 6176 | 14227 | A | 6937 | 61 | 742 | |
| 6177 | 14228 | A | 6938 | 7 | 238 | |
| 6178 | 14229 | A | 6939 | 1 | 213 | |

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|------|-------|---|------|-----|------|---|
| 6179 | 14230 | C | 694 | 70 | 225 | MNIQYIQHESVYQNVRSQRESTGRWSH CCPSQGRSRRIPFTVEEIQQHGV* |
| 6180 | 14231 | A | 6940 | 1 | 257 | |
| 6181 | 14232 | A | 6941 | 3 | 279 | GSGWDGRGQSGRVADSS*ARVLSAL*RE VNK*RLQDLRSCLSPKPPQGGQEQQED EVVLVEGPTLPETPRLFLKIRCRADLVR LPLRMVSA |
| 6182 | 14233 | A | 6942 | 73 | 816 | |
| 6183 | 14234 | A | 6943 | 1 | 484 | |
| 6184 | 14235 | A | 6944 | 1 | 1758 | |
| 6185 | 14236 | A | 6945 | 1 | 1420 | |
| 6186 | 14237 | A | 6946 | 186 | 209 | QLWPN*LLSRNKEATLRYSQLPTCHSICY *MPAF*HTISDLSFNKNINCKSYHLRVFY KYV*IVCHF*VPKVYWTKYQTSCRT*W R*SGVE*PPISSSSSACCLLRRLPTEGTC EIFWNPRLGISAECDSCGPTSF |
| 6187 | 14238 | A | 6947 | 2 | 2948 | |
| 6188 | 14239 | A | 6948 | 1 | 616 | |
| 6189 | 14240 | A | 6949 | 1 | 1913 | |
| 6190 | 14241 | A | 695 | 277 | 396 | EAP*HPDFIKNMITGTS*ADCAGLIVAAG GGVFKSWDLQK |
| 6191 | 14242 | A | 6950 | 3 | 185 | |
| 6192 | 14243 | A | 6951 | 112 | 569 | |
| 6193 | 14244 | A | 6952 | 1 | 1210 | |
| 6194 | 14245 | A | 6953 | 75 | 333 | |
| 6195 | 14246 | A | 6954 | 271 | 512 | GAVGRPRSQQKSIGVPGWVSPGF*ECGK RRMTFVLLKHIMLLFPARFQQIMRNIPRR LAEHMQQLFSSCPSLMRAFEVT |
| 6196 | 14247 | A | 6955 | 2 | 184 | |
| 6197 | 14248 | A | 6956 | 13 | 163 | |
| 6198 | 14249 | A | 6957 | 627 | 847 | |
| 6199 | 14250 | A | 6958 | 3 | 144 | |
| 6200 | 14251 | A | 6959 | 1 | 2008 | PAAADARRPRAPATMRPRKAFLLLLL GLVQLLAVAGAEGPDEDSSNRENAIEDE EEEEEDDDDEEDDLEVKEENGVLVLND ANFDNFVADKDTVLLEFYAPWCGHCKQ FAPEYEKIANILKDKDPPIPAKIDATSAS VLASRFDVSGYPTIKILKKQAVDYEGS RTQEEIVAKVREVSQPDWTPPEVTLVL TKENFDEVNDADIILVEFYAPWCGHCK KLAPEYEKAAKELSKRSPPIPLAKVDAT AETDLAKRFDVSGYPTLKIFRKGRPYDY NGPREKYGIVDYMIEQSGPPSKEILTLKQ VQEFLLKDGDDVIIIIVFKGESDPAYQQY QDAANNLREDYKFHHTFSTEIAKFLKVS QGQLVVMQPEKFQSKYEPRSHMMDVQ GSTQDSAIKDFVLKYALPLVGHKVSND AKRYTRRPLVVVYVSDFSDYRAATQ FWRSKVLEVAKDFPEYTFIAADEEDYA GEVKDLGLSEGEDVNAAILDESGKKFA MEPEEFDSDTLRIELVTAFKKGKLPVIK SQPVPKNNKGPVKVVVGRTFDSIVMDP KKIDVLIIFYAPWCGHCKQLEPVYNSL A'KKYKGQKGLVIKMEAPANDVPQRP AIRVEGFPTIYFRPPVGDKKDPV/KFEG GDRDLEPFEPFSFIEEHA/TKLSRTKEEL |
| 6201 | 14252 | A | 696 | 549 | 707 | SQNFWRPMWADHLRLGVRDQHGQHG TPSLLKIQLAGHGGRL*SQLVRKLR |
| 6202 | 14253 | B | 6960 | 137 | 214 | ASQFPIEWRPVKDAATVDSEPALPQQ* |

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|------|-------|---|------|------|------|--|
| 6203 | 14254 | A | 6961 | 1 | 625 | PSLKGQKLELHRGAAALELVDPPGCRSG LVHARGCTYSQWRSRSHPFCCSRGPLA MAGILFEDIFDVKDIDRKAKKFDRVASRL HCESESFKMDLILDVTIQIYPVDLGDKFR LVIASLTLYEDGTLDDGEYNPTDDRPSRA DQFEYVMYGVYRIEGDDETSTEAATRA LSAYVSVYGGLLMRLQGDANNLHGFEV DSRVYLLMKKLAF |
| 6204 | 14255 | A | 6962 | 1 | 273 | |
| 6205 | 14256 | A | 6963 | 135 | 233 | |
| 6206 | 14257 | C | 6964 | 198 | 449 | |
| 6207 | 14258 | A | 6965 | 1 | 1278 | |
| 6208 | 14259 | A | 6966 | 1 | 325 | |
| 6209 | 14260 | A | 6967 | 525 | 661 | TEILSGSLGSEIFTSES*RPGLGPSFVIFLF SSSVCLNIFRVL |
| 6210 | 14261 | A | 6968 | 1 | 293 | MAGTPPPALLPPCSLISDCCANNQRDSV GVGPSEPGAGYNLVVRSFLSPSEKRSVR VGVTRLFQGRPSPLSLTQKGNPLTPCAS QFTSTISDGRIMV |
| 6211 | 14262 | A | 6969 | 1 | 1372 | |
| 6212 | 14263 | A | 697 | 82 | 417 | AFQEMELKRPQEEDVAALPEGMRPHSN LYGFSWE*VICAADVGLFAALFFLWRSF RTVRIHVGRRERKLALMLSGLNQ*KSEL LGHCILAQNEYDGYELDE*FVDLRVDKE |
| 6213 | 14264 | A | 6970 | 2 | 277 | KNEMTLDAYIFLADMAAYQEEQMQLP RADAIRSLIDTFSLIEHLQGLSQAVPRH TIRELLGQQPISSLI*I*DSYPHPLHLRVEN SGEV |
| 6214 | 14265 | A | 6971 | 434 | 563 | ETTFYNEQRGPQPHLEVKKKYRGN*EA KTK*LRPENWKGDL |
| 6215 | 14266 | A | 6972 | 197 | 1247 | ALVRLDSWMGLNTTANLGGGEMTEMAR GVTPWICPRSSAERARSGIPAAVPISVK ISGPQLLIGPNPPGSKRWARNSSCSSEH CR/SQGAQEESCLAQHH/TPSAPSQMT*T PNC*CAGAPLAAVHR/GITQRCQMNEVQ VAHMPPTLP*ETGDHNAELSGAPAIYLP QGAQHSPVH*DQLL*FPIS*TY*EPTKLQ DLLRTKSPGGTPQLFCFAH/ALPAVPQAQ VLGLLQIMSGSPQSLRAPSLQSLQTRLL GMSLVHLHNLAAQVLEDPQQLVAPP/T/D YQGCFLGSKLWLPQLSN/VCSAPSSAAF LEAAPGSLDPRPPGFVPSLPGLPGGGGS VPAAALELFAPAPPPT |
| 6216 | 14267 | A | 6973 | 232 | 476 | IFVSSYYHVNLFRRFT*AHSSSH*TNPD LYPYQHGNKVKDIPGTLLENRKVG*PL KKDLQDENKQDKPSCHLQGGQLQWP |
| 6217 | 14268 | A | 6974 | 442 | 698 | |
| 6218 | 14269 | B | 6975 | 546 | 1820 | LLNCPLFCYGLTSVLHVTCFFSHHGYY DTSKDNQAKQPKDEIDAAEDATDFRH LPDVLKQCIPMIQASQPADSAVPATSGK VYGTPELTETPTNIEAAPLAEEEHASSA TSITECDKLSSFATSV AEDQSVASLTAPQ TEETGKSSLLDVTISIPSSRTEATQGLD YVPSAEDKGFKSPCEDFSVTGESEKRG EIIGKGLSGERAVEEEEEETAHVEMSEKL CSQYGTVPVSAPGHALHPGEPALGEAEE RRSPDDSTVKMASPAPSGPPSGTHTPFH ESPVEEKSEPQDFQEADSWGDTQRTTSV GKRKAAEELRCLVRTGRSIRGLSLPPACT RAERREVERVVVDALSGLKGDLGRYY RLSEMTEAEQQQLIDHFLFDKPVSPLLT AAGMARDWPDARGIWHNNEKSFLIWW N* |
| 6219 | 14270 | A | 6976 | 2 | 480 | |
| 6220 | 14271 | A | 6977 | 1 | 2043 | |
| 6221 | 14272 | A | 6978 | 1259 | 1497 | |

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|------|-------|---|------|------|------|--|
| 6222 | 14273 | A | 6979 | 2 | 425 | |
| 6223 | 14274 | A | 698 | 751 | 1063 | FYQDKRHQPGIVAAACNPFGRSRQEDLL RS*VGDQPGQHSESPSMQKI*KL AGHGG AHV*S*LLRRPRQDNPLSPGGQGCSVL*S HHCTPAWATQGDPGSKSKN |
| 6224 | 14275 | B | 6980 | 259 | 329 | XFRKKEQQIKQCKGTAGQALIKE* |
| 6225 | 14276 | A | 6981 | 1 | 1251 | |
| 6226 | 14277 | A | 6982 | 1 | 421 | |
| 6227 | 14278 | C | 6983 | 120 | 371 | MSAHSHPCTCINGHTPVSIYXXXXXGG PFKRTLGGPKFNGGGQKIFFFMGGLFK PSLGFLEKNLFXXXXTYGATPPPKFKP* |
| 6228 | 14279 | A | 6984 | 76 | 251 | ALKFCRGVFPFSPQKKFLFQNSPGGFFF PPLKEKNFSFPP*KSSSPKPLNFVGGFFP FFPPP/NKKFLFQNSPGGFFFPPLKEKNFS FPPPVKFGPPQGSF*TPPP |
| 6229 | 14280 | C | 6985 | 193 | 315 | MGGQLKPSLGFLEKNLFFGGEKNHXX XXKFKPLGXXXXF* |
| 6230 | 14281 | C | 6986 | 363 | 413 | |
| 6231 | 14282 | A | 6987 | 1 | 1088 | |
| 6232 | 14283 | A | 6988 | 64 | 1279 | LAPGAVGKGRGHTLPCSAARMGVKAS QTGFVVLVLLQCCSAYKLVCYYTWSQ YREGDGSCFPDALDRFLCTHIYSFANIS NDHIDTWEWNDVTLYGMLNTLKNRNP NLKTLLSVGGWNFGSQRFSKIASNTQSR RTFIKSVPPFLRTHGFDGLDLAWLYPGR RDKQHFTTLIKEMKAEFIKEAQPGKKQL LLSAALSAGKVTIDSSYDIAKISQHLDFIS IMTYDFHGAWRGTTGHHSPFRGQEDA SPDRFSNTDYAVGYMLRLGAPASKLVM GIPTFGRSFTLASSETGVGAPISGPPIGR FTKEAGTLAYEICDFLRGATVHRTLQ QVPYATKGNQWVGYYDDQESVKSXVQY LKDRQLAGAMVWALDLDQGSFCGQ DLRFPLTNAIKDALAAT |
| 6233 | 14284 | A | 6989 | 3 | 174 | |
| 6234 | 14285 | A | 699 | 3 | 17 | |
| 6235 | 14286 | C | 6990 | 116 | 181 | MCSTSRSRFTNILKSCNLLKY* |
| 6236 | 14287 | A | 6991 | 20 | 111 | |
| 6237 | 14288 | A | 6992 | 120 | 426 | |
| 6238 | 14289 | A | 6993 | 2 | 112 | |
| 6239 | 14290 | A | 6994 | 24 | 316 | FLFLFFETESCSVARLECSGAISAHCKLC LPGSRHSPASASSQVAGSTGACHQA/QA NFVVFVLVETGFYRVSPG*SG/LSLELVIR PPRPPKVLGLQV |
| 6240 | 14291 | A | 6995 | 80 | 326 | |
| 6241 | 14292 | A | 6996 | 1 | 233 | |
| 6242 | 14293 | A | 6997 | 1941 | 2223 | RTPRMKQSPAPIPCQPTTCSGCMASRAT RTGWTSVCAYCRLFRAHACVPVALPE MVRALSAQQQTLKQIVICGDRQAKDTK ALGAVRPLCLHS |
| 6243 | 14294 | A | 6998 | 211 | 544 | |
| 6244 | 14295 | A | 6999 | 31 | 230 | |
| 6245 | 14296 | A | 7 | 46 | 1069 | ESKHGNFFWVIFLCYCTKEERTQLQKQK TDEYFRMKLQWKSISQEQEKRNSRLRD YRSLIEKDVNRTDRTNKFYEGQDNPGLI LLHDILMTYCMYDFDLGYVQGMDSFFS PFLYVMENEVDFAWCFASYMDQMHQN FEEQMGMKTQLIQLSTLLRLDLSGFC YLESQDSGYLYFCFRWLLIRFKREFSFLD ILRLWEVMWTELPCTNFHLLCCAILSE KQQIMEKHGYFNEILKHINELSMKIDVE DILCKAEAISLQMVCKELPQAVCEILGL QGSVAVTTPDSVVG*RTKMLVNDFLGPT VCISKVTALPTLSASGARNDSPQIPVSS RCLQD |

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| 6246 | 14297 | A | 70 | 170 | 340 | TDSALGSPCLHPTALCAVCGTA*SST/GL VALALMRLELILKSSVPAVMAGIITIYNL |
| 6247 | 14298 | A | 700 | 3 | 443 | |
| 6248 | 14299 | A | 7000 | 1 | 861 | |
| 6249 | 14300 | A | 7001 | 55 | 406 | |
| 6250 | 14301 | A | 7002 | 1 | 361 | |
| 6251 | 14302 | A | 7003 | 1 | 1725 | |
| 6252 | 14303 | A | 7004 | 1 | 1271 | |
| 6253 | 14304 | A | 7005 | 3 | 329 | LKLCCKSAKSCENDLEMGMLNSKFCKT RYQAGMRNSENLTANNTLSKPTRY/QGE LKEIKQDISSRLRYELLEKSQATGELADLI QQLSEKFGKNLNKDHLRVNKGKDI |
| 6254 | 14305 | A | 7006 | 1 | 801 | |
| 6255 | 14306 | A | 7007 | 21 | 373 | |
| 6256 | 14307 | A | 7008 | 3 | 63 | |
| 6257 | 14308 | A | 701 | 147 | 437 | WYVKKERKKERKQERKKERKKERKKE RKKRKRERKKER*REREREGRKEGRKE GRKEGRKEGRKEGRKKGRREGREKERE RKKEREISREYDSEK |
| 6258 | 14309 | A | 7012 | 1 | 521 | MSSKRTKTKTKRPPQRATSNVFAFDQ SQIQEFKEAFNMIDQNRDGFIDKEDLHD MLASLGKNPTDEYLDAMMNEVAPGPINF PQWFSPLVRSNAPDPVENVIRNAFACF DEEAPGPIQEDYLRELLPTMGDRFTNEE VDELHREAPIDKKGNFNYIGFTRILEHG AKDKDD |
| 6259 | 14310 | A | 7013 | 106 | 693 | TTTMSSKKAKTKTKRPPQRATSNVFA MFDQSQIQEFKEAFNMIDQNRDGFIDKE DLHDMLASLGKNPTDAYLDAMMNEA PGPINSTMFLTMFGVEKFKSHRSPEDVI/ RANGLCFCSDDEEATGHPFQED/YTLRELL TNPWGD/RFPDGGKWMNLYQRKHLIGP KKGEFSNYIGVHHGILTGRPPKHKDDLK ELLA |
| 6260 | 14311 | A | 7014 | 78 | 188 | |
| 6261 | 14312 | A | 7015 | 2 | 93 | GGSCL*SQHFGRPRWADHEVRRSRPSWL TR |
| 6262 | 14313 | A | 7016 | 2 | 93 | GGSCL*SQHFGRPRWADHEVRRSRPSWL TR |
| 6263 | 14314 | A | 7017 | 2 | 93 | GGSCL*SQHFGRPRWADHEVRRSRPSWL TR |
| 6264 | 14315 | A | 7018 | 2 | 93 | GGSCL*SQHFGRPRWADHEVRRSRPSWL TR |
| 6265 | 14316 | A | 7019 | 2 | 94 | GGSCL*SQHFGRPRWADHEVRRSRPSWL TR |
| 6266 | 14317 | A | 702 | 505 | 637 | CLLNSIYRRHQGR*DGKERKKDRKKE RKKERKKERKKERKKERKKE |
| 6267 | 14318 | A | 7020 | 1 | 418 | RRLRTAMKLRSRHPDQTDWHDDQYKNA HLGAALQANPLGGAHAHAGVLEKVRV EATQPKAISAMK/CVRVQLIKNGKKITAF VPNDGCLNFIEENDEVLVAGFGRKGHAV GDIPGVRFKVVKVANVFILALYKGKKER PRS |
| 6268 | 14319 | A | 7021 | 2159 | 2334 | SATNYRNLTVLELGNSTHRHSHKTNST* KNCTRIPQTSQNLK*VKKHQSHICQSNCP F |
| 6269 | 14320 | A | 7022 | 1748 | 1821 | |
| 6270 | 14321 | A | 7023 | 2179 | 2485 | |
| 6271 | 14322 | A | 7024 | 3 | 502 | TARAWLLGPVWPCVSRWSSKPSPRG GRDPSDRDPAFAAARSTVPPRISAYERPV PWPGEWNPGRPGRRASAVVSPREGNW GVLRDPRQLQARKPRMVRSRQMCNTNMS VPTD/GCCNHLTDSSFGTRDPG*TKAIAF EVIKVCWCTKRHLYYERGSFSLWPFVYY D |
| 6272 | 14323 | A | 7025 | 89 | 291 | |

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|------|-------|---|------|------|------|--|
| 6273 | 14324 | A | 7026 | 1295 | 1429 | |
| 6274 | 14325 | C | 7027 | 332 | 763 | MTGCLNFIENDEVLVAWIWSQKVMLL VIFLESXFKVQSSPMVSLALYKWL YGETKIINMNGENTVVINFHMPKNVCILLSP VLTTKIMFITTTTPPYFFYPKPNAGPVPI LGNNKTGLFQDSLELITFVTWHSFHPVE * |
| 6275 | 14326 | A | 7028 | 89 | 184 | |
| 6276 | 14327 | A | 7029 | 2 | 274 | LDLDSIKIVKKLKTGFYKIFKNTSFI/ KDIVFMRTWYVPSIPAFYNPVTSLKPV/ GEKDTWSGMWTTGHLGL/AHGVRKTN KDSLYKGLV |
| 6277 | 14328 | A | 703 | 220 | 476 | HNSLVVYVFEIWSRILFVYSCSIHTSVVT H*SLLSLGHLKYIWAGHGVSHL*FQHF GRPRWENHLRPLG*DQPGQHSETPSLLKK |
| 6278 | 14329 | A | 7030 | 178 | 619 | PPRHVQLNHAEFEDQDDEARVQYEGFR PGMYVCVEIENVPCEFV*NFDPRYPILG GLGNSEGNVGYVQ/PIPTQGTGFLAIQSV SGIMPDFRIAATGVVLDLDSIKIVKKL LTGFYKIFKNTSFIKGMFNSALEVAKFE GAVF |
| 6279 | 14330 | A | 7031 | 159 | 484 | DPITPQGTGFLAIQSVSGIMPDFRIAATGV VLDLDSIKIVKKLKTGFYKIFKNTSFI KGMFNSALEVAKFEGAVIRTISGIRGQIK KAL*APEGAFRASFEKLL |
| 6280 | 14331 | A | 7032 | 19 | 3881 | IATMEAKDQKKHRKKNSGPKAAKKKKR LLQDLQLGDEEDARKRNPKAFAVQSAV RMARSFHRTQDLKTKKHIPVVDRTPLE PPPIVVVMGPPKVGKSTLIQCLIRNFR QKLTEIRGPVTVSGKKRRLTHIECGCDIN MMIDLAKVADLVMLIDASFGFEMETFE FLNICQVHGFPKIMGVLTHLDSFKHNKQ LKKTKKRLKHRFWTEVYPGAKLFYLSG MVHGEYQNEIHNLRGITVMKFRPLT WQTS |
| 6281 | 14332 | A | 7033 | 182 | 374 | |
| 6282 | 14333 | A | 7034 | 2 | 198 | |
| 6283 | 14334 | A | 7035 | 1 | 457 | |
| 6284 | 14335 | A | 7036 | 2 | 145 | |
| 6285 | 14336 | A | 7037 | 55 | 193 | |
| 6286 | 14337 | A | 7038 | 564 | 882 | |
| 6287 | 14338 | A | 7039 | 257 | 513 | KFFSFLSSACCLEQVLFVFFVFFLLII FSFFSFSSFFSSSSSSSSSSFFFLR WS/PRSVAQAGVQ/WS*FGSLQPP |
| 6288 | 14339 | A | 704 | 1 | 554 | DLILNHLFFCFVIRQQFSFLFFFSFFHFI AMLTHQSYVIFLSVYTVIIHLDIFYISLFLT YDIMYF*TKINT*AKLLLIYENMLIVL*CS AFLSNYTVLIVQIIASLIHSSTK*ISQCANII KI*ILH*L*SSVEINSYL*LFCYLVYSAIL ELVLQSQFSYMYILRIQLDFLNEEMHI |
| 6289 | 14340 | A | 7040 | 936 | 1317 | ILVLHGCFCWYLCLSMYFFNFME SRSVAQAGVQWCA/DLCSLQAPPAGFTP FSCLSLPSSWDYRHPPLAKFFVFLVET GWFHRVSQDGLDLLTSGDPPTSASQSAGI TGVSHRARPLKHL |
| 6290 | 14341 | A | 7041 | 1 | 1218 | |

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|------|-------|---|------|------|------|--|
| 6291 | 14342 | A | 7042 | 1 | 1169 | MAPPSPSTTSSNNNSSSSNSGWDQLSKT NLVIRGLPPHTTDQDLVKLCQPYGKIVST KAILDKTTNKCKGYGVDFDSPAQAQK AVSALKASGVQAQMAKQQEQDPTNLYI SNLPLSMDEQELENMLKPFQGVISTRILR DSSGTSRGVGFARMESTEKCEAVIGHFN GKFIKTPPGVSAPTEPLLCKFADGGQKK RQNPKNKYIPNGRPWHREGEVRLAGMTL TYDPTTAAIQNGFYSPSYIATNRMITQT SITPYIASPVSAQYQVAKETRENKYRGSJ KVQSPSWMQPQPYILHDPGAVLTPSMEH TMSLQPASMISSPLAQQMSHLSLGSTGT MPATSAMQGAQYLPQYAHMQTTAVPVE EASGQQQVAVETSNDHSPYTFQPNK |
| 6292 | 14343 | A | 7043 | 1 | 743 | |
| 6293 | 14344 | A | 7044 | 2 | 171 | |
| 6294 | 14345 | A | 7045 | 1 | 350 | |
| 6295 | 14346 | A | 7046 | 2 | 1685 | |
| 6296 | 14347 | A | 7047 | 47 | 218 | |
| 6297 | 14348 | A | 7048 | 3 | 1716 | GRCCCFSPDGKALAVGLNDGSFLMANA DTLEDLVSFHHRKDMISDIRFSPGIWPI GEVTDVTVASCLTSDKMVLATGDDLGFV KLFYRPTKASSEQGPPTARETPDKQCRQ EKETYRATAPSIHIWDAMNKQTLILRC YHSKGVCSVSFSATGKLLSVGLDPEHTI TIWRWQEGAKIASRAGHNQRIFAEFRP DSDTQFVSVGVKHKVFWTLAGRALLSK KGLLSTLEDARMQTMALAFGAGKILVG TRNAEIEVGEKNAACNLVNGHVDGPI WGLATHPSRDFFLSAAEDGTVRLWDIAD KKMLNKNVNLGHAARTVCYSPEGDMVAI GMKNGEFIILLVSSLKIWGKKRDRRCIAH DIRFSPDSRYLAVGSSENSVDFYDLTLGP TLNRISYCKDIPSFVIQMDFSADSSYLQV SSGCYKRHVYEVPSGKHLMGSAIDRIT WATWTSILGDEVLGWISRHAEKADVNC ACVSHSGISLVTGDDFGMVKLFDFPCPE KFAKHKRFLGHSPHVTNIRFTSGDRHV SAGGDDCRLVTFSAAHEEQTMLLVKRLN TTTTPTALVYEIS |
| 6298 | 14349 | A | 7049 | 1 | 5853 | |
| 6299 | 14350 | A | 705 | 1039 | 1560 | SLVLDLTGLPRPTSPSHERGLDSSSSGPG LSTGP*ECSPDPNPMCPKVLPGPDQRCW NSHSTAPIAFPEPVRSR*SGSWTPVPATG ATLNPQRQGLAIPNSLVSSP*GPAGWRE LPSSQQAHPHPR*GALRSENREQEPDQ GCGNCFVKYGGVRVGRVGYSGPVRTGCS RASN |
| 6300 | 14351 | A | 7050 | 1 | 426 | LKQQIEEQRVQVQVVERAQQVAVQEIE ARAEAEQMAKKA/AFQLYQEAQQLDM LLEKLPQVAEEISGPLTSANKITLVSSGS GTMGAAKVTGEVLDILTRLPIESVERLT GWTILPRLNHKAF*RTALSLQPSQMPSLI AE |
| 6301 | 14352 | A | 7051 | 162 | 1449 | |
| 6302 | 14353 | A | 7052 | 57 | 389 | |

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|------|-------|---|------|-----|------|--|
| 6303 | 14354 | A | 7053 | 162 | 1581 | TMFFTCGPNEAMVVSFGRSPVVMVAG GRVFLPCIQIQRISLNTLTLNVKSEKV YTRHGVPISVTGIAQVKIQGQNKEMLAA ACQMFLGKTEAEIAHIALETLEGHQRAI MAHMTVEEIKDRQKFSEQVFKVASSD LVNMGISVVSYTLKDIHDDQDYLHSLGK ARTAQVQKDARIGEAERDAGIREAK AKQEKVSAQYLSEIEMAKAQRDYELKK AAYDIEVNTRRAQADLAYQLQVAKTKQ QIEEQRVQVQVVERAQQVAVQEQEIARR EKELEARVRNPAEVAERYKLERPAEAEKS QLIMQAEAKVAASVRMRGEAEGLCP*GP EPRAEAEQMAKKAEAFQLVPRGVAQL DMLRRESCPRWQEEISGPNLNFSPIRSPLV SSGSGTMGAAKVTGEVLDILNSPCPES VERLTGREHLPRVNHKPLKNSLEPSAL HRCPASLAEVALNDPPVACNPLGLPEHV H |
| 6304 | 14355 | A | 7054 | 1 | 327 | |
| 6305 | 14356 | A | 7055 | 1 | 202 | |
| 6306 | 14357 | A | 7056 | 1 | 493 | |
| 6307 | 14358 | A | 7057 | 409 | 521 | |
| 6308 | 14359 | A | 7058 | 296 | 869 | |
| 6309 | 14360 | A | 7059 | 1 | 848 | MPGLRVKMPGPGISQDEAVWSMDDNF EVNKKQHPVWRAATLAKDCKNQSAQAV TVYNKPASFKEAPLDLQHRLFMKLGST HSPFRARVFFCSFISEPEDPATERLAFTER DAGSRLVTLHERPALLVSSTSWTGKGP LREYYSRLIYQKHQHIQVCTPWLGAED YPLLIGSADLGVLCHTSSSGLDLP/*KV VDMFGCCLPVCANFKVFTLKVHEEN GLVFEDSEELAAQLQMLFSNFPDPAGKL MSFRKNLPESQQL*WDESWWQTVLPLV MDT |
| 6310 | 14361 | A | 706 | 644 | 930 | EGSHGLGVVAHACNPSTLGNRCGVDHL SSGVQGPQGHGKTPFLQKIQKLAGHG GTRL*SSYLRLRWEDEGGRGCSEPRSRH CTPAPWATE*DPV |
| 6311 | 14362 | A | 7060 | 738 | 1902 | FHHLTETNSPNYFITMALNVAPVRDTKW LTLEVCRRQFQRTGCSRDEECKFAHPPK SCQVENGRVIACFDSLKGRCRECKYL HPPTHLKTQLEINGRNNLIQKTAAML AQMQMFMPGTPLHPVPTFPVGAIGTN TAISFAPYLAPVTPGVGLVPTLPTTPVI VPGSPPVTVPGSTATQKLLRTDKLEVC EFQRGNCARGETDCRFAPADSTMIDTS DNTVTVCMDYIKGRCMRECKYFHPPA HLQAKIKAAQP/QAAATVMTQSTAKAM KRPLEATVDLAFPPGALHPLPKRQALEK SNGTSAVFNPVSVLHYQALQALQQA AAFIPTGSVLCMTPATSVPMHSAAT VSAATTPATSVFAATATANQIILK |
| 6312 | 14363 | A | 7061 | 1 | 240 | |
| 6313 | 14364 | A | 7062 | 3 | 354 | |
| 6314 | 14365 | A | 7063 | 1 | 621 | |
| 6315 | 14366 | A | 7064 | 362 | 720 | |
| 6316 | 14367 | A | 7065 | 1 | 2610 | |
| 6317 | 14368 | A | 7066 | 122 | 1840 | |
| 6318 | 14369 | A | 7067 | 1 | 1433 | |
| 6319 | 14370 | A | 7068 | 3 | 324 | |
| 6320 | 14371 | A | 7069 | 3 | 421 | |
| 6321 | 14372 | C | 707 | 185 | 397 | |
| 6322 | 14373 | A | 7070 | 3 | 552 | |
| 6323 | 14374 | A | 7071 | 3 | 600 | |
| 6324 | 14375 | A | 7072 | 3 | 550 | |
| 6325 | 14376 | A | 7073 | 1 | 102 | |

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|------|-------|---|------|------|-------|--|
| 6326 | 14377 | A | 7074 | 3 | 1451 | GAVRTWGRGFQTEKQASLLNFWNPPT TAQVTIEAEPKVSXGKDVLLLVHNLPO NLAGYIWYKQGMKDLHYHITSYVVDGQ IIHYPAYSGRETYSNASLLIQNVTRDA GSYTLHIVKRGDGTGETGHFTFTLYRH SLDSALSLEVTGSSQPL*DTWENCPTLW LHCLMTELTSGLDVLPVISAIEVPSPRS GFPVSKGFKDNWKFHHPSLGCPWQGKL QRKHTSGGKVRLLKRRFQHCMLQVRTT SVETPKPSISSNLYPREDMEAVSLTCDPE TPDASYLWWMNGQSLPMTHSLQLSKNK RTLFLFGVTKYTAGPYECEIRNPVSASRS DPVTNLNLLPKLPKYITINNLNPRENKDV LAFTCEPKSENYTYIWWLNGQSLPVSPR VKRPIENRILILPSVTRNETGPYQCEIQDR YGGIRSYPVTLNVLYTTKHSGLYACSVR NSATGMESKSMSTVKVSAPSGTGHLPL NPL |
| 6327 | 14378 | A | 7075 | 3 | 435 | |
| 6328 | 14379 | A | 7076 | 79 | 1516 | |
| 6329 | 14380 | A | 7077 | 9970 | 11210 | MKDACGGIKGATQDNLLSTQ/PKLPMP YITINNLNPREKKDVLAFCEPKSRNYTY IWWLNGQSLPVSPRVKRPIENRILIPSVT RNETGPYQCEIRDYGGIRSNPVTLNVL CEYPLFLCGPGHQLNSKRPEARPLSLSPV QV*TTLLDIRPGHDSLPWEILGRHSLNQ EYKGRGALVMGH*GPTACNERNRGIPO AWA**T*MGFGCHRLCLGSEGHCVPLR DQEHPLPLDDITCGFILFPDGPDLPRIPP SFTYYRSGENLDLSCFADSNPPAEYSWTI NGKFQLSGQKLFIPQITTNHSGLYACSVR NSATGKEISKSMIVKVSXGWIPASLAIGF *VESIWLSEKSENICIPRLCPMGTSKSOI LLNPPNLSLQTLFCLFFCFLMADLVSGL RKVGRGLYQP |
| 6330 | 14381 | A | 7078 | 460 | 1832 | QPVLEFLDPRLISTEENTQAAETMGTL APPCTQRIKWKGLLLTASLLNFWNLPTT AQVTIEAEPKVSXGKDVLLLVHNLPO LTRATIWAYKQGMRLHYHITSYVVDG EIIHYPAYSGRETAYSNASLLIQNVTR DAGSYTLHIKRGDRTRGVTFYFTNLY LETTPKPSISSNLPREAMEVILTCNPET PDASYLW*LNGQNLPMTHSLQLSKAN RTLYLFGVTNYTAGPYECEIWEIRECQ ARSDPVTPEFSSRKLKPYITINNLNPGEE *GCL*TFICIEPKSENYTYIWWLNGQKPP/ VSSPRVKRPH*KTGSLIPTPVFTRKWQOG PYSMWNYGDRYGGVRLSPSSPLNCSSYG SRTSPRILPFHFTYVRFREENLDLFLGFT GIFNPPAQYSWDN*WKSFLTRGQKLF YSGHITTKHSGLYVCSVRNSATWQGA PNP |
| 6331 | 14382 | A | 7079 | 2 | 315 | RWSLCPLQAGVQWRDLCSLKPPEFEKQ FSCLSLPSS*DYRCPPPCANF/SFFFVFLV ETGFHHVQGAGLNLTSRDLLTSASQSA EITGMSHCPRPTLSNSRVL |
| 6332 | 14383 | A | 708 | 3 | 521 | CKMDAGFFRGTSAEQDNRVSNKQKIKL LKQLKFAECLEKKVDMKVNLEVIKPAW ITKRVTIELGFEDDVIEFIFNQLVKA*T KMEVPCV*SIAPSPY*VTAE*VSQCRSDP TPLMMQCVFGNPD SKMMQINLTGFLNG KNAREFMGELWPLLSAQENIAGIPSAFL EL |
| 6333 | 14384 | A | 7080 | 1 | 534 | |
| 6334 | 14385 | A | 7081 | 1217 | 1545 | |

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|------|-------|---|------|------|------|---|
| 6335 | 14386 | A | 7082 | 2 | 1665 | KKKKKQKNKKSSTGEASENGLEDIDRIL ERIEDSTGLNRPGAPLSSRKHVLYVEHR HLNPDTELKRYFGARAILGEQRPRQRQR VYPKCTWLTPKSTWPRYSKPGLSMRLL ESKKGLSFFAFEHSEYQQAQHKFLVAV ESMEPNIVVLLQTSYPYHVDLSLLQLSDA CRFQEDQEMARDLVERALYSMECAFHP LFSLTSGACRLDYRRPENRSFYALYKQ MSFLEKRGCPRTALEYCKLILSLEPDEDP LCMLLLIDHLALRARNYEYLIRLFQWE AHRNLSQLPNFAFSVPLAYFLLSQQTDL ECEQSSARQKASLLIQALTMTFPGVLLPL LESCSVRPDASVSSHRRFFGPNAEISQPPA LSQLVNLVYLRSHFLWKEPATMSWLEE NVHEVLQAVDAGDPAVEACENRRKVLY QRAPRNIHRHVILSEIKEAVAALPPDVT QSVMGFDPLAPSDTIYSYVRPERLKSLS SHGNTIALFFRSLAPNYTMEGERPPEG VAGGLNRNQGLNRLMLAVRNDMMANF HLNDLEAPHEDDAEGEGEWD |
| 6336 | 14387 | A | 7083 | 420 | 627 | |
| 6337 | 14388 | A | 7084 | 2 | 380 | |
| 6338 | 14389 | A | 7085 | 2 | 657 | |
| 6339 | 14390 | A | 7086 | 2 | 842 | |
| 6340 | 14391 | A | 7087 | 174 | 463 | GSLKQGMFPSGLNRRLPTESPLQILRATF L*KEVA*GLHQYHLPLQLLSGPVFGLTH LQSAPVFREKPDPPPELPSLRVLRRTLDS WGARTHNYGI |
| 6341 | 14392 | A | 7088 | 69 | 194 | |
| 6342 | 14393 | A | 7089 | 1348 | 2204 | TWRLDPQIISSPKPQPGGTYTLEVVKSSK SKKVLSHP*WPLRLWQRIGGSPEGGT QAPDGLPPPPRPKSERVSGPKLSGGKR /EGSHPGGPPHITHP/DGEEKAKSSWFGL REAKDPTQKPSHPVKPLSAAPVEGSPD RKQSRSSLSIALSSGLEKLTVTSGSIQPV TQAPQAGQMVDTKRLKDSAVLDQSAK YYHLTHDELISLLQRERELQRDEHVQ ELESYIDRLLVRIMETSPTLLQIPPGPPK |
| 6343 | 14394 | A | 709 | 730 | 983 | GAVAHICKSQFGRPRQAHQLRSRV*DQ PGQNDETPSILKIQKLAGHGGTRPLSQLL RRLRH*NHLNPGGGGCSELSRHCIPG |
| 6344 | 14395 | A | 7090 | 2 | 762 | |
| 6345 | 14396 | A | 7091 | 2 | 218 | |
| 6346 | 14397 | A | 7092 | 7 | 78 | |
| 6347 | 14398 | A | 7093 | 553 | 954 | SRSRRGQKRRRWSTVWRLSAGACALSM QTPSRTSWPTAPFRAIWRAETVAAWCRL RRPVWRVWSWCLPTPITRATPLGARS WPGWRMWPLQAGSAVPTLR*PLKF PLPRVPGRRPSGAQSHREQCLQT |

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| 6348 | 14399 | A | 7094 | 1 | 1215 | MTLKEHAAFKHLFNKAHLAPPLIHLTSL GHSTCFREHWVGDIVHRDLKLENIMVKS SLIDDNNEINLNKIVTDFGLAVKKQSRSE AMLQATCGTPIYMDRGWNSLEGSEQDR KMWDSLELPRDLLNVFEQNADNDMDDD EIQAEVLSGDGEELGNWSKGDSCYVLL KQLAAFCPCRLDLWNFKLERDDLGYLV EEISKQQSIQEATWVLLKAFSFIREAEHK NLENLQPDNAIEKKIPFSEEKFKLAAEICI SNQEANVNPQDNEKNVSRACQRSSQOP LPLPRVLGGKSGFVGWAQDSHAEIYTFG RILGKGSFGIVIEATDKETETKWAIKKVN KEKLLLMKSNFLQPVRTTLICAVQVSHL ANSFQLKSREKWRKPL*LKEHAAFKHLF NKAHLAPPLIHLTSLGHSTCFREHWVGDI VHRDLKLENIMVKSLLIDDNNEINLNKIV TDFGLAVKKQSRSEAMLQATCGTPIYM DRGWNSLEGSEQDRKMWDSLELPRDLL NVFEQNADNDMDDEIQAEVLSGDGEEL LGNWSKGDSCYVLLKQLAAFCPCRLDL WNFKLERDDLGYLVEEISKQQSIQEATW VLLKAFSFIREAEHKNLENLQPDNAIEKK IPFSEEKFKLAAEICISNQEANVNPQDNE KNVSRACQRSSQPLPLPRVLGGKSGFV GWAQDSHAEIYTFGRILGKGSFGIVIEAT DKETETKWAIKKVNKEKSTAYEKQFPAT SKDNFDMCSSSTSSKLLPAEIKGEMEKT PVTPSQGTATKYPKSGALSRTKKKL |
| 6349 | 14400 | A | 7095 | 1 | 770 | |
| 6350 | 14401 | A | 7096 | 7265 | 7684 | IVSLFLFILLVFWWWCFFFFFFFETVLLFS PRLQCRDV TSAHCNFCFPGSSDSRASAF RVARITGAHHD TWLIFCIFS RDRVLSCWS GWSRTSDLR*SALPKCWDYRCEPPCRA* FFFFLYPLTIPTSLPAPHYPPSLW |
| 6351 | 14402 | A | 7097 | 1 | 344 | |
| 6352 | 14403 | A | 7098 | 3 | 285 | |
| 6353 | 14404 | A | 7099 | 346 | 517 | |
| 6354 | 14405 | A | 71 | 134 | 450 | QSPDSMNAREFRRRGMEMVDYVAYYM EGIEGLLVYPDV*PGYL RALIPAAAPH*L DTCEDIISDAEKIIMPGLSHWSPDLFVY FDSVSSYARML EDMQCGALDC |
| 6355 | 14406 | A | 710 | 108 | 418 | GWGGLLIARPPFKRGKSSGPVGH LKPRG VGRRRG*NVNLC PKSSNPQGGLGERPRE LRDKATVSALANFTARKGC*LRGPEGGQ PGPRGKLFPGVPGVQGGQ |
| 6356 | 14407 | A | 7100 | 3 | 173 | |
| 6357 | 14408 | A | 7101 | 256 | 352 | |
| 6358 | 14409 | A | 7102 | 1 | 203 | |
| 6359 | 14410 | A | 7103 | 1 | 112 | |
| 6360 | 14411 | A | 7104 | 1 | 1213 | |
| 6361 | 14412 | A | 7105 | 3 | 413 | |
| 6362 | 14413 | A | 7106 | 45 | 537 | |
| 6363 | 14414 | A | 7107 | 2 | 224 | |
| 6364 | 14415 | A | 7108 | 179 | 393 | DKWRRLPWKRGVEVG TAGSLAKAFGFF AEAKTEPREGCSES GVRISYQ*VQQTNS KCLKY*MEPARPTFSP |
| 6365 | 14416 | C | 7109 | 21 | 410 | |
| 6366 | 14417 | A | 711 | 274 | 394 | SPFPKEVGGGKFLNLGGQRFWGPKFGPL FSAKTKKGTSFLK*GFKNPQAQGGKPPFF LKIQN*PTLGGGPLNPHFLRRLGGENF*T SEGKGFGDPNLALCSPPKQKKGLLF |
| 6367 | 14418 | A | 7110 | 3 | 178 | |
| 6368 | 14419 | C | 7111 | 134 | 295 | MNSVPGLAKSVGLLRTRYDSPKQPLLCS EAVVLICKDL SRGWQKPGTQGIGG** |
| 6369 | 14420 | A | 7112 | 3 | 864 | |

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| 6370 | 14421 | A | 7113 | 3 | 155 | |
| 6371 | 14422 | A | 7114 | 1 | 122 | |
| 6372 | 14423 | A | 7115 | 84 | 579 | NWKAGMGRPSTADYAMFKVVHEVDK YRFTYAYFAGGDAEDAFDGYDFGDDPS DKFFTSVHNGMQFSTWDNDNDKFEGNC AEQDGSQGWWMNKCHAGHLNGVYY\QG GTYSK\ASTPNGYDNGI\WATWKTRWYS MKKT\TMK\IIPFNRLTIGEG\QQH\HLGGA KQAGDV |
| 6373 | 14424 | A | 7116 | 19 | 418 | VEMGFCQADQAGLELLTSGDPPASVSQS TGITVLSLFFFETESRSVAQAGVQWRDL GSLQRP\PPGSRHSPASASRVAGTTGARR HAWLIFLYF/LVETGFHRSQDGLDLLTS *SARLSL\PKCWGYRREPSAR |
| 6374 | 14425 | C | 7117 | 207 | 401 | MGXXIFXPLXKTPFFPGVWGKNFSPGP GXPXPP\PRGGPPPLFFPQKKGXPPPPFP KVLGLQA* |
| 6375 | 14426 | A | 7118 | 2 | 681 | FFEMESRSVAQAGVQWRDLGSLQAPPP GFTPF\SCLSL\PRSWDYRRPPTLLANFFVF LVETGFHCVSQDSL\DLLT\RSARL\FFFFF ETESRSVAQAGVQWRALGSLQAPPPGAS RHSPASASQVAGTTGARHYARLIFVFLV ETGFHRSRDGLDLLTS*SARLGLPKCW DYRREPPRPAVRVYFYNRSVFIEYVQFC KLLFTFKINVR\SNILGSPN\ILKSLLKNLN |
| 6376 | 14427 | A | 7119 | 3 | 265 | FFFETESRSVAQAGVQWCHLGSQPLP\A GSSDSPASTSRVAGVITAT*VAGITV RHHAWLIFVFLVETGFHHVQAGLEHL DLR |
| 6377 | 14428 | A | 712 | 59 | 306 | FGTDRTAVQTSSQRLCLPWVAQKTYW LLVPSSLLKDLKEKKEVVEEA*NGRDAP ANGNAVSVCFAP\EPWQLPPHKIFPVLL |
| 6378 | 14429 | C | 7120 | 359 | 583 | |
| 6379 | 14430 | A | 7121 | 279 | 566 | FRRRFLISL\FFFFL\FFFCFF\FFETESRSVA QAGVQWRDLGSLQAPPPGFTPF\ALSPRL ECGAILAHCKLLLP\GSSHSPA\ANRVA GTTGTRHH |
| 6380 | 14431 | A | 7122 | 237 | 523 | PQEFKTS\PGNVARPQLYN\FFFFFETESR SVSQAGVQWCDLGSQAPPPGSHSPA SAS*VAGTTGAHHHARLLAFVFLVETGFH CVSQDGLDLLT |
| 6381 | 14432 | A | 7123 | 1023 | 1459 | KGTRKRGQGIKVHLPILLFNLCFCTFG LFLVFLFP\FFFFF\FEIESHVAQDGVQ WCNLGSLQPTPPGSSDSPASAS*VAEITG TRHYAWLIFLFL/VEMRFHHVQAGLEL TSGDPPASASQSAGIRVMSHRLVFLYY K |
| 6382 | 14433 | A | 7124 | 1794 | 4614 | RFFS\FFFFFETESHVAQAGVQWCNLGS LQAPPPGSRHSPASASRVAGTTGAHHH ARLIFVFLVETGFHRISQDGLDLLTS*SA RLGIPK\CDYRCEPPHLASI |
| 6383 | 14434 | A | 7125 | 2 | 441 | FFFFFETESRSVAQAGVQWRALGSLQAP PPGSRHSPASASQVAGTTGARHYARLIF VFLVETGFHRSRDGLDLLTS*SARLGLP KCWDYRREPPRPAVRVYFYNRSVFIEYV QFCKLLFTFKINVR\SNILGSPN\ILKSLLK NLN |
| 6384 | 14435 | A | 7126 | 3 | 226 | CETESRSVTQAGVQWSDLGSQAPPPGAS RHSPASASQVAGTTGAHHHARLIFVLLV ETGFHRSQDGLDLLTS |
| 6385 | 14436 | A | 7127 | 153 | 504 | KH\FFFFFETESRSVAQAGVQWRDLGS LQAPPPGSRHSPASASRVAGTTGTRHRA WLIF/VYFLVETVFHRSQDGL*KL\YRE NSIENILVQKCLKVYFSHCSRSEITVTGN NLL |

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| 6386 | 14437 | A | 7128 | 3 | 313 | FLFFETESCSVAQAGVQWHDLGSLQAPP PGSCHSPASASQVARTTGTRHHRLIFF VFLVEMGFHHVSQDGLDLLTLGSGHLSL PKCWDYRCEPPHPSSPSY |
| 6387 | 14438 | A | 7129 | 3 | 307 | FFFFFETESRSVAQAGVQWRDLGSLQAP PPGSRHSPASASQVAGTTGARHYARLIF/ VVFLVETGFHRFSRDGLDLTS*SARLGL PKCWDYRREPPRPAYF |
| 6388 | 14439 | A | 713 | 171 | 565 | TLAFLIPICIGSPACPTMSDAAVDTSSEIT TKGLKRRRRKLWEEAENGKRRPCLTGN AENEGK WGSREADNEVHQKEE*CGEEQ EEEEEGDGEEDGDEDETL SATVTRAT EDEDDDAVAPTKQTTRLDE |
| 6389 | 14440 | A | 7130 | 2 | 91 | |
| 6390 | 14441 | B | 7131 | 3686 | 14131 | MTNAFQYVQKNRGIDSEDAYPYVGQSY YNLVSSSQEESCMYNPTGKAACRGYR EIPEGNEKALKRAVARVGPVSAIDASL TSFQFYSGVYYDESCNSDNLNHAFLA VGYGQKGNKHWIKNSQSAQTVLTPDE CLLLGYLDKGKLRKDKAGSLQWAYM AIARLGGFMDSMPTGIAIWGALX* |
| 6391 | 14442 | A | 7132 | 8044 | 8378 | YIDVKTFFFFFLPETESHVAQAGVQWH DLSSLQPLPFGSSDSPASASRVAGITGTH HHAWFIFVLVGTRFHHLGQAGLELLTS SDPPASAPQSAGITGVNHHHTQPQKFI |
| 6392 | 14443 | A | 7133 | 3 | 283 | |
| 6393 | 14444 | A | 7134 | 2 | 177 | |
| 6394 | 14445 | A | 7135 | 1 | 491 | |
| 6395 | 14446 | A | 7136 | 3 | 612 | |
| 6396 | 14447 | A | 7137 | 2 | 137 | |
| 6397 | 14448 | A | 7138 | 1 | 2631 | |
| 6398 | 14449 | A | 7139 | 2 | 112 | |
| 6399 | 14450 | A | 714 | 1 | 1497 | |
| 6400 | 14451 | A | 7140 | 67 | 245 | AYNLSGQYGLVDPEFEYFYLCCWLP L*LGGKCLWVLPVSVSGDRNDNDQAER NGSHL |
| 6401 | 14452 | A | 7141 | 356 | 2252 | RSFLDEEFPHYDSLSCADAIQQPLQEKLK QCCHKLYGGQEARIHQTPLTKHTCWY TPLLDALSLDSFTAVPTLESTPFSGVANQ IHTLCERPTYGEVKDGLDVKRQHKCPG PTSGPSPGTNLSGCIRMNDPSPMEENG ERVCPESLLQSRGYSSLPLRHTSSDGTI TSSDPGLEILNMASCDLDRNSLCKKEED TRSASPTIEAQGTSPAHDNIAFDSTSKD KTILNLEAKEPETIEEHKKEHASGDSVV SPLPVTTVKSVMNRQSENTSANEKEVEA EFLRLSLGFKCDWFTLEKRVKLEERSRD WAEENLKKEITNSLKLLESLTPLCEDDN QAQEIIKKLEKSIKFLSQCAARVASRAEM LGAINQESRVSKAVEVMIQHVENLKR YAKEHAEELELKQVLLQNERSFNPLEDD DDCQIKKRSASLNSKPSSLRRVTMALLF LPRNYLGNAGMVAGMENNDRFSSRRSS SWRILGSKQSEHRPSLPRFISTYSWADAE EEKCELKTKDDSEPSGEETVERTKPSLS EKKNNPSKWDVSSVYDTIASWATNLKS SIRKANKALWLSIAFIVLFAALMSFLTQ LFQKSVDAAPTQQEDSWTSLEHILWPFT RLRHNGPPPV |
| 6402 | 14453 | A | 7142 | 1 | 835 | |
| 6403 | 14454 | A | 7143 | 1 | 3735 | |
| 6404 | 14455 | A | 7144 | 2 | 1161 | |

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|------|-------|---|------|-----|------|---|
| 6405 | 14456 | A | 7145 | 126 | 572 | NFSSNKWNTSQNFANMDNSAQKNERTG KHPRRASEVQKNDIPGPGFYNVHQSPV SNSVSLSKKGTCTMFPSMCARLDTIVSKY PAANAYTIPSDFISKRDFNSCSCSMFQLPS FMKALKFET/PLAPNYYNASVSCCKRRN NVCTRAGF |
| 6406 | 14457 | A | 7146 | 1 | 1261 | |
| 6407 | 14458 | A | 7147 | 107 | 227 | |
| 6408 | 14459 | A | 7148 | 3 | 407 | |
| 6409 | 14460 | A | 7149 | 3 | 608 | |
| 6410 | 14461 | A | 715 | 32 | 3730 | NSERRGLGMSLADELLADLEEAAEEEEEG GSYGEEEEPAIEDVQEETQLDLSGDSVK TIAKLWDSKMF AEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIEN ELNIIHKFIRDKYSKRFPPELES LVPNALD YVRTVKVSAEKELGNSLDKVARAIEEPW QQILT NATIMVVS V TASTPQGGQLSEE ELERLEEACDMALELNASKHRIYEVES RMSFIAPNLSIIIGASTAAKIMG |
| 6411 | 14462 | A | 7150 | 2 | 212 | |
| 6412 | 14463 | A | 7151 | 3 | 91 | |
| 6413 | 14464 | A | 7152 | 1 | 115 | |
| 6414 | 14465 | A | 7153 | 1 | 1279 | MGDTPRQFGGARPRSGGALRGCRSRGG GNRRGLCLSRALANGDRRLTMDDDIAA LVVDNGSGMCKAGFAGDDAPRAVFP VGRPRHQGVVMVGMGQKDSYVGDEAQS KRGILTLKYPHEHGVITNWDMEKIWHH TFYNELRVAPEEHPVLLTEAPLNPKANR EKMTQIMFETFTNPAMYVAIQAVLSLYA SGRRTTGIVMDSGDGVTHTVPIYEGYALP HAILRLDLAGRD L TDYLMKILTERGYSF TTTAEREIVRDIKEKLCYVALDFEQEMA TAASSSLEKSYELPDGQVITIGNEARFRC PEALFQPSFLGMESCGVHETTFNSIMK/C DVDIRKDL YANTVLSGRTPPCTLGADR MQKEITALAPSTMKIKIIPPERKYSVWI GGSILASLSTFQQM WISKQEYDESGPSI VHRKCF |
| 6415 | 14466 | A | 7154 | 1 | 111 | |
| 6416 | 14467 | A | 7155 | 143 | 295 | |
| 6417 | 14468 | A | 7156 | 186 | 437 | |
| 6418 | 14469 | A | 7157 | 3 | 356 | |
| 6419 | 14470 | A | 7158 | 1 | 220 | |
| 6420 | 14471 | C | 7159 | 102 | 407 | MDAGLEAMQKYGKAAPGDRTMLDSLW AAGQELQAWKSPGADLLQVLT KAVKSA EAAA EATKNMEAGAGRASYISSARLEQP DPGAXAAAAAILRAILEVLQS* |
| 6421 | 14472 | A | 716 | 3 | 117 | HKRPLMASYLLFFCSFVRVE*TIITCLT** ECHRYNR |
| 6422 | 14473 | A | 7160 | 1 | 2302 | |
| 6423 | 14474 | A | 7161 | 1 | 178 | |
| 6424 | 14475 | A | 7162 | 60 | 413 | |

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| 6425 | 14476 | A | 7163 | 2 | 1420 | NSGVGAGARRAARCRAAAAVGTARS PALGMALLVLGLVSCFFLAVNGLYSSS DDVIELTPSNFNREVIQSDSLWLVEFYAP WCGHCQRLTPEWKKAATALKDVVKVG AVDADKHHSLSGGQYGVQGFPTIKIFGSN KNRPEDYQGGRTGEAIVDAALSALRQLV KDRLGGRSGGYSSGKQGRSDSSSKDVI ELTDDSFKNVLDSEVWMVEFYAPWC GHCKNLEPEWAAAASEVKEQTKGKVKL AAVDATVNQVLASRYGIRGFPTIKIFQK GESPDYDGGRTSRDIVSRALDLFSDNA PPPELLEIINEDIAKRTCEEHQLCVVAVLP HILDTGAAGRNSYLEVLLKLADKYKKK MWGWLWTEAGAQSELETALGIGGFGYP AMAAINARKMKFALLKGSFSEQGINEFL RELSFGRGSTAPVGGGGFPATIVEREPWD GRDGELPVEDDIDLSDVELDDLGLKDEL |
| 6426 | 14477 | A | 7164 | 547 | 980 | |
| 6427 | 14478 | A | 7165 | 3 | 1290 | LYSSDDVIELTPSNFNREVIQSDSLWLVEFYAPWCGHCQRLTPEWKKAATALKDVVKVGAVDADKHHSLSGGQYGVQGFPTIKIFGSNKNRPEDYQGGRTGEAIVDAALSALRQLVKDRLGGRSGGYSSGKQGRSDSSSKDVIELTDDSFKNVLDSEVWMVEFYAPWCGHCCKNLEPEWAAAASEVKEQTKGRVKLAAVDATVNQVLASRYGIRGFPTIKIFQKGESPDYDGGRTSRDIVSRALDLFSDNAPPELLEIINEDIAKRTCEEHQLCVVAVLP HILDTGAAGRNSYLEVLLKLADKYKKKMWGWLWTEAGAQSELETALGIGGFGYPAMAAINARKMKFALLKGSFSEQGINEFLRELASFSGGSNGTL*GGGGFSLPIVEREPWDGQCGRFPWGDDH*PSVDAELDDLGLKDEL |
| 6428 | 14479 | A | 7166 | 335 | 519 | ILFPGSGQGLRSSDQKAACLALL*FQKRS EMYKTK*FWGRKMSQFFSVVRHTNPG SRLWA |
| 6429 | 14480 | A | 7167 | 2 | 386 | |
| 6430 | 14481 | A | 7168 | 311 | 493 | |
| 6431 | 14482 | A | 7169 | 2 | 82 | |
| 6432 | 14483 | A | 717 | 1007 | 1118 | APGPCPNQTLARDSGWVG*KNHQLCTC VCVCVCVCVC |
| 6433 | 14484 | A | 7170 | 51 | 347 | |
| 6434 | 14485 | B | 7171 | 188 | 353 | XDVVVPVANCQVQEYNSNPKEHVTLRD YITYWKEYIQAGYSSPRGCLYLKDWHLCS* |
| 6435 | 14486 | B | 7172 | 188 | 353 | XDVVVPVANCQVQEYNSNPKEHMTLRD YITYWKEYIQAGYSSPRGCLYLKDWHLCS* |
| 6436 | 14487 | A | 7173 | 753 | 1216 | QVVEVGPPRGRHPSAAGCPSPA*RRWKT RRAGWAARSPAQRRRRRRPPRRRLP GPEPGRRRGHRPPGLSGCRRGRASRGP SSSARVEGPSSSLPPERKR*GPASEPEDA GRRVSAPPAPGARACTHARGSPRSSLRR RRAAEAARSALGLV |
| 6437 | 14488 | A | 7176 | 27 | 285 | VFFFFFFLRRSLALLPRLECSGTIVFLVE TGFTMLARMVSIS*PRDLPALASQSAGIT GVSHRAPASFNFLTINILPILLWTF |
| 6438 | 14489 | A | 7177 | 12 | 336 | SPVQL*F*LFLVFC*LWSWSAVVYLGPL GTPSADAHT/AGLSKTPPHWAARARLDD VFSRLTFSSHSLNMELVQDLTASAPMYS STSRDPP/CLGLPKCWDYKREPPRAH |
| 6439 | 14490 | A | 7178 | 74 | 463 | HISQHDSRYLQVLLASYKTASLFFFLRQ SL/DSVTQAGVQWRDLGSLQAPPGFTPF SCPQSPK*L/SSWDYRRPPRPANFFCIFIV EKECFILLARMVSISWPRDLPASASQSA GITGMSHRARPAQVS |

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| 6440 | 14491 | A | 7179 | 1 | 412 | TRMGLPDASRRRTCRMDEPGWQEAMSS A*GRITLQRLSTGPEGQGGREKVGPEGG SENPQQPKAAGVLSKHLPGAPAPPPQRP PSSPPPLAGPLTERVEKVCDFLDAAGDY LN/GTPG*PSPGESPAADPPVPPWPP |
| 6441 | 14492 | A | 718 | 1692 | 2123 | SQPRFSWTQERLRLFPGLLNSLIVSQAT QGPKLKSCLGSLMAFTFKKMEPSPMSCS PQCFGKPMGRLSGGQKFKNQAGQYH KTPSLRKSCKLASHGGVHLWS*LLRRLR QEDCLILGIRGCSEL*LHLCPPSATQRDP LS |
| 6442 | 14493 | A | 7180 | 117 | 295 | |
| 6443 | 14494 | A | 7181 | 279 | 1065 | IQHPRLSADDFRVNCETEPAM/*HAVEN DIHGLCELQLETEIQAFKEELL/FMKKNH EEEVKGLQAQIASSGLTVVVDAPISQDFA KIMADIWAQYDEVAQKNREELDNRSQ QIEESTTVVTTQSTEVGAAMTELTR TVQFLEINLDSMRNLKASLENSLREVVA RYALQMEQLNGILLHLESELAQTWAEQ QCQAQEQALLNIKVKLEAAIATYRRL EDGKDFNLGDTLDCSNMQTIQKTTR R*TRQIVDGKVVS |
| 6444 | 14495 | A | 7182 | 60 | 846 | IQHPRLSADDFRVNCETEPAM/*HAVEN DIHGLCELQLETEIQAFKEELL/FMKKNH EEEVKGLQAQIASSGLTVVVDAPISQDFA KIMADIWAQYDEVAQKNREELDNRSQ QIEESTTVVTTQSTEVGAAMTELTR TVQFLEINLDSMRNLKASLENSLREVVA RYALQMEQLNGILLHLESELAQTWAEQ QCQAQEQALLNIKVKLEAAIATYRRL EDGKDFNLGDTLDCSNMQTIQKTTR R*TRQIVDGKVVS |
| 6445 | 14496 | A | 7183 | 645 | 861 | KYYRKRGIHSAIDASQTPDVVFASILA S*ATCKDLVFI*CWVQEGISFHPCEAM GGNDRTGKEKLPSG |
| 6446 | 14497 | A | 7184 | 2 | 1327 | RPQSLSPVLSLSPDSMSFTTRSTFNYS LGSVQAPSYGARPVSSAASVYAGAGGS GSRISVSRSTSFRGGMGSGGLATGIAGGL AGMGGIQNEKETMQSLNDRLASYLDRV RSLETENRRLESKIREHLEKKGPQVRDW SHYFKIIEDLRAQIFANTVDNARIVLQIDN ARLAADDFRVKYETELAMRQSVENDIH GLRKVIDDTNITRLQLETEIEALKEELLF MKKNHEEVKGLQAQIASSGLTVEVDA PKSQDLAKIMADIRAQYDELARKNREEL DKYWSQIEESTTVVTTQSAEVGAAETT LTELRTVQSLNLDLSMRNLKASLEN SLAREVEA/RRTPLOMEQLNGILLHLESE LAQTRAEGORQAQYEALVNIKVKLE AEIATYRRLLEDGEDFNFGDALDSSNSM QTIQKTTPPG*VGLGKVVS |
| 6447 | 14498 | A | 7185 | 2 | 345 | FFFFFETESRSVAQAGVQWRDLSSLQA PPPGSRHSLASAS*VAGTTGVCHHARLI FVFLVETGFHHVSQDGLNLLTS*SAGLG LPKCWDSEKLFFFGDKSFRFCCPGWST MV |
| 6448 | 14499 | A | 7186 | 178 | 388 | RREPLHPANLLFFFFFEMESPSVAQAG VQWRDLSSLQAPPA*GCHSPTSLS*VAG RLRNKNCLNPDAW |
| 6449 | 14500 | A | 7187 | 546 | 850 | FSVLFFFESESCSVLQAGVQWRDLGSL QPPPPGSSHSPTSAS*VAGTTGTCHHTQL IFIFLVETGFHHIGQASLKLLTS*FAHLGL PKFWDYRCEPPHPA |
| 6450 | 14501 | A | 7188 | 4 | 410 | PIERPHELKHRLPHVQKLVEDVGDGVIP AALEEGQAGWSHGFLVFLVEIKSAEGP/P GPADSRVRGVRPQRSQSAGPA*RAGRQ DGVCRSLGQGRGGGRATSLVLHPPGY GCWFSVGVPSLPQYTGIRSSSPRTRG |

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| 6451 | 14502 | A | 7189 | 148 | 268 | LQPR*PLTCAPPPCPVQTQTHPISVSQTLL GLEFCCSLSL |
| 6452 | 14503 | A | 719 | 1 | 371 | HRHCHPSHTVDGRMESIDVATDGG*RTG VLAVSGLSVSLRTAELSTRKLLMNSEQRI NRIMGFHLGSGGAVE*RHTQSMQHDSD KLNSLIIPSVSKRVVLVDSVCTGTTDHQG GVLERKVTTL |
| 6453 | 14504 | A | 7190 | 397 | 1449 | RSHPSGTGRRTSRLESWFLGVSCKKSKV REGPLGPA**AG*RGVRPQRSQSAGPA*R AGKRQDGG/SPEPRAGVGGVGTQSP/GP SGASGYPGMLVSKPVGGTSASWLPAGC PIPS*LS*QRSQSGSPSSCLIGHLLALWAAF GLGVTSLPQYTGIRSSSPTA*ATVQGDGSG HKGGTGGTGLGRGRNTQPDAAACGRGHR SSPTR/RPHGNPNNGNTGCAEGGQARSLLP KLAPKLPWPVSPVAVGPGDFGWRRQ AQYQSSLWDLSSPRNTLGRSATSAGPAP PALLGAGSGRSSGTSPAAPGCSSRCHCW ASAPAGVSGGPGGRGAEAPPSPTLAQR GSPPGAIAIFPPACGIPP |
| 6454 | 14505 | A | 7191 | 47 | 1654 | LHVPARPPGCCGAFLAGGPCPGWGQPR AQLWPQ/SAAPGPPHPALPSPVFETWP RLLSH*S/RPA/VEQCPEPHVYPDPASS WVPKSASPPRVACPCPPAL*/PFGDSCSCL LCTAGLRGPGHDTLPQVWVRPHPGAS AEM*AHKPPPLAQKPPRPSISVPQPSAQL WYPAGPWVPT*AGTWLGYGAI*SPQGLF SFYEMEHGVPA SLNPPKWEPHDRV*LGG GR*GKSEVPRGTPSLTGLFRGVPGPPAI TGTQKHPFNDMVSFLISFFCLFCFGFQL G*/PPGL*SIHIEPLTGLPGCQG*Å*P*VLL STAGSAHAV**GSELVHLQS*LHFPSCFP PPVLALDLQVCRPALSAFLACGPPAIPGS WSPEGVSLWMGVRGVPLCGLSLYPA L*NLARRGPGQPFTGK/IGEGTPTPHKPC NHQVRKLGVLPGQGVKTKIEVGFWGPT R/PKAGETR*VGRVPQSLA*PQCVSPEM LP*LSGTPGRSWG/PVLSPTPAHSQALRL CGHSPPCWSLVIGLELYFDAMKTLFISNV YIF |
| 6455 | 14506 | A | 7192 | 4 | 496 | NRRTERLGRWCPCTGAWPAPVNLAKLA PS/HDSEQVSGCVPLAQSMAPPGPAWR AGHHRRRSENPRPGFFGSFFKRFGTNR GWSRRDDDPGGPGSGSRWPPAPRRGGQ WRCPREPG*RRSSSAGRGSSPCALRHRA TKASSSCSPCPPTPTKRERALAAASC |
| 6456 | 14507 | A | 7193 | 3 | 514 | SVPKREELQGHHRVRGGEHRVWTRQDV LQHRLPATSVWTHPVLPTARAPALGRA SGAARRTAARAAPLAPVAAAAAPGRA RPTTTWPASPPSPRSASPPTAPSSACWSP TP/GSPFALRPLRAGLGAVYTRSRAHPRR PLPAHLCLVRHRATKASSSCSPCPPTPT KR |
| 6457 | 14508 | A | 7194 | 2 | 324 | GGGFRPLFPPLWRPKPVGPVRVEIFGPAC PPWENPFSLKIPNLPGVVGPSDYSRFSEG LARKLPLTRKGRFR*PKFPPLPSFLGKKR EIRFPKKTKKKIFINSSSC |
| 6458 | 14509 | A | 7195 | 3 | 344 | ERQKLHYKYSKQFLTQFDWNTNWKAE EPEEQKLATMFREQQKSC*ARMVQRQ RH*NKLN*NQQFLRSLEDLEENQSSFTD EQSDLRKEMARLQTKLMKETLQQDLALI HSC |
| 6459 | 14510 | C | 7196 | 68 | 319 | |

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| 6460 | 14511 | A | 7197 | 56 | 945 | HRKLDNRNYSRHMGGSPGPEPRRAEEPC PPRCMPTKETGAFRSHTRSRLGPF*SLAE PPF/PRVPVSRGPLSASSPPPLSSRDAGLQ TSQLLP/SWGWSIPNSIPELDLGPLSPTGR LSAAFPSCRSPSTGNGKDATSQVDSHPA PSFRSPGLELSRCPGDPVTATSPHEWTQQ GKDWRPCSCPLVMQAPPTSHIFLPPPSRS SLRRPRAPSGCPWGCLG/RPPAGPWATP LAGLPSWSGVRLPG*GVLPASRGSG*G PPRHRPDAGSERPAAAAAGFAGP*VCSN SSALPSVYEGLL |
| 6461 | 14512 | C | 7198 | 161 | 262 | MLKGIPCLHPPLASSSQSDNSQKCLQTLF SLPR* |
| 6462 | 14513 | A | 7199 | 132 | 1007 | NPQAPQATKKEGRKNARKGGSVCSGVP WGPPPRKVPTVPWRAESPGPGESHAGFE SLRHGHAGAGPKGMPRLPTENTVSAE GSTGGESGARVPDTGKGL*PATHPLPWG SLSGF*ETQRL*G/PCLEGG/YPGEGQSL ETFLAVV*LGAAG*GWVEARDTFKHPTV CRTAPTKESSPETQQSGAGIGEAAVWC QPHIGRRALQEACGEHGDGRFGGNHA E/PDRGGNEAAPTNNNPTHPDGHTSL*G/ VTGPSP/PGRWGN*GPESSEPLDPPPH PPTS WCGLFLRSFRLHS |
| 6463 | 14514 | A | 72 | 218 | 428 | LSSLPTTISR VFYNLS/CSHL*YSLKHFIY LFIYLFYLFYLFIFETESPLSPRLECRSGI SAHCNRL |
| 6464 | 14515 | A | 720 | 3 | 408 | DAWANARSVRLEVAGLRRDL*R/CSER WPLARATPFCFGSAMPYQEESENLSLQ ALESRQDDILKRLYELKAAVDGLSKMIQ TPDADLDVTNIQADEPTLTNTALDLNS VLGKDYGALKDIVINANPGFPPLF |
| 6465 | 14516 | A | 7200 | 59 | 326 | TGLSPGSEIGALPGNLV*APFFFNPKNLP GAVGPVGPVPPFWGG*ARLGGPRSSEFP LVGLGPLAFRLGTLGPVFKKNQESKKK TSV |
| 6466 | 14517 | A | 7201 | 3 | 263 | TLRKKFFQPGKTRFSPHTPFSFFPQKK EKL*GGNPPKFPPPKKKPPPKP/HPSSS PPPKSSSSQSHAPPKGPPPEPLKKNPP |
| 6467 | 14518 | A | 7202 | 1 | 348 | RYRSGIPGRRTRAGETPSLLKIQQPG/GD GARS*SRLRLRQENRLNPEGRCSEL RLCHCTPAWARE*DSLKKKKKEFKIPIY FLTLLWDFRTQYTY SIPMCLLCGEMVT DI |
| 6468 | 14519 | A | 7203 | 3 | 441 | SSGSRSECRFLPLEFNVVLEILAGAIRQ/Q KE/IKGIHIGKVVSIKLTEVINKFKVA*Y KIN/SNKSVCYLTNNEQLEKKFKISSSS SSSSSSSSPNH*GKDLYNENLKTLLKEM KENKWINIPCSWIRRLNNVNISILSKVTY KF |
| 6469 | 14520 | A | 7204 | 3 | 310 | TINCVDITDIYRLLHPSTADCTFCPSSNGI FTNIGHILGKTHINKFISIEFI*CLLSDHRI KLEINNKTWKIPKYL*INTLIKEKCEEQF *NTVN*NPNTI |
| 6470 | 14521 | A | 7205 | 3 | 88 | |
| 6471 | 14522 | A | 7206 | 2 | 1053 | TMPSSVSWGILLAGLCCLVPVSLAEDP QGDAQAQTDTSHHDDHPTFNKJITPNLA EFAFSLYRQLAHQSNSTNIFFSPVSIATAF AMLSLGTKADTHDEILEGLNFNLTEIPEA QIHEGFQELLRTLNQPDSQLQLTTGNGLF LSEGLKLVDFLEDVKKLYHSEAFVNF GDTEEAKKQINDYLEKGTQGGKIVDLVK ELDRDRTVFALVNYIFFKGKWERPFVK DTVEEDFHVDQATTVVKVPYELKRLGM FNIQHLKKLSSWGAA**KYLGNATR LLSCLDGGGNLQHLGKIELHPTIHSFSL GEIEGQ/DRSCPALHFTQIVPLLGTYGFLK SVLGFNWGIH |

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| 6472 | 14523 | A | 7207 | 2 | 334 | RDPPGPGPAITARERKCAKHPSLHQTTV THLKL*VVLAQLTLEETHCHANPDLIFE DMEAMTDLELHELCCQDRHINNQLDM DLILDGKGFQVVGILSELKQKDSSN |
| 6473 | 14524 | A | 7208 | 1 | 306 | LRRS/LCSVAQAGVQWWDLSSLQPLPG PMPFPRSLPSSWDHRRRPLPANFLYF* *RRGFTVLARMVVIS*PCDPPASASQSAG ITGVRHRTQPPRYVFM |
| 6474 | 14525 | A | 7209 | 156 | 331 | QPLILRCLPPRSIYRFNSIPIKIQVTFF*EK EKSLLKFIQNLKGP*ITKTILRKKKVD |
| 6475 | 14526 | A | 721 | 25 | 494 | PLTVSERWPLARATPFCFGSAMPYQV KPYHGGGAPLRVELPTCMYRLPNVHGR SYGPAPGAGHVQESNLSLQALESQD DILKRLYELKAAVDGLASRRIKPPRATLD ETNIIQADEPTLTNNALDLSVLGKDYG ALKDIVINANPGSPPLS |
| 6476 | 14527 | A | 7210 | 50 | 269 | FRNIKHQRDYNEQ*YG/NKLDNPEDMNK F*ETRYT*/PNLHQEEIGMLNRPVTNKVL *LVIKIPLTKKSPEPDGFV |
| 6477 | 14528 | A | 7211 | 584 | 1001 | ILKLWGVGTG*TKVPPQVPPTPHSRA*GP PRRECLRRQ*PRP*SPGFGPLSFTSVELM GVKTVLSQASRERGSWG*KGSPLNGR QFWAQGGA/LSWVAWGGGGGWRGSNG KG*QPGEQSSQLPLPPRTWRMGPGQ |
| 6478 | 14529 | A | 7212 | 79 | 315 | ERDFLFVPRVGFQGNL*LFPLPGLPL FSGLTLP/RNWGLRGPFITPG*FLDFLKK RGFNIVAQVGLKFWTSGDPPPL |
| 6479 | 14530 | A | 7213 | 247 | 827 | KYLEIVLLKY*RNSCSCVILKCSFSLIL LELTMKKKILCLYI*LLTVQTVTQWIFV CPPKTF*S*AIFNKDV*IILILIVKLLLV WVQYILSFLILLKLN*DVCFVLLH*VLF KNSLCVYELILDFLYSMIKDN*KFCTFL GPWKVFV*YFLRMSIYFVHNKLALYMK MGLNQIKKVMLLSSKKK |
| 6480 | 14531 | A | 7214 | 1 | 311 | LNREKLKAFPLTSGT*QE/CPLSPLLNFNV REVLATAIRQEKEIRGIQIGKEEVTLSLFV DDMILYLKPKDCTKKPLEL/NTFSKVA* YIINIQISVAFLNAKSK |
| 6481 | 14532 | A | 7215 | 6 | 375 | ESLRSPSRFS*PSPAYRGHGCSRPAETH NGDPCRAEALSDTPVPQSSGSDHNEKG PSRPFQLH*PGPWGPAGCRGPAPTPW RLAPAGPLRDSQEDPPSPPEPGSGGAAGQ GGG*GLSCFP |
| 6482 | 14533 | A | 7216 | 80 | 251 | GKFHISKTL**NINILL/VQLSVVAIGINY RTSNVEVLLQFLEDQNTFPNFEHLAYR |
| 6483 | 14534 | A | 7217 | 161 | 333 | GKFHISKTL**NINILL/VQLSVVAIDINIY RTSNVEVLLQFLEDQNTFPNFEHLAYW |
| 6484 | 14535 | A | 7218 | 3 | 299 | PPFRTHQARRFAPTQDWQIGFTQH/RP/G VRKQKYL*VDTFTG*VKAFPTRSDKA TAVITSLSDIIPRIGLPTCQSSSTLALISQ ISHPSCQAATIQ |
| 6485 | 14536 | A | 7219 | 526 | 1108 | TQTKNSKIYFN*LLF*ETGPHSLSPQAGV WWHSHISLQPOPGLKHPPHPSLLSSWD YRHTSLRPANF*KIFVETGSLHVAQDGLE FLGSSPPVSASQSARIAGMSLGARARPC LK |
| 6486 | 14537 | A | 722 | 358 | 445 | NSFGRTIFFFY*FFFFFFFFFTIQTFKGGPL SPFFLLFFINPFRFFFFF*TPFLRALAFF KPPFFFKIVLAEPYFFFTNPQILMRGGGG FSGRGS |
| 6487 | 14538 | A | 7220 | 181 | 272 | IQSWFNILKSIHVIHHSNRLK/NVNHIVSS SSSSSSSSSPFLIKKQ*KG |
| 6488 | 14539 | A | 7221 | 2 | 334 | YDEEWRRSTVHPDEVGNLK*EDR*ALQ NRLRVFLSLMDTGWLDNLLDIDKADVI VKMLDA*SVIKMEGGTDNDLNLDQDVE DEHA*KPGESKNEEGRAVSGLDGERK |

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| 6489 | 14540 | A | 7222 | 1 | 323 | VVSYLLVFESSK*KKIIYQDCIGFVQDC LNINDPIDSLRGKNVIISLDTEKVVGKIQ* PFMTKIFSKLGIEGNFLKWLYQSSSTVS LLNV*ILKAFLSRTE*GCM |
| 6490 | 14541 | A | 7223 | 2 | 690 | ATYIVDFGFQYNIREGQMLTAFCGMYP YVAPERSLGQACQ*PARDIQLSVILYFR NTVGRRTLPFYS/AEASKLQEKILTGR YHAPPLFALQLDSL/KLLMLNARKGPSL *LMKNPVWKRIQKMPLIPEEPL/RGPPQ TIQLMVAMGFQAKNISVAIERKFNYPM ATYLIL*HTKQERKCSTIRELSLPGVATS PSPSTELSTFPLSLMRAHREPAFNVQPPE ESQ |
| 6491 | 14542 | A | 7224 | 2 | 338 | SSSYTPEYWQ*RSRSHSPMSNQRRTGR RANPDNPNTCLR/VFGLSLYTTDRDLREVC S*YGPLNGANVVYNQQTGRSQGFVH F*GIDDSKEAMVRANRKELDORRVRD YS |
| 6492 | 14543 | A | 7225 | 604 | 841 | RPGGQFCLMEASPSGFNPFFLLNLPREW ELRVPPPTRGNFF*FLKKNQFI/EVNPGGF DFLN/SNDPPAFASKGVGLTALTP |
| 6493 | 14544 | A | 7226 | 3 | 343 | HEPNGFYAEIECERCNSPELDEEGYSIIPD EPGSTNGKHFYSSSESEY*E*SHKNIYIQI PSLSTDILNNAAPVDELKASIGNIALSP*P EGAIKRNLSSREEVARPRRFTSP |
| 6494 | 14545 | A | 7227 | 3 | 304 | HEEKNEKIRNVGLCEAIVQFTR*YL*VCL *RSVNS*NCCWRIVPNIFF*PL*VTFSPSKP AKSLHTQKNRQFFNEPEENFWMVMVFT YTVYLSEIVWVELW |
| 6495 | 14546 | A | 7228 | 1 | 167 | SARGPDGFTAIFYQTFKEELVQILLKQFQ RIKGEVSSLKSL*ETSITLIPKTRKGT |
| 6496 | 14547 | A | 7229 | 2 | 334 | ARDRAALETVIRRARPELRRPGVQGIPR VHELKIEYVQRLQVGLDQPLNLAL ALYAHVA*EKRVVSLSRILIVILVESLI LLIIVLTYGYQLSILCTCSVGNIF |
| 6497 | 14548 | A | 723 | 452 | 764 | LLFSKCRAVEKNLSKEDPHMETIKVAFV MTSGERDTGLTEPMAG*RGSG*SG* ARGHETSLGHRGVSGDGGSMGSPSLTAN ALPSISRPFPDSVTDSGSAPL |
| 6498 | 14549 | A | 7230 | 1 | 792 | FFYREVKPSLFVDCKILITEIPKES/NRVL QITRELSKMLAYKVSMLKSILFILTREYK KVKMPFNIVY/NNTKYSRINLMKDIYDL YTAIYPSTAALKYRYMCNLQNIARRN*R PPLNKWW/REE*YSWIEGLVVKILVFPKQ IYRFNASPNKSPPLFNKLIPKFP*KYKG RRISQTNLGRJ/TLQDLKIYYKTLKNIV WYWYEVQRLLPPAPQSAPIPRTCWQLS PSDLQGLKGAEGLTDWGGKQSGTEITS GHLPLSTFG |
| 6499 | 14550 | A | 7231 | 1 | 2541 | |
| 6500 | 14551 | A | 7232 | 560 | 901 | GNPATPSHCSLPQPPTPQEGAA/YNPDDF FF*KQP*QPKPVSSQPPWPLSTSLPPACP SCSRRAPAVPAPIQAPSAILPLPGQSVR LCVDPRHRQGPVNLLSDPEQGVETG |
| 6501 | 14552 | A | 7233 | 13 | 2931 | EEGRQSPAADVKTGLRAPLAASAWPH RCCVRRLLARITMKPPRPVRTCSKVLVL LSLLAIHQTTAEKNGIDIYSLTVDSRVSS RFAHTVVTSRVVNRANTVQEATFQME PKKAFITNFSMIIDGMTYPGIIKEKAEQ AQYSAAVAKGKSAGLVKATGRNMEQF QVSVSVAPNAKITFELVYEELKRRRLGV YELLKVRPQQLVKHLQMDIHIFEPQGIS FLETESTFMTNQLVDALTTWQNKTKAHI RFK |

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| 6502 | 14553 | A | 7234 | 3 | 338 | DAWVSVLCCNLSEAKRRINSLSYNCEN IRRLPSF/RDVWNGENSRYVEKQASEQQ VELLTNERYLMEESQLLLQYLHVYHMN YFLDLTCRPTFYCYLTEAPIG*PMCKGYL S |
| 6503 | 14554 | A | 7235 | 147 | 380 | ASCRFDFFCLLCYRVLFSLNLTVCFAFR YFNIYMSFCFTFFLYFWWL/FCYDFLL/D YVF*TLILVLCFFPVSVFMFLI |
| 6504 | 14555 | A | 7236 | 1 | 257 | PTRPDFFAQQHLTPDKIYHVTVMPCYD KKLEASRPDFFNQEHTQTRDVCVLTGGE VFRLLLEEGVSLPDLEAPLDSLCSGAYA *EPTSHRGGGSGGYLDHVFRHASLQFLD S/DVV*VSSIHLR**DFFAQQHLTPDKIY HVTVMPCYDKKLEASRPDFFNQEHTQTR DVDCVLTGGEVFRLLLEEGVSLPDLEAP LDSLCSGAYA |
| 6505 | 14556 | A | 7237 | 2 | 502 | PVWWNLQRRTSAGPGTAVPGLAVA*FR QTGLTRSPSSGRDGAGVRDLWNPPPPVP IPLPLGFHLRGPDSLAEQPSACLPGS/PP CRNGLGQPQGHGLWPG*IGIQFRLGFH GNQGPSPGNLPPYPPFLAAPLHTRHVP /LHCCPLTWAALPTPLCLWRCSAIQD |
| 6506 | 14557 | A | 7238 | 1 | 828 | |
| 6507 | 14558 | A | 7239 | 2 | 775 | NISREMLQQSKILKIRKKNLVKKCLELFT ELAEDKENYKKFYEQFSKNIKVGVNNH* FSNWPL*FFFFFFNSESCKEHTLFLQGIH EDSQNRKKLSELLRYTASGDEMVSLEK DYCTRMKENQKHYYITGKRTLCSYHT RRSYNLVGSVGFSTQVALLQLVLI*AR* LT*TRSFVSLGSA*VSG*QEKSEDETILN C*KV*K*LCNTSGETKDQVANSAFVERL RKHGLEVIYMIPIEDCAQQLLEEF*GK |
| 6508 | 14559 | A | 724 | 209 | 384 | KYETIRYRDSVKGRFTIF*HLTKNCLHLR AIGLGADDSHFYSCANDVADSGTTLFFD S |
| 6509 | 14560 | A | 7240 | 1 | 2303 | QLLQRPQVAVPLVLCGHLAKMPEETQT QDQPMEEEEVETFAFQAEIAQLMSLIINT FYSNKEIFLRELISNSSDALDKIRYETLTD PSKLDGSKELHINLIPNKQDRTLTTVDGI GMTKADLNNLGTIAKSGTKAFMEALQA GADISMIGQFVGFGFYSAYLVAEKVTVIT KHNDDEQYAWESSAGGSFTVRTDTGEP MGRGTKVILHLKEDQTEYLEERRIKEIVK KHSQFIGYPITLFVEKERDKEVSDDEAEE KEDKEEKEKEEKESEDKPEIEDVGSDEE EEKKDGDKKKKKKIKKEYIDQEELNKT PIWTRNPDDITNEEYGEFYKSLTNDWED HLAVKHFSVEGQLEFRALLFVPRRAPFD LFENRKKNNIKLYVRRVFIMDNCEELIP EYLNFIIRGVVDSDELPLNISREMLQOK/S KILKIRKKNLVKKCLELFTLAEADPANY QKIFYEQFSKNLKALEYHEDSQNRKEA FPELLRYTASISDEMDTLKD\YCTARM KENQKHYYITGETKDQVANSSLCGTV FRKHGLEVIYMIPIDEYCVQQLKEFEG KTLVSVTKEGLAELPED\EEKKKKQEEKK TKFENLCKIMDKIEKKVEKVVSNNRLA VTSPCCIVTSTY\GWTANMAERIHGKLQ ALKETTSTMGFTWQPKKHLEINPDHSIE TLRQKAEADKNDKSVGILVILLYETAL LSSGSLEDPOTHANRIYMIKLGIDE DDPTADDTAAVTEEMPPLEGDDDTSR MEEVD |
| 6510 | 14561 | A | 7241 | 158 | 405 | RMNLSDGMDDIISQESSLDMEGNYKK AQKNEREAIRLILAL*SFDDGSRIYIS/CE QSGKQIFSPH**GINFQIGLSSTWSP |

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| 6511 | 14562 | A | 7242 | 3 | 442 | TLLMFNNVSLTLTFCMFLEFSLPCTED VPTCGDSCDKVLECGIHRCSQRCHRGPC T*VIYFHA VFQAGPECLHCEEGCSKSRL GCLHPCILRCHPGECPPCVQMLGTAESA VLPQACHCPQFCLQSPFFLFTHKEPQSSW SSG |
| 6512 | 14563 | A | 7243 | 2 | 322 | SGWSLTEQDPYNNIVRTAIEAMAAVFGG TQSLHTNSFDEALGLSVTKSSLIPFSLHF LFS*QFSLSYISIFLFIFFYFYLSELLHFFY IFYLISIFLFFFLFIY |
| 6513 | 14564 | A | 7244 | 1 | 361 | RELLAFWQNFKL RPQGPFFSP/GPGGEKK R*SLPKTPPKGGPPGP/SPNGRLPSGGQLP PPRGG/SPQGSSSLPKGPQGWGPPFP*RS PCPPHRIGVPQVSSSPTGLVFRGPLNPG NLGG |
| 6514 | 14565 | A | 7245 | 115 | 313 | LVRSLTSLPHSPNP TLSPS*LPPYGPVY LSHYPPSPITSLTHPPSPSPPTSLPPASPI TPTS |
| 6515 | 14566 | A | 7246 | 2 | 326 | NEGECRKDVEMEPVLQAEKTNFQNHKG HEFIPTLWHFPANCDAKPLWHVIKPP PALECRCHVKCHRDHLDYTDLDIFPCN IRYDVSSTLRYS*LLHFSDEITII |
| 6516 | 14567 | A | 7247 | 1 | 364 | EHTRAEDHMLEEREER*RAERAQREE*L PEYQERMKTL*EADRNIRPRELEIEERER RTEEERILGDSSLRKDSRWGDRDSEGA WRTGPEAHSEWTIGSPQMEWRP*EWLY DDRSYTG |
| 6517 | 14568 | A | 7248 | 86 | 512 | RGRVEAAPGYGSHLCHNFPCTYWQKF GQPPGLQRTAASYSSDTMLGKAEHTPT FAFFPAQGPCKESWQSRDTSARSETLGT ACSNTGNWAGAAAHGDTEDLQWLQ RKRE/RSEKTRTDLKGVRTSNGTARDD NCAYSP |
| 6518 | 14569 | A | 7249 | 2 | 703 | PDCPSRPT/YARGTSPGNKTENAHKGPKS VSSAPKMR*SLQDTG/REDTREPVRFHDT TGTEQTVIFAD*KIAGRCKT*GQFPRQR PPHGGGSTPQLFSAAGTSFPAFPVAVKV HGFKTSPTGRGGGHWANTRISFSWLATK KRESERKTRTDLKGVRTSNGTARDDNC AYSPHRRERGAPPAHGLYRRSVCARKN HIVLSKTGGRSVRRHDHRRSRSWRLRPG VSHHMRRSQR |
| 6519 | 14570 | A | 725 | 68 | 362 | SLPTIRECIYIHVVHAGDHIGNACWELCY L*HGIHPDGHMPRLTIGGGEDSFNTFFT ETGASEVPRAAFADLEPTVIDEVTVTY GQYLQL*QLIK |
| 6520 | 14571 | A | 7250 | 148 | 357 | LGIDLTKKVKKLSKKNYKTLMKKIEDDS N*KDNSCL*IR/MTILPKAIYRFNTISVNIP MRFLPDADAW |
| 6521 | 14572 | A | 7251 | 1 | 389 | RGAQAIIVF/NLNDVASLEHPSKWLADA LKENDLPSVLLFLTRAQYALMEKDALQ VAQEMKAEYWAVSSLTGENVREFFRV AALTFEANVLAELEKSGARRIGDVVRIN SDDSNLYLTASKKKPTCCP |
| 6522 | 14573 | A | 7252 | 1 | 144 | |
| 6523 | 14574 | A | 7253 | 174 | 809 | DQRGGNWAYECQWEGPCRLTHPLLSTS HGRQWLADALKENDPSSVLLFLVGSKK DLSVSVPVGGPLPSLVRECPLTAFPPQTP AQYALMEKDALQVAQEMKAEYWAVSS LTG/EGGFRALL*HSCALLSLLHLQLC PVSPDPALPLSTYLLSVGENVREFFRV AALTFEANVLAELEKSGARRIGDVVRIN SDDSNLYLTASKKKPTCC |
| 6524 | 14575 | A | 7254 | 1 | 524 | MERFEVLGIPFSLQLWDTAGQERFKCIAS TYRGAQAIIVFNLNDVASLEHTKQGV AECLKEE*PSRVVLFLLGFKKDLSTPAQ YALMEKDAFPGGPRRLKAEYWAVSSLT GENVREFFRVAAALTFEANVLAELEKIG CLDUQVMDPSSDDSNLYLTASKKKPTCC |

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| | | | | | GLDVIGMFVRIN\SDDS\NLYLTASKEEAP HVCP |
| 6525 | 14576 | A | 7255 | 1 | 258 |
| 6526 | 14577 | A | 7256 | 2 | 562 |
| | | | | | RCFARYRPVHADPLYCQGHAAVPVGYST VSRTHAPGG/VQLPPPPPYTA/GRGAQVG RGCSPARSGAWPHRSGAVDHPLTQGDH TAPDHSSGLNDHSHHGAGARHLPPQ HAAWPP*DLNPCRTQPS*PSHSPRPGSPL APVAPPWALGWNQYFPPKSDSLLLLAK LYLIQWVFPCTVDFPNVINFNK |
| 6527 | 14578 | C | 7257 | 30 | 323 |
| | | | | | MRLQLPSTSHLPVKGXKEGEAVVLPEV EPGLTAREQEATPRPRETTQLPTTHQALG WNQYFPPKSDSLLLLAKLYLIQWVFPCT VDFPNVINFNK* |
| 6528 | 14579 | B | 7258 | 249 | 374 |
| | | | | | RLRWPLREVQSVQDQRCITKPREPVSGI RYCDFLPGVYDCT* |
| 6529 | 14580 | B | 7259 | 77 | 867 |
| | | | | | XAGALQDITLSQQTPTWKDTQLLTAIPT SPEPTGLEATAASTSTLPAGEGPKGEAV VLPEVEPGLTAREQEATPRPRETTQLPTT HQASTTTATTAQEPATSHPHRDMQPGH HETSTPAGPSQADLHTPHTEDEGGSATE RAAEDGASSQLPAAEGSGEQDFTFETSG ENTAVVAVEPDRRNQSPVDQAGATGASQ GLLDRKEVLGGVIAGGLVGLIFAVCLVG FMLYRMKKKDEGSYSLEEPKQANGGAY QKPTKQEEFYA* |
| 6530 | 14581 | A | 726 | 1 | 1254 |
| 6531 | 14582 | A | 7260 | 93 | 1049 |
| | | | | | TSGSHSGITQFLPCFSGAQPTGQSP*KR SPGPQHRAARCTHFPEGSFFGSSCSRPR NRAWVSAWWAGS*RPQWSQELTQTP KQAGGQWRGPAPSRTPMPRLLEPPQHP KEQERHGVALEQSR/PRTLPPALGHTCV* DQPSAFPVPAQFWGNPSMGS/HERSWV CHVL*LSSHPLIQRRGSPCPPVGLGISP SPCPGGQPRQPD\SSLLGA*ASGFSGTPK FKGPGTHHGPCQPLPSPAGLGSGLGEDL EAVGRTQPSNA/PLAPGQ*ATGGSALQPP VHTASNAPGPVSPDAPPPLDQAQRLQD QAKAKPCPR |
| 6532 | 14583 | A | 7261 | 2 | 643 |
| | | | | | PRVRLNGIVDR*VLGCLPCYDLGIFTDRD LGVHADADHDLVENLAKDLIA**IPFLAEGI RIHGDKVTVALRPFHERMEACFKQKE MVENEYGVIMPSSLLDD*RGIRPRSMVR AFTMPSSSRPLSVASVSSSDSTPSRPGS DGFALPLPKMLSRSHDKLYKDDLD DKKDYMTYNWTCRQFQISRDKMKRTD VSLYIMLVSPNPNSY |
| 6533 | 14584 | A | 7262 | 59 | 339 |
| 6534 | 14585 | A | 7263 | 2 | 519 |
| | | | | | ILFLFLFYFISFLRWSFTFVAQAGVQW*D LDSLQSPPPRFK*LACLSLLSSWDYRHMP PRPANFLYF**RWGFTMLARLVLDSPQ/ CDPPASASQSVGITGMSHHAGPTMKLLN PQSEVIFSPRNSHSTLLTPLSRHLHPHISIS TWCIIHYAPLHTVSIASAEAPWLFACPOS |
| 6535 | 14586 | A | 7265 | 3 | 317 |
| | | | | | EESFTAHLRHRGVQPFPCGQCDKAYG TQRDLKEHQVVHSGARPFACDQCGKAF ARRPSRLHRMTHQVQLPMPLAHALCG AAPGSQGFLWNHMLRHT*KKPFL |
| 6536 | 14587 | A | 7266 | 285 | 672 |
| | | | | | PLCTREKSEYMCTSYSLARSRVGQTLCK GVQWRHLSSL*PPPPGFKQF/SCLSLPSR WDYRCPPPHLANFFYF*QRQGFILARL ALNS*PRDPPASASQIAGITGVSHRDRLII NFLDFEGYT*SATDS |

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| 6537 | 14588 | A | 7267 | 3 | 231 | QIEQLHRRF*AA*/RGDQPTIRKENFNINV PDLELNPIRSKIVRAFFDNRNLRKGPRGL ADEINYEDFLTIMFYFLSI |
| 6538 | 14589 | A | 7268 | 88 | 360 | KINMGILLKL VYRFSIHPVKTPAGLF/TK NEQ**TEFDKRLKSIWKCKE/PYSTRTMF KKTEAKGLPS/P/DFKTYEATEFKTS*D QQKDRYKE |
| 6539 | 14590 | A | 7269 | 2 | 355 | RRLLLLFFFFLRRSL/DSVAQVGVQWHNIG SLQAPPPGFTPFSCSLPSS*DHRPPPCP ANFLYF**RQGLTMLAKLVSTS*PCDLPA PAHQSAGITDMSHRARLIVSLFKRQKTY GNN |
| 6540 | 14591 | A | 727 | 65 | 1552 | PLKAKMGKEKTHIWINIVIGHVDNGQVSP LLGHLIYKC\GGINDKRTIEKFEK\EAEM GKGSFKYA*VLDK\KAER\ERGITT\DISL WK\FET\SKYYVTYPFDAP\GHQRLLSKN MIYRGHLKA*PGLGGPLFGGVLP*LFAA GVWWNLKAGISKNG\Q\TREHALLGLHT WVWKQTKLFGVNKNWIST*GHPTAQKK ILKEIVKGKSALT\LRKIGYNPDTSSILCPIS GWNGDNNAWSPNANMPWFQGDGKVT RKDGNASGTTLLLEALDCILPPTRPDKPL GLPLQDVYKIGGIGTVPVGRVETGVLPK GMVVTFGPVNVTTEVKS\SEMHEALGE ALPGDNVGFNVKNVSVKDVRRGNVAG DSKNDPPMEAAGFPAQVILNHPGQISAG YAPVLDCHTAHACKFAELKEKIDRRSG KKLEDGPKFLKSGDAAIVDMVPGKPMC VESFSDYPLGCF\AVRDMRQTV\AVGVK AVDKKAAGAGKVT\KSAQKAQKAK |
| 6541 | 14592 | A | 7270 | 1 | 336 | RGDTGRTLAQRGARSSG/LPTV/LNPGRQ LTSAG*PH*YGKARAAMPTPSLVRPVLK VGHSPEVSGSAAEIAPWTISSPLYNPSS LPGPASSMPPIPNSPLASPVSYTVLV |
| 6542 | 14593 | A | 7271 | 1 | 371 | RSRPELNDYKDKKAATKNVQKK*MQRQ KG/DIAIDATETQRIIRDCYEHYNKMSSSS SSSSSSSSSS/PSSSSSSSSSS/PSSSSSS SSSQSLPSKKNSGSEGFTAIFYQRYKTPL ILKLFKK |
| 6543 | 14594 | A | 7272 | 2 | 406 | ARAARVFLHRTSLNLSNGGTQC*KTMOV VHDEYSEPCMTSPKEGTLIVRQTQSAS STLQKHKSSSFTPFIDPRLLQISPSGTTV TSVVGISCNWMP*SIKHYPQKGSLSF* ISTHTYPSAFCVIFLHYC |
| 6544 | 14595 | A | 7273 | 1 | 165 | GSLLPLLFNIILEVLAKAIRQEKSIQNEKE KV*LSLLTDHMI/YM*NPTVKKLT*KL T |
| 6545 | 14596 | A | 7274 | 110 | 409 | |
| 6546 | 14597 | A | 7275 | 53 | 930 | ARSYRQLTMEANGLGLQRIHTDTYPHPH LIARPQGFPELKNDFLRAAWGEETDYT PVWCMRQAGRYLPEVRETRSAQDFST CRSPEACCELTLQALRRFPLDAAIIFSDIL VVPQMFSPPP\ALGMEVTMVPKGPSFP EPLREEQDLERLR\DPENVASELGVVFQ AITLTRQRLAGRVP\LIQFAGAPWTLMT YMVEGGGSSTMAQAKRWLYQRPQASH QLLRJLTDALVPYLVGVQVVAQALQLF ESHAGHLGPQFFNKFALPYIRDVAKQVK ARLAREAGLAPVPM |
| 6547 | 14598 | A | 7276 | 86 | 552 | KQPQPTAPLWQPLKLSKLGAPGHGPC CLHLLSALGSLPGLVPWLPSPRVGC/SS*G LLLTSPQPSADPGQRRVALHHVL*VEP FASQEAQPPSLP/WW/PLRGDTESPGGPS PLSARCTHPGCRSVRGRWGRARGWPAR CQGAGGPGGWRTTCPCR |

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| 6548 | 14599 | A | 7277 | 176 | 779 | NSVSKLGLAPGHGALLPPPAERSREASQI PRGRAPGVHYLCLKQPRPRGLLGPQONE RPLPSKPHLCAGLCLGGPGTSPLPFETIR NWARRPPEA*PQGACI/LLSLGDPRGVG *PWV*TPGGLVFWMSLWHFGPQLKPPPL PRSLRPRPSLDLLGRKRHQGQDEKPGGA APQMRAL*PVLPLPPHPGTAPQLVTATR KP |
| 6549 | 14600 | A | 7278 | 32 | 492 | FALVGQAGTQ*CDLGSVQPPPLGFK*FSC LSLLSS*DYRHVPPCWLFVFLVE/QGFVI LAKLVSNP*PQ/CDPPILASQ/SAGITGVS HCAW/L*LSFSFFC*DRVSVTQAGMQWH DLSSLQPLPLGFN*FSCSLPSSWDYRCV PPHPANFFIFSR |
| 6550 | 14601 | A | 7279 | 19 | 253 | LENSFLKTLPLAJACRNIKYMNLTKCESC KLRENKDLNKWGSTPCSTIGKLRIVKMS FLPKLIYKSQKTFFLQTLIK |
| 6551 | 14602 | A | 728 | 344 | 803 | KRDPSLSAYPFFKCNLLSTLHFMTAYAS LYFIYTEPVFVQHDWLHASKAL*IPFHISPS TTIPLTMVSQPYTEHYIVTKLGEFQVSK GNYIHKRFCAIAQFTI*LVIQTPTMLR*ISD YLDKYIGFCPPQPMKQERHTYSPPYQGC VYSVVQS |
| 6552 | 14603 | A | 7280 | 3 | 1023 | FLNWKSKILYSTDDMIYIENAKESRKKL LE*VN*SKLLDTRSMYKSNAFLYTSNNL GKPAF*KPYPLAJACRNIKYMNLTKCES CKLRENKDLNKWGSTPCSTIGKLRIVKM SFLPKLIYKSQKTFFLADIDKSCFF*DSFT PGLPRLEWPWPRSQAHA*KPSNLPGSSNSP GLSLPSSWDSTSACHRRLANFFVFLVEM W*CMPTVPTTWEAKERAHLSPDVRGYIS CDCATTLPQGQNEISASNKTTVINIVSY WCKVIHTRKWCPEQTTSMSLRVFTNL* RLGHWESRVSTNRTEPTNHTDKKVNLD PYHIWYTKMNSKWITDLNVKGKTIKVP |
| 6553 | 14604 | A | 7281 | 1 | 407 | DVCKPDLTVGLRYAPHQYKSVVATNLP EAKYWFLNWIADLSKAAPRNNDVALGTS AQAYYGYRKQEQUILL*EEDALTGTNESL ERQMREMEENFAVEAANYQDTIGRLQD EIHNMKEEMARHLREYQDLLNVKMGMP |
| 6554 | 14605 | A | 7282 | 1 | 3003 | MNIDAKIHNKILANRIQQHIKKLIHHDQV GFIPGMQGWFNSTKSNVQHINRTNDK NHMIIISINAEKTFDKTQQPFMLKTLNKL IDGTYLKIIRAIYDKPTANIIPNGQKLEAF PLKTGTROGCPLSSLLFNIVLEVLAIR QEKEIKGIQLGKEEVKLSLFADDMIVYLE KPIISAQNLLKLTNSNFSKVSQYKINQKS QAFLYTNKRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKKIYQSLN |
| 6555 | 14606 | A | 7283 | 2 | 178 | PRVRWN/RKVQKQIISIHGGQ*IVDKGSR TIQ*RKNSVFN**C*DK*IFTCKRMNLYL YFVSSSSSSSSSSSSSSSSSSSL*EENTGI NLHDLGFGNGFLDMPAKAQTATA*LYL YF |

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| 6556 | 14607 | A | 7284 | 699 | 2526 | MQYNIFQVLYILDELHGILGNLTNKFH RSIVANNLDDLDEKTHQLTKLAQKEIKN PNRPVTSKEIEPVKNLPATKESPGLENEFT GQ/YYGQTY*RKELTLILLELSQKMEKEG /V/FPVTFYKADITLTPKPKDLTGNYRPI SLMNIDAKKLAKILAGQIQQLIKMITQHD QVRFIKEMQGWFWHIQMSIDVIIYHNRM KGKKVHMITSIDKKKHLTKIQHPFMVKTL CKLGRKGNFLNLIKTSIKTHS*QHNSKTL KIFPLIS*KFLISPLLFNILEGLARAIQEK EIK*IVQIGRSKTTFAENMVLYIKNPKEST K*FRLI*KFSNVAGCKINTQKSKKNLRG N*/RQF/PFTIT*KRIKYLEINLTKKVQDLD TEKYKTLKKEIKEDLNKWK/NILCWQVG RLNIVKMALLPKLVYRFNTIPIKJPV/LF TETEKLTLEFIWGLQV/N*RYSSLFKTLN KNKVEGLTFSNFKIYCKATSIKTVLCWY KNI*SNRVEWKVQKQITPAHLWSIDFWP RGSRTIQ*RKNSVFN**C*DK*IFTCKRM NLYLYFIPYIKINSR*IKDPKCKSVNPIKL *EENTGINLHDLGFGNGFLDMPAKAQAT TAKKKKK |
| 6557 | 14608 | A | 7285 | 2 | 577 | KKIKNIKGSIQEGLTVVNMYAPNDKPS TYMKQKLT*LKGEVDNSTLIVGVNITISV VDRT/SQYLSKEI*DFHNTINQLDLTTIYR TLYPTMKYTFSSIHRSKIGHKLSLN*F *KTAINIFPDHNGMNLVIIPKKKTGKFKN HRN*HTLNH*IKKETTRHWLKITPRLWP WQVRVFGAQSLOQPQLTAR |
| 6558 | 14609 | A | 7286 | 17 | 377 | QRKACAPRAWSGDPSACRPSVRS*GSTT *G/KPVNFDDYGDYIPAVNLKTFLRELA ESLLTFQAYDQILGITCEYLPWRRSGGLS PHMLSIIYWPMVRLWGGRGDVYPSCYC CHMALYGM |
| 6559 | 14610 | A | 7287 | 1 | 893 | SISSQQT*SSWAPCYRSLPASTWASSLCS SSLSISFSFSSVYSSPPGSSTPLASILSAFF *PLDFSSLASVSSLLPSLNLTFVSWLPPAS PLSSLAFPASTLVSGLPASSLMSSLPSPGS ACLSSPTSQHACSS/STLSQSLPSTSCCLS LQTP*TLPDWGFERSQKGT*VW*ALRKTS SPFSSSTSGLGAESREQQLGAKTNCASS RDRSSRCGSTENSST*GPTPRSSSR*PIPGS SSPGEKAAPAASAWAASPSSAPTHSGYE LLESSRKEKESCTSWDESSRAGAKSSGP ES |
| 6560 | 14611 | A | 7288 | 827 | 1393 | ARCRQAREDGRLVQRLCRRGHFVPLQH RRGAQERAPGIAHSSCAAEPRLSLRTDI SSALVWPRASCARSCPEMGPPLKWA GA*TLIECPPALSGSPRKNLD*PPGLEEPS RLEGGTPSSALLKG/PAPTYLPPYALD PKPTSA/VQHSPTYPHVLPIPTPSSWR VVAVGALCSRQDNLHDQRL |
| 6561 | 14612 | A | 7289 | 104 | 464 | |
| 6562 | 14613 | A | 729 | 209 | 372 | KRKKILRINKTKS*FFEKINKIYKMLTHL RRDKRQKKSEIKKGDTITDITEMKK |
| 6563 | 14614 | A | 7290 | 2 | 394 | PRVRNHPIQKWAKKGLADSHLSKEGPQ/A AISHMKRCPASPATRE/VQIRATGETHLR GCGNIGTLTRC*WGCK/LLQPLWKPVW WFLRSLSIGLRCD/PVATPLLSV/WPQAC KPGTQRDLHTTVFTAALFTVAEQ |
| 6564 | 14615 | A | 7291 | 2 | 344 | DTRTHVAEEDKLAIVEPEKRGKYVWF DPLDGSSNIDCLSVATIFGFYITNSSD*P SFNHVALST*RNLYLVSLPFHLAFLSTFHL SFLFFFLSFLSLFSYLLFFLSSFFSS |
| 6565 | 14616 | A | 7292 | 1 | 348 | RYRSGIPGRRTRAGETPSLLKIQQPG/GD GARS*SRLRLRLRQENRLNPEGRGCSEL RLCHCTPAWARE*DSLKSKKKKEFKIPIY FLTLLWDVVRTQYTYISIPMCLLCGEMVT |

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| 6566 | 14617 | A | 7293 | 10 | 436 | EYYRFLEAKENRTATY*NL/MDHAAKAE LRGKFISIIYAIKKLEKFQIKNLTMQSKK LEKF*IKKSSNVFQARKEQTKPQISQRK *ISEKE*TKLRLNQCHKKSLKQPLLS*TK KDQNK*MRKEKGDIKLSGRVGRPEYLQ T |
| 6567 | 14618 | A | 7294 | 2 | 403 | CPTSTSTSWTMWGPACREHL*PLPTFP GQQPNTLP/RPTLRP/SP*TPTSACS/RP*P AVPSRPSHPSHLPPSCPPQFTFNPHL**G GPHPTHNLPPNPCALLQLPGFSTLPRLS P*TPPTPPICHCVSRFLAP |
| 6568 | 14619 | A | 7295 | 27 | 88 | CREEDDDLVESEDS*QWGESLKRVSFTL LDDEATEDAGDLNVKKSDEVKSFETR QEKESA*VGRKMMTWLKVKTNNGEK A |
| 6569 | 14620 | A | 7296 | 109 | 409 | KFKNMWKLNDTL/LNNHWVKEEIKKEIR KYLKRNNENKNTTYQNL*DSAKPVLREFV VINAYIKIEEGSYISNLTLYLKDLEKEIKA KVNRRKDIRITEIN |
| 6570 | 14621 | A | 7297 | 13 | 811 | VCRRWSGGLARRFGSGCCSSCPORRA ARRSQVQNGKYL/FDQINRSLENYEPCSS QNCSCYHGVIEEDLTPFRGGISRKMMAE VVRRLGLGTHYQITKNRLYRENDCMFPSR CSGVEHFILEVIGRLPDMEMVINVRDYP QVP*MDGACHPS/SPSVRHQS/DHDIMY PAWTFWE/WGTCCLANLSYRSWTEGPL QRRSGKVSITQWPWKKKNSTAYFRGSR TSPERDPLILLSRKNPKLVDAEYTKNQA WKSMDTLGKPAAKDVHLVDH |
| 6571 | 14622 | A | 7298 | 22 | 426 | IFSHYFFQKFLRLPFIMFIMHLLGCKVDL FIFQCFHFLVFYFLFYLLKLCYTFKFT NCFLYSFSFTVHLI*YIFPSDIMFLYEV* FKSFF*RYLPLCHVHAFISFLNILSLFSS* **LTIFYCPYLLFYH |
| 6572 | 14623 | A | 7299 | 131 | 353 | IFLPEKKLYKLEKWDRAFDNT*NF*T*K/I HTGEKS*KCKKWDRAFKGWPHFIIGKIV HTEKNFYKGEQCGKTFN |
| 6573 | 14624 | A | 73 | 702 | 1281 | AVEMYLVVCGTV AISRVRMSAVCVLRT WSRNAGQL/ICFTVFQPCSNVHVL/KGP NYVCFGVPSPFKYSHPHNFVKTNVAVC GQLVQFRFPDTEEGIRKVTV/KCYVKEG DTVSQFDNIGKVQSDKASVTIASPYDGV I/RKL*HSLDDIAYVGKPLVNIEEALKGT VNLFYQIDYCPFFVIGSQLKVTFKKKK |
| 6574 | 14625 | A | 730 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDSFGNLSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGT AQLSELHCDKLHVDPENFKLLGNVLT LAIHFGKEFTPEVQASWQKMTGVAS LSSRYH |
| 6575 | 14626 | A | 7300 | 131 | 418 | IILTEKKLYKLEK/CGQGF*QHLKLLNIKN HTGEKS*KCKKWDRAFKGWPHFIIGKIV HTEKNFYKGEQGGKTFNEGSHLIAQESI YT*KKLSKYKD |
| 6576 | 14627 | A | 7301 | 305 | 326 | KTFRSQKKK*IHWDYIKILNFCARKNTIS KVKRQPT*EKIFANHISA*G |
| 6577 | 14628 | A | 7302 | 3 | 416 | FLR*IGSHSVTQAGVLWRDFGSLQPLPPG LKLFSCLSLSS*DYRRVPPCLAKFCIFS/ VRRGFAMLARLVLS*L*VVCPPCHVD LYN*SASQSAGIKGVSHHTWPHKYHLK NLNVFSYQSKSTVNNQLSSQILLN |
| 6578 | 14629 | A | 7303 | 3 | 474 | |

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| 6579 | 14630 | A | 7304 | 2 | 1050 | REDTKAAVLLHLLHNVRPQDQTVVVFV ATKHHAEYLTELLTTQRVSCAHIYSALD PTARKINLAKFTLGKCSLTIVTDLAARGL DIPLLDNVINYSFPAKGKFLHRVGRVA RAGRSGTAYSLVAPDEIPYMQDLHLFLG PLPHRPPTPQGALRVWAGVDGHAGVGV PQSVVDEEDSGLQSTLEASLELRGLARV ADNAQQQYVRSRPAPSPESIKRAKEMDL VGLGLHPLFSSRFEEEEELQLLDLVNSIKN YRSRATIFEINASSRDLCQVMRAKRQK DRKAIARFQQGQQGRQEQQEGPVGAPPS RPALQEKQPEKEEEEEAGEKCEDIFSEVG GRKRQRSGPNR |
| 6580 | 14631 | A | 7305 | 3 | 872 | PKSWNGPPHPPGHRHSRSHSNFSGCSVD EERSRTSKDSSSPVNDHRGRQ*MR*KNP FAASSRSTSSSSSSSPPLWSTAGRTPT TRSGPSPALDKVQIYMEHLLATAST/EPA GSAHVPGLHFAE*VLPAL*GRALLGTP VTNNLLGEIAKPSLSQSKRLKAAS/AAKY PHDVVNHLSCDEARNHYGRRGQPHPPH PRTK*KNGSPTPRSCARCCST*VSPRRT RRAPGDPLVLP*GPSPGPLNTSVDSQ KPASNPQDVQNHPPGGLLVGNCNSEPGA PSAESFAV |
| 6581 | 14632 | A | 7306 | 99 | 433 | KLKVKGGKRYRMLTLIKRK*H*IKIQCNSC VFLYTSN*ELENK/IFGRYVSFMA*KIKS/ LGIILMKDV*NLHSEDYERLLTKIKDDSN KWTDMQFTRIR*YHKMLILK*PIIY |
| 6582 | 14633 | A | 7307 | 18 | 146 | LHDSNTRSPQFQKSLGFSTGRHRCVP*EG L/RSVTQAGVQWPIHSSLQPRPGLQSDP PASACQAARTLCRWY |
| 6583 | 14634 | A | 7308 | 1 | 240 | LVCLSKSECLQPLFYHHLTLKNCQFHLC RILLHPQC*KQALRHGKACPLCHCCSHA ALYMICLAKED*KTFDPQELMYSL |
| 6584 | 14635 | A | 7309 | 2 | 1790 | ANQLQGEVVRFFVDCRPAAEQYGAGHL STAFHLDSDLMLQNPSEF/DTAIL*SLLEA QKQSIESGSIAGGEHLCFMGSGREEEDM YMNMLAHFLQKNTEYVSASGGFMAL QHHLADINVDGPENGYGHWIASTSRSR SINSVDGESP/KWLCKLRWILKHQV |
| 6585 | 14636 | A | 731 | 99 | 641 | APSPDAMGHFTEEDKATITSLWGKVNVE DAGGETLGRLLVVPWTQRFDSFGNLS SASAIMG/NTPKVKAHGKVLTSGLDAI KHLDDLKGTFAQLSELHCDKLHVDPENF KLLGNVLTVLAIHF/GKAEFTPEVQASW QKMAEDVTGVASALASTYPLSSLAHDS ELSRDRLFLCKQIKI |
| 6586 | 14637 | A | 7310 | 1 | 1424 | ARILLDNHDYAMEKLKKRVLEYLAVRQ LKNNLKGPILCFVGPPGVGKTSVGRSVA KTLGREFHRIALGGVCDQSDIRGHRRTY VGSMPPGRIINGLKTGVVNNPVFLLEIV DKLGKSLQGDPAALL*/EVLDPENHN FTDHYLNVAFDLSQVLFATANTLATIP AALLDRMEIIQVPGYTQEEKIEIAHRHLIP KQLEQHGLTPQQIQIPQVTT*WITRYTRE AGVRS�DRNLGPLCRAVAVKVA*GQRT EPIWTVLM*LREKVAENTS*KMKNLNL /RDTDLALPPEMPILIDFHALKDILGPPM YEMEVSQRLSQPGVAIGLAWTPLGGEIIF VEASRLDGEQQLTLTGPSSTVMKESAH LAISWLRKQKESTKLTNAFGSFDLLDN TDIHLHFPAGAVTKDGSPSCWEVTISNLSR PQLFSGRLVRSVDVAMTGEITLRLALPV GGIKDKVLAHRAGLQVPIPR |
| 6587 | 14638 | B | 7311 | 169 | 379 | VSQRLSQPGVAIGLAWTPLGGEIMFVEA SRMDGEGQLTLTGQLGDMKESAH LAISWLRKQKESTKLTNAFGSFDLLDN TDIHLHFPAGAVTKDGSPSCWEVTISNLSR PQLFSGRLVRSVDVAMTGEITLRLALPV GGIKDKVLAHRAGLQVPIPR |

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| 6588 | 14639 | A | 7312 | 3 | 411 | HHFLTCRIKNKINYTIATKTIKYLRINLRN F*SLTKPKLLKDIKVDLNKWKNISSYWL R*FKLTNISVLPILIYNKIPI*KINTFFIKLD KLMPKFI*KNKHVKIGRK/ITKKKSYKGI LTLSDIKTYKVSIIKTV |
| 6589 | 14640 | A | 7313 | 2 | 423 | SFPLPFPLPPCSSPQGPQLLRKAITRPWPG TCPYPASTQVGEFTLRTRPQLSVGV*EEG CPYPSPADSPMSEDPGAAPPHHPRSPL*R NR/C/SSKGKTAVFAWPASHLASPLQPTG LPGKRNNMLSVPNNTQPDAWVAPE |
| 6590 | 14641 | A | 7314 | 2 | 416 | ILSTLFQICHCLWSSQLLLTSHCQYHYCC SSKNKNLAWLLKLFLYNLEA*FIHLA VIFLYLSCLGFTALYEFVVCFLLLVLRSY SVLLFLSF/LFWNFSVTHILELLCPICLLNF VLLFMYFSFSVLQFGYFLFLCLQ |
| 6591 | 14642 | A | 7315 | 2 | 411 | RQGLTLSHGPEVQWHDLSVLQPLPPGLK KIFPPSASRVAGNTDVHHHAWLVFFPFF VRRGFAIVAQAVLQNPGLQAICPPMASP KCWDYRRGPPHPAQE*EHFLRSLPSTGE SYFGEL*HISTRKIKILVHFEETN |
| 6592 | 14643 | A | 7316 | 2 | 333 | TEPALSPRLECSGTISAHCKLR/LPGFMLF SCLSLPSSWDYRRPPHPAGFFVFLSRRT GFHC/RLARDGLDLLTS*SARLGFPKCWA DYRRDDPMPGPVSNRMENLMETVD |
| 6593 | 14644 | A | 7317 | 3 | 232 | AASTPRPLRFLPSPTRGLVPN*RP RRRT SSAAUTPAPEAPTSARPTRSNTHRRLS WSSRPVTEEMQSAAKHNG |
| 6594 | 14645 | A | 7318 | 1 | 385 | IPWSRVG*NHPVKNAHLPKAVSKFKTISI KKPPLFFPRMEKTILKFLWDSSSSSSSLPV *SSSSSSSSSSSSSFSSSSSSSSSSSSSSSS SSSSSSSSSSSSSPTHKIKPNTYRQLIFD KANKN |
| 6595 | 14646 | A | 7319 | 2 | 409 | DRKEERLRSPRSGAAATMSSGGKGVAE WDPLPCLDPCLWDQFDNLENHNSLEKFI SAKERTIEISYTKQLRNLLKTCQPKRN WKEKEYIT*NSPSLPVNKMSDHARQH*V IFFEVLNFQITVELQGHVQNOQKE |
| 6596 | 14647 | A | 732 | 154 | 411 | AGQPGPEGIQLG*PQIRDKGDQMGP HPC W*VCGTLTPNTSF*VFCCVAGRDGAPGV KAHFPAQKPWDGGFGPGP*SAGVGPPPI PR |
| 6597 | 14648 | A | 7320 | 58 | 501 | DPRVRPGTRGPRSGTAGGETTWEGPFGV IVRVLMLFSYELRAAELGEVGAGGPRGA RRPSQTETAA*PASRFVRGLGPQTLRPTS PGPRRSRPLLGDEPPRRRVGGASFPTRN GSGAWALWRRPCWECSSRSFLRTTKLF LFFGFG |

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| 6598 | 14649 | A | 7321 | 381 | 2378 | AASMEHIQGAWK TISNGFGFKDAVFDGS SCISPTIVQQFGYQRRASDDGKLTDPF*T SNTIRVFLPNKQRTVVNVNRNGMSLHDCL MKALKVRGLQPECCAVFRLLEHKGKK ARLDWNTDAASLIGEELQVDFLDHVPLT THNFARKTFLKLAFCDCQKFLNGFRC QTCGYKFHEHCSTKVPTMCVDWSNIRQ LLFPNSTIGDSGVPALPSLTMRMRRESV SRMPVSSQHRYSPTHAFTFNTSSPSSEGS LSQRQRSTSTPNVHMVSTTLPVDSRMIE DAIRSHSESASPSALSSSPNNLSPTGWSQ PKTPVPAQRERAPVSGTQEKNKJPRGQ RDSSYYWEIEASEVMLSTRIGSGSFGT VYKKGWHVNVAVKILKVVDPTPEQFQ AFRNEVAVLKTRHVNILLFMGYMTKD NLAIVTQWCEGSSLYKHLHVQETKFQM FQLIDJARQTAQGM DY LHAKNIHRDMK SNNIFLHEGLTS*KFGDFGFA TVK\SRWS GSQQVEQPTG SVLAWMAPEVIRMQDNN PFSFQSDVYSYGHRCMELDGRGELPYS SH\NNRGFRSIFHGWRGY\ASPDLSKL YK\NCPK\AMKRLVADCVKKVK\ERPLF WQILA\SIELLQHSLPKINRSASEPSLHRA AHTEDINACTLTASSPRLAGLPS |
| 6599 | 14650 | A | 7322 | 3 | 419 | EPQWQALMPEKEPARQSRGGALRTDSS EPSRNEVKKTISFIILAKRTYLEIYATQDA *NLCTEKYKIFLKG IKEYRTKWKDILQS WITRHN VKMAKLP/KFIYSFTICKMP\LS FYKLILIFMRKYKGCRANTI*RER |
| 6600 | 14651 | A | 7323 | 3 | 222 | DAWVTSTNADKEFEKIQHPLMIKLSSK* VYNMSYIYPLFKIHKGIYDKSLVNIILNVE KLKAFFLRTGTRE |
| 6601 | 14652 | A | 7324 | 2 | 395 | GRQPRWRLWGQLLSSGRRPLEPGWHRP SRGERGHASFPPEPGPCPGPQRPQG*V PVPEP\PPKGGPEPRSSGRKASGPSAQPPP AGDGARERRQSQQLPEEDCMQLNPSFK GIAFNSSLAIDICMSKRL |
| 6602 | 14653 | A | 7325 | 63 | 451 | KNQE QESEETLPNLFYKASITLIPKLDTQ K*KKRKEKKRKKKK\EN*KPITHRNIYAK ILNKILAHQIQYIGKIIHHDQVGCIP/GAF DKIQYRCMIR/TLQKM GIEGTHLNIKA IY IRPTDSIENREKP |
| 6603 | 14654 | A | 7326 | 2 | 137 | SKAKINGWDYI*LKCWYTAKKAISGVKR QPT EW/EKIFAN*SSDRR |
| 6604 | 14655 | A | 7327 | 755 | 1287 | GGWDFAPAEGRERLAPCQIWDPSCLPTH W*PLSGLLSRPPPGTQSPQLSPYSCAKSW CPCPSLSPGSPMN*PSVPRTTGPSHPEPSA HGSHTSPIVATTERAPERISGGDSLGLSPS GLEGVNREPLFTPPSSSGSSVSLMSSTPAP PAGHSAA*SPQPGRCSGPAQQQATSRSV RGP |

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| 6605 | 14656 | A | 7328 | 1 | 2239 | MEERKGHKEIHLRRLKVRILSVRMSAIK ESPRLLIGNQEPLKQLKQESKMNRVYFN TDYSGCIRLIQSRLSHFPSSGQQNPKPY MRKFKTPLMIAEEKYRQQKEEIEKQKQE SSYYNIVKTQSQNQHTEVEKEMPLQKT NEEVSLSGIDSECTVVQSPSGSQSNARIL GVCSDNQLSTTSPETVAAKRLHHVLAAS EDKDKMKKEVLQSSRDIMQSKSACEIKQ SHQECSTQQTQKKYLEQLHLPQSKPISP NFKQSEIDVQTFKKQYLKTKKTEASTE CSHKQSLAERHYQLPKKEKRVTVQLPTE SIQKNQEDKLMVPRKQREFSGSDRGKL PGSEKNQGPSMIGRKEERLITERKHEHL KNKSAPKVVKQKVIDAHLDSQTONFQQ TQWQTAESKAHEHKKLPQPYNSLQEEKC LEVKGIOEKQVFSNTKDSKQEITQNKSSF SSVKESQRDDGKGALNIVEFLRKREELQ QILSRVKQFEAPNKSGLKTFQTLNTIP GWLISEDKREYAVHIAMENNLEKVKEEI THIKTQAEADMLVSYENIIQTAMMSKTG KPANGA/ALVSTKTSPKVSNVHVSNNEN SEQEN*IAEKTQVQHQAHADEATVRS HVKTHQEIKLDDSNIP/LP*KHSPPSPFTI TIESTARRTENPTKNELSQSPKDSYVEP PPRRPMSQKSEIHRANTSPSPRSRSEQL VRLKDTTAKLSKGAIPCAATPVPIVEKR SEIIMSPATL |
| 6606 | 14657 | C | 7329 | 110 | 298 | MPWISEGRATRPCLRVPSARRGDEGLHQ RATANSVYKSRNTWLCWICKPPQSSSPK ISEKRF* |
| 6607 | 14658 | A | 733 | 233 | 353 | STAPGSGRQRTVSEEP*PHSTEDGQRGQ WGGTSLQHQAQD |
| 6608 | 14659 | A | 7330 | 127 | 742 | LVRVFPWREDKVWWHCQE/CRPKR*KS KPGLSGPV/APGHSWDSTETTEATGLLLI PGPTRRPPTLYHTPCCLSVPRWCRPSSPL LAEGTRRQGLVALPSLIHQIPMGLEW GLASPPRPGRKWHR*KDKMATQALSVC RA*TCILPPSTKTSRPRPHSTPRGPAPTTV QRNSRRVNGSPESPLPRPGLPVSEPHVA GTRTARDG |
| 6609 | 14660 | A | 7331 | 2 | 433 | FEDIK*VIGKVKKMMSKQQRGNINKGKIJK RNQKEIVELKSTVTIKINLLGGFKNRL*Q TDK*ISYF/EDTTVEISQSGKQSSSRLEGR EQSLKNLWNTIKLTRVYTVGVSEKEKKE QIV*KISAGNFSNLIKNMNINIQAQRTP |
| 6610 | 14661 | A | 7332 | 1 | 281 | PR/PPDRDSEAPGADGAGPRGALPVPGGH GQDPAEDGPGVHAGGARDGGDPARGA YPPMPSTRGCRKGSANLP/PVGFQYVH PFF*FPGVTAKIQRMDQVFLAVRETE ALIPPEVPTRQCPAHEAVGKVHWLICH WFSICPSLFLISRAQYFYP |
| 6611 | 14662 | A | 7333 | 33 | 427 | GSPAPGLPKGWGFRGGPPGPGKFVFFKL PKGGFPAGAEIFLGEFFQRGKKGLGPIPPP VFLKTEEGGTL/NSFFKGRVFLVFKPKA GSSSSSSSPNYKPIYLNNTDTKFFNNMLA NRI*QCIKEVMQYDRTRG |
| 6612 | 14663 | A | 7334 | 491 | 731 | DRGLCLPTLEVQWAPILGSLQPPPGFKQ FSCLSLPNSWDYRCMPTCPANFFVFFCIF **SRFHQVQGAGVQLLTSSDL |
| 6613 | 14664 | A | 7335 | 2 | 575 | AGQVQQLGFPGWAGGEGRGRPPLL*LSL PGRQLPREEGLTSVSGHPCWP/DSFFGLP GVEKPQGNLAAGGALLPKLQRQSGPGNH KTLPISRGPADPGAVPVCHSTVGPRG*HS LALHTVPPEKFNIYFFTCPENSSFNLSPLP FRSSLEGIAQGVSSAWGHSAGPGLGLS GDGRQRQARRFSLHSLPCSP |

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| 6614 | 14665 | A | 7336 | 19 | 422 | GEKTDKIQHPLMIKTLTNLGIEKAYISIHK VIHNRPMACIINGAKVKAFVRSERQRC SPSPLLFNIGLKVPVRAIEKEKEMKGI*IG KKEIKLCLSGNDWMTLYLKHPKNSTKTIR TDTFSKVAGYKNTDAWV |
| 6615 | 14666 | A | 7337 | 33 | 193 | GNLGETLMDIGLGKEFMTKTSKAQATKP KI/DWDLN*KSFCTDTNIMHMLIYL |
| 6616 | 14667 | A | 7338 | 87 | 713 | DIYYNCFGFASRKTDCLSTRIPCFTERTSS NS*TQNLTALE*IKYDCATVQACRSRNRK WEVRDALNKFSGTNSIFYIIRFYIYIYIF FFFFFFETESHVAQAGMQWRNLGSLPA PPPGFTPFPCPSLLKWLGPTRRPP/RQTL ANFFVLLVETGFTMLARMVLIS*PRDPP /ASASQSAEITGVSHCTRLKKIRFAKHV EFFFESHVE |
| 6617 | 14668 | A | 7339 | 2 | 105 | ENGWCWIATYGKRKLDLSYLSLHARVNS R/WDLDLGTETMEILEENLGEVLLDIGLG /KEFMTKTPKADSTEIKINR*DSYIWKNE NWIPISHYMQELTQEGLGSRN |
| 6618 | 14669 | A | 734 | 1017 | 1880 | TLAKWWTRREQRSQSTQASSYHQWQR VGACGQAARMRSAPAVIPTRPGEFVHQS LESASNSRLQPVSTGHRSALEAGLLTG CVLMPGCSASQASMEHLSWSPCPDGFCT YRVLRSCPLCNCSPDGPEKENHGOEPE AAVRSQPEGPEGGTRAGRPEPGGGPHLQ EPKASETHNPGIPSREGAAAQGHLCQSG THVRGGKQPSAAGPGRIARVLSGPPGPR ARGRGCADGS*ASPRARSSCRSGGRSRA AAPRRRRGGAGAACARAGCAGG*AGS AARGSSGR |
| 6619 | 14670 | A | 7340 | 2 | 362 | STHETFSKIDHMMSTSLSKIKETIVLSIPS SSSSSSSSSHSKSNLQNYTNTWK/LNLLQ NDF*VNNEIKMET*KFFEMNDNDTSYQS LWD TAKAVLR*NRKDHKLTT*HLKELQ KHEQTQS |
| 6620 | 14671 | A | 7341 | 58 | 341 | IKKFRWGPKPPLKEPPGV/SPDFPII/NFGN PGPVPGKDFKFPNFSSSPWGGAPPVVP TTPGG*MGRFP*PPAFGVPRGGDGSPPPG APKEGPLS |
| 6621 | 14672 | A | 7342 | 2 | 428 | FLRRVSLYCQAGVQWPTSVTEPPPPGFK *F/SCLTLPSSWDYRRAPPRPAKFCIF/M* RLYFTILARMVISIS*PCEPPASASQAGNT GVSHRAGLVFLNKPVTGLGFDSDHHPYH SQISEKDPPPISSIFNKKSIHTNLLIPN |
| 6622 | 14673 | A | 7343 | 2 | 686 | PGPPPEVRQHIRVPGTRTGRAAIWPGSFP VGFLHRAQGRGQSPFPQGTGLGLE WKGCCHAGAQTGSLPIMVHFSGSWE MVSRGKPSS*QLEA*GRGRAPGLGSKAG PRLHQDTPASQCMWVCLNTPSRQVRG PDTQGYVCVPLPPQPHAPRMNQGLPPG APPPPPPSLVPKYFPSSQSSWDRKIPRLQ APPCPPRH/GPPS/AVTNALPNGPRLSAEA PWLG |
| 6623 | 14674 | A | 7344 | 1 | 603 | SGCSRRCPGPWACWTPQKGRGGRKRR SGLWGLCCWCRRPHSHRRAGCHHQDGE CDRWGLLPRDHSRLWIFLRNYWHQLGG E*KANAGGSDRVYQFWG/AGPPSAAPSG AAYLQHSTLNRGSPREDASFTPVGWGT CTMSTRQSPVTPWTASAS*R*EATPVT AVTSM PAGAQSPPPTMSSASAAARTG CTWNGWFWAL |

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| 6624 | 14675 | A | 7346 | 19 | 1562 | GRYWRVVDHGRESRVSGPRFRPSFLAA LPPGRHPWPWDAAGGSPAS*GGAA*S ALGLSQPRPPGASDAAPDSTPAGV*TASS SALIPSRAR*KGSGTLEETKSRRPHSHRS GPVDLSRSSHSDSTPVHGPYFRSAPDP \GAPPRPSAGQSQLGGSSGSPGNSIPCAF VQQ*LERARSHS/SPGSEHRA*SGGLR QGVQGIEVFGLGHPPGGYSCGPQOEKS PPPAHPLGVEIWCRLYIGWKSHPHPA LAEDWQPVPPAAMAVGAPGLRRIQRTS RRWGQCPNEAGHAADPRDSGPPGNYQP VSLHILHMDPGTC*PE*QHPRPPL*MAG KQWPCT*LDKGQSLGLAGSHQHQCQW W*QQLQSHTSLCRSPPPR*RASASPC*AS WGRSSAGAAGFRALGR*HLGTSLPGSAG SLPPCTAEPADASP*LSPTVLAELGSEG ASEECHSCPHGSPQSLSGSHRPAESQYH VER/WKQDMGPISVKSPTRRGPTSGSGL LRLARSSL |
| 6625 | 14676 | A | 7347 | 473 | 792 | MLARALDARFLRWCRDQPLVYHSP*PP GASDAAPDSTPAGV*TASSAPAGEKDA NQMEWARR/VPRAPPPGSPGPLIPSRAR *KSGTLEENKSRPPTQSPFGAG |
| 6626 | 14677 | A | 7348 | 3 | 411 | LCAAVNRALDEGIPLTSALYYATVTLTQ VRNLRSDTDVSMPLVEERHRLYDTG KILLEKFGGCFNLCVRENSAQKLMHS WAESCPSYRDVTLVEGKRASFYKRTQIL VSYTCIVLEGK*DACLODILSITML |
| 6627 | 14678 | A | 7349 | 2 | 331 | AGGPGLPCVPHLPAGARAWRCQPPGA ACCPGRRLPL/GKPSPGSSSRQRGQS CRTVSVLPSSPGC/RGSQVRPDLGPPKA EGCSPWGLRAESCGATGARVRCHRCVV |
| 6628 | 14679 | A | 735 | 1000 | 1211 | VPSTVLDALHILFCLISFLKNKLGWCSGL TPVIPGLWEAEAGLLESQEFTRLVNM AKPCLY*KYKKLA |
| 6629 | 14680 | A | 7350 | 1 | 1062 | EAGPGGQAARSQRGSSSLGLVLPRLRQ CGAPEGHASPTPAGGAPNQLAAPWLL WPCA*PPPGLCYPAPPPPPQKHP/GLLPA PRALPSPRELPGEEPSAHPVHQG/PSRA TRPASASFKSHSGEFRQGLISAAHILQELP GPAGVENFQVFNGAAGPAARHGPPSSRS SC/PCTHGTSGNREKPLSTKSKKNKKA WQATTQAGGPGLPCVPHPAKQVLAHGD ASKPPGAACCPGRRLPL/GKPSPGSSRS RQRGQSCRTVSVLPSSPGLPGTKVRPW *GHLASLVWPGPPGKSPGQSTRPVGTLK RGVHPLPQVVGQSRFVILVLFGRQCQEG RAGMLGTCCLLAKPEVTV |
| 6630 | 14681 | A | 7351 | 423 | 826 | QKVCAHT/CLRGITC*IFTHLCVLRGLCW LLGCCEMCM*MKYVCMCEK/CCTFVG RC/M*VCVCAGDREHLAECVRGCVRHV CTRA*VRMCI/CVCTC/LCV/CV*VSGVCI CKSPCVLCKSIVN/CV*A*THTWFCVHVC V |
| 6631 | 14682 | A | 7352 | 310 | 863 | STHLSLPKCWGLQA*ATLAQPNRSLLK YKFIYMSKGHYSVKVEKQPTWGRKIF WQTMVSG*GGLESRIYKELLQLSNKKTN A*LKSGAKAQHRHFSREHMHMGQHQ QRCLIASLIREMIQMT/LRGYFTLIRMIIT RKSDNN*CWQECAEIGTLL/HYWWECE MVHGRGKIVWQFLKNIQLP |
| 6632 | 14683 | A | 7353 | 3 | 357 | SISNENFPTKESQGPETFTGEFYQTF/DLS PILLKLFQITD*AGTLPSFYEISITIIPKE* KSQENYSAMYLNMIDTKIFHKILATQI*P YINVIIHYDQVGIFPGWQSSFNVIN |
| 6633 | 14684 | A | 7354 | 2 | 207 | GRVDHTHPGLPRPLCPHSPDP/PQRM*SH SAVGASGLADPYERIVVS*DGNSSPNH QGDGASQTSGEQI |

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| 6634 | 14685 | A | 7355 | 1 | 801 | QPRDPSSGTHHPDGRGGQPAPICPRQG SCSHSPLEHAPCPILPGSWPRWHL/DLL SLLGDPKVGGPIACPPGSPPHA WTGPVA CPGLGQPCSCPTILIPHPICQHPKAPGGH PLCSKLLTCLPATPAVPSQPGHHHPLFIM SGLMGAWPSPEAGPGVLPSTTAE*GTR HWTHEEEAALGATDAVTS*PGFGRQVP APRMPAWKPCIRGLLHSLPSEKPLQVH RECVQPC EGLPLAQTGAPQAQAWGPT DLSPQLPHRKHLK |
| 6635 | 14686 | A | 7356 | 3 | 926 | SSGTRHPDGRGGQPAPICPROGSCSHSP LEHAPCPNLPGSWPRWHL/DLLSLLGD PKVGGPIACPPGSPPHA WTG/PLWPVRAL ASPAAAPPILIPHPICQHPKAPGGHPLCS KLLTCLPATPAVPSQPAIITPCSLCQASW EPGLLQKLAPA/PPKLDHVGPRSQGGPD VGVPVCTPKSRPSTCDTTPPLPGLNEER ATGHMRKRLPWELLM/PVTSPLWLWAA GPCT*DACLEMSLHSWPPSQPPPREKPLR SAQGVCAAL*RAGTTLPLRLPLRHKAW GPTDLSPQLPPQKASKINTRGMESVK |
| 6636 | 14687 | B | 7357 | 73 | 255 | XGSSEQDTC SNPGPCSSPTGNPEWGLR DTALLEDLGKASGLLLERMVMDMPANNK CLIFRKN* |
| 6637 | 14688 | A | 7358 | 1 | 710 | PIEITSQCGGIPRFAPITVGV RVSSLPHHS RGEGLQPPPSQSG*GSPAS/HHHSRGEGL QPPPSQSG*GS\QPPPSQSG*GSPASGPGF CWGQ/RP/PLPSCSYSPGALQSSRTPAQT QGPAHHLRGSGPVHGGPPAPSPSCCLLP/ SLRVLPPGLPAPPATSTVCPLPVCTPP WVICQPPYPLAHQAGLG*LPLGDREGVP FHSPNPSLQVCPRPLRKPRWSSGLGPH AHNPMPSMGRSPPRATWTLT |
| 6638 | 14689 | A | 7359 | 3 | 750 | GRGAEQGSHLARAAAVPGSGPAWRPRP RGGLGLRPARSALRAGLPPGRVAAVGR GPALPGQG/HLQSSRTPA/PNPGPCSSPTG EGVPFHSPNPS/H/GKSVPGSSGKYDPLGP VGLCPHAHSPMPSMGRSPPR/GKRG L*P DAQMQEP/SKWGLSGHSPPGGPGKGQW PAPGEDGGHASQQQMPDLPEKLSPSFTP AHLHSLPEA/PVRHEPCLPR/HGPCGRQP HPVCARHRRARRAQAQNKACPAAGKK KKKPVPN |
| 6639 | 14690 | A | 736 | 109 | 346 | PRSLSPHRPAPPSVSVGFRPRGKRG TQG DKGKCLGYRGPQQL*PHGTPGPTQGRR ARGCYLQPGAWGPLLSPWEC DV |
| 6640 | 14691 | A | 7360 | 102 | 380 | GKKIPMLYFAEIEQCILKFVKRS*KAK*I LPKNNKAGGLKFPDFKTYKAAASKHQ VGGLWKELRSTLQAQQTWVPREELRST SPSYQTQVQ |
| 6641 | 14692 | A | 7361 | 190 | 375 | VIYRVSIISIKIPTTFTEIEKTYNLG/WND NRP*IPKAILSL*NKVGDIPLDYEYHLN MN |
| 6642 | 14693 | A | 7362 | 102 | 345 | GKKIPMLYFAEIEKCILKFVKRS*KAK*I LPKNNRAGGLKFPDFKTYKAAASKHQ VGGLWKELRSTLQAQQTWVPREELR |
| 6643 | 14694 | A | 7363 | 12 | 380 | DPTVCCLQEHLTFKDT HRLKVKSWKKI LHANRNQKKAGIAKLISKIDFKSKTVK RDII*MIRASIHPRRLINSYI/WAPNIGNT*I HKILKDLKGGINCNTIIVGDFNTVHR*SRQ KINKHWA |
| 6644 | 14695 | A | 7364 | 3 | 298 | RRSI/NSVAQAGVQWRDLSSLQAPPPGFT PFS*LSLPSSRDYRCLPPCLANFLYF**RL GFTVLARMVLIS*PSDPPTSASESAGITGV SHCAWPISFS |

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| 6645 | 14696 | A | 7365 | 82 | 526 | NHSELQLKLRVA*KMKCTADLSLLEKDT *IKLEENR*QERIMLRAEVNEIENKIENIN KTGSSSEKYYKIDNPLTRSIRRK*T*ITS FRNEKGSVTTNPTEIKRTVKEY/YYEKLY ANKFNNLDEMKKFLKHNLPKLTQKINR KSECS |
| 6646 | 14697 | A | 7366 | 146 | 588 | LPQVMAEFRNNPGEVEGRKAKSMKGQT TGKNQDNPNVIDEIDFLEAFKNIQPS/LFE ASLGLMGIKPVDWEEIGGLEDVKPEVKT AH/WSLRQKSGHCPV/GARLPTGLLATL GSGSGSGRATEAVSGPAG*KRASIGGSS QPRRRFPTVP |
| 6647 | 14698 | A | 7367 | 2 | 1041 | CREAAMHALLHSEKDNPNVIDEIDFLEAF KNIQPSFRSVIGLMDIKPVDWEEIGGLE DVKLKLKQSIESPLTFPWEFVRMGLTQP KGVLLYGPPGCAKTLVRLATSCHCSF VSVSGADLFSPPVGDSEKVLQIFRQAR ASTPAILFLDEIDSILGAS/RQPSKTGCDV QERVLSVLLNELYGVGLKTIERRGSKSS QQEFQEVFNRSVMIAATNRPDVLDLAL LRPGRLDKIIYIPPDHKAARLSIYKRLYK KPCPIGPDVLENLAAETCFFSGADLRNL CTEAALLALQENWTRPQLTVKQEHVF*N HLRL*NRSVKVARTWLVMKTYLRKKDF LTVEGI |
| 6648 | 14699 | A | 7368 | 1 | 2046 | |
| 6649 | 14700 | A | 7369 | 1 | 4340 | MSAFESVPDDEEVDVDAVPENKLTFDNL AEGFRLFKTACDFLYHMDLSMNEDIEKE VKEEIDPDEEESPKKKHLDKKRKLKEMF DAEYDEGESTYFDDLKGEMQKQAQCLG GRSSVSMQAHRRPVVHGGDSCSDPAAM LTTVKAFFTGGVLQRGGLQSSWQAPIF MDVGEWEQRNWRLNCRKLLWGFAAER SREMKPLLVEEVESKGFEIRERTEGRAV GIKSRSKGWCLGCPRRTENQPAQLQSDL NSDPRAL |
| 6650 | 14701 | A | 737 | 134 | 387 | PRSLSPHRPAPPSVSLGFRTRGKRGNGQ RQGEVSWGTGGPQQLWPHGTPGPTQGR RARGCYLQPGASGFLRPPWECDEV*ERG |
| 6651 | 14702 | A | 7370 | 18 | 731 | KEELYGDFENLQTDVH*GKFGPDSLNE DVQUIQEEIDPDEEESAKKKHLDKKRKL KEMFDAEYDEGESTYFDDLKGEMQKRS TGKQHTRFPPRAPHVQLNHAEFEDQD DEARVQYEGFRPGMYVCVEIENVCEFV *NFDPRYPHILGGLGNSEGNVEHVQMRL KKHRWYKKI\KSDPFISSVGRRFQTI PLYIYIEDHNGRQRLKYTPQHMHCGAA VFWGKI*LQ*LAYCRD |
| 6652 | 14703 | A | 7371 | 97 | 373 | TYESEYFLLLLFLFRRQSLALLPRLECS VKIIAHS*NVKLLDSSDLPDSASRVAGIA GACHQAQLIFIFVEMGSCSSFLSVGL NQLF |
| 6653 | 14704 | A | 7372 | 1 | 464 | LVFFSWCLFVCLFVLKTESHIAQAGVQ* RDLSSLQPPPPGFNRFSCLLLSSWDYRR A/PTMPN*FYCWPAAGLKLTTSGDPPASAS PSVGITGVSHCAQPRIVSFTSNIILKFKN LSKGCLIEAYFDKTVKATVLEYLALRNP KPEEHIWGLY |
| 6654 | 14705 | A | 7373 | 181 | 652 | QNRDVHPAASPNSAAQGS*RAKTHSVE GPLSVPGSPAA/PARSL*EQNPVKPHSL P**LSSQLGSPLEDVGNLTLRHKPQSP PSRGRPRPEGTRLHFTEPQRLRSSRQPTI TAHVVLPMPLPTPPAAHACPLPTHAR GTSSKQAEPPPSACS |

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| 6655 | 14706 | A | 7374 | 56 | 480 | TRPTEHLKLSSAVSPGFCRWPPSAPKAEL SPA VPRS PAAGAATIAVVRSRWSPGEPR CPLQTTASVRCAPMHRPVDGACSPPVV *ACRAAARLGPREGPPWDPQSPQSRAEQ KMLPVFGRASDAFFIDKKGFFCLISCCG |
| 6656 | 14707 | A | 7375 | 265 | 2253 | LSILSHCKRGVGCWLFVALGWDHEQP CAPSTHGRAQPE/GPRVLPGRSRP/GTQ TLAAPQPEPGECTSQARSGGPVSPHKAG SEAQES*EGSEDPQD*ELQQERTAKNILG KRLPQ*IILYCHSHLGEQPOT*NPGERRV *PPEFGLGCG*D/STLLAEESGSGWRGP/P WPAGASTPLEAQAPV*AGGCGPPAELPP QPGGAGHPGRPGGSLGHQAGG*GQ** PHPSGPA*PSA*GPRSRP/PSGGRSQPAVS GPGWAWHCPASGPPGTSSFEPQLWLWP LPGLPGQQRPPRLSAARGPQAHGPPRGP FSSPGDRHGPAGGPAVHPARHQR*PAVP AGVTQPGAVQLLLPPHRAGPLQGPGLGS LAWASCEGPPSLLLALPRASWLQTENW CQWLPPPSQVVSCLGNRQ*RPDFAQGIP LRGAPLGPRLPWRGLARAPAPGPWGAP SQCQLPWGRHPSGHLASCPGLP/GGSVS GPPSGGPAGSPPTGPS/GAPGSAG*GPGM AQGGPQEL*GQGPKAGEADSPSPWPCL QGPPGLWAPLPRALDAPPPAWVYPPRPP ASAGGSPCAAPRSPPAASAPGASGF/SA APACSLITLKQDGGGPSISGPASFLQLAW PPGFHPARLHGPSAREARAGSPGPGAGF SAGRGGFPFWSLSSAGCPVSPA |
| 6657 | 14708 | A | 7376 | 58 | 412 | RPAGCGSTRGTCEWARPSAAPCQTAAG GACSPWTPAPRSPAGRSWASSWPG*C WAPPSGHGAQPPSPSGQWWVMRWAP AS/WLPSGATPGPRFLALGTIGVPAGPRS PSPSFTQRF |
| 6658 | 14709 | A | 7377 | 1 | 1548 | DKDNSGPTVLHLTARFGHPKVNVNLLH HGGGDPTAATDMGALPIHYAAAKGDFP SLRLLVRHYPEGVNAQTNGATPLYLAC QEGHLEVTQYLVQECGADPHARAHDG MTPLHAAAQMGHSPVIVWLVSCTDVSL SEQDKDGATATHFAASRGHSHKVLSWLL LHGGEISADLWGGTALYDAEENGELC CQILVVNGAELEVRDRDGYAAADLSDF NGHSHCTHCLRTVENLSMEHCVLSDPS VELEAKQPDSGMSSPNTTVSVQPLNFDL SSPTSTLSNYDSCSSSHSSIKGQHPPRGLS /KH*SCRHTELHGHAEPAGPALGHDWE AHTPTTPTQLPPATPAPRHPTAPTPT*LPI SQASCGTTGS*HLHADQEQTPRGDRGP QEGAE/PPATATTGYGGRTPAASPALSAS SPARGTTTGSWAAAPARRWSHARAWRT ARRRNSLGTTCLTAAPRTPRRPGSSSCRR RRRRRPCPRPRVRRRRSRLCPSRALALA AGSAAPPRPPAAPSLST |
| 6659 | 14710 | A | 7378 | 2601 | 4758 | |
| 6660 | 14711 | A | 7379 | 1 | 741 | |
| 6661 | 14712 | A | 738 | 33 | 509 | VSVSVGLRPPWELQVWVLCVPRGQAKT RLEPAGRAPEAPLPAHSVLAGSDSDSRF RQSLSSAAAPGADSLGARTELVEPGPS RPRPRPRRPSWTTASTADASRRRAAGAR GRGNESAGSGAEVRSEQKVRESIGNR* KRKNKTHSKRKKTLQKQK |
| 6662 | 14713 | A | 7380 | 3 | 5650 | |
| 6663 | 14714 | A | 7381 | 1 | 1131 | |
| 6664 | 14715 | A | 7382 | 421 | 582 | LPGAQGMPRPGVQ*PSGLHIPQGGSTRTS GLKAMRSPKHNHQPDSRAGPWAYC |

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| 6665 | 14716 | A | 7383 | 3795 | 5290 | WNWTVHGDGSAGQGPWLHLFCHKRQH GGISWPLVQREGRDEHFRNQREIAPPAG REQTAVQKQREMFCNSTGRLPGQPTTE IQV*RV*RPHKIYAEERQFKEEKLAEQL KQAEELRQYKVLVHSQERELTQLREKLR EGRDASRSLNQHLLQALLTPDKPDKSQGQ DLQEQLAEGCRLAQQLFQKLSPENDEDE DEDVQVEEAKEVLESSAPREVQKAESK VPEDSLEECITCSNSHSPCDSNQPHKNI NITFEEDKVNSTLVVDRESSHDECQDAV NILPVPGPSTSSATNVSMVVSAGPLSSEKA EMNILEINEKLHPQLAEKKQFRNLKEK CFVTQLACFLANQQNKYKYECKDLIKS MLRNERQFKEEKLAEQLKQAEELRMGS GKYLNEHFVFTENDEDEDEDVQVEEAE KVLESSAPREVQKAESKVPEDSLEECAI TCSNSHGPCDSNQPHKNITFEEDKVNS ALVVDRESSHDECQDAVNILP |
| 6666 | 14717 | A | 7384 | 125 | 605 | EAEALENQSQPCDTG/PQSAFSPPGSTQH PRSQLSQCKQRYQDLQEKLLSEATVFA QANELEK*RVILSEPLLKQDSKQVQVDL QDLGHETCGQSKNEAEQEETWPPAPYL VPRAPSCRPEQSRRGRRYPERSQRRPR GRPPPPCPRIKVKDGKNKTQG |
| 6667 | 14718 | A | 7385 | 310 | 327 | TVKLL*HVGNISLFPSP*MLNTQWGK KSFNEWWWENWISTCRRIKLDPYLLPYI KTN*KSIKDLNCKTTK |
| 6668 | 14719 | A | 7386 | 310 | 327 | TVKLL*HVGNISLFPSP*MLNTQWGK KSFNEWWWENWISTCRRIKLDPYLLPYI KTN*KSIKDLNCKTTK |
| 6669 | 14720 | A | 7387 | 3 | 642 | GKGLFDDEDEESDLFMEAPQDRQAGAS VKEESSSSKPGKKIPAGAVSVFLGDTDFV GAASVPSLKEPQKPEQTPRKSPYGPPT GLFFFSAPHKPSKTRKVQSTADIFGDEE GDLFKEKAVASPEATVSQTDENKARAE KKVTLSSYKLNKPSSETKTQKGLFSDEE DSEDLFSSQSASNLKGASLLPGKLPTSVS WFDDEDEEDNLLGVQ |
| 6670 | 14721 | A | 7388 | 1 | 3096 | MVTHQQPAARKPNMTSKPKPMGPKA HGIFSGTRKNNLEIYMDQTRTGIATKLS KNNKSGGMTLPDFKLYYKAIVAKIACG GSMYNSDTDEDEETEPSSSGQHIENSIT MNKMKLLKAKMKNMNLSKKHITQVSD EEEDDDGCDLFADSEKEEKDIEDIEENTR PKRSRPTSFADELAARIKGDVGRVDEE PTTVSYEDDRRGKNQDAYTEGGLSTIKT VNCSSSLPSGEAKLRKTL/KEKKERRTPS DDE |
| 6671 | 14722 | A | 7389 | 1 | 238 | |
| 6672 | 14723 | A | 739 | 2 | 349 | PASSIQQGGRRACLEVWSCSIWNPTAT GGLDRGSRHSREGGGEAPVRVQGPGE MIPAVPKSSWTLHKMQLPGHVCSTLGR RGDEKGEAGPEAHAYDPSTLGGRGQRIT *GQEFK |

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| 6673 | 14724 | A | 7390 | 1 | 1374 | DDIFATEAIKPSQKTREKEKTLESNLFDD NIDIFADLTVPKPEKSKKKVEAKSIFDDD MDDIFSTGIQAKTTKPKSRSAQAAPEPRF EHKVSNIFFDDPLNAFGGQLRSPSRCCQA DCCPPDSGLVWVGALVGLGGARAAQHI TQVSDEEEDDDGCDLFADESEKEEKDIEDI EENTRPKRSRPTSFADELAARIKGDVAG RVDEEPTTVSYEDDRRGKNQDAYTEGG LSTIKTVNCSSSLPSGEAKLRKTL/KEKK ERRTPSDDEEDNLFAPPKLTDEDFSPFGS GGGLFSGGKGLFDDDEEESDLFTEAPQD RQAGASVKEGKGLGSCSVSVCVPKLSF SLGDGTLRRHGCAASVPSLKEPQKPEQP TPRKSPYGPPTGLFDDDDGDDDDNDFFS TPHSPKSTGKVQSTADIFGDEEGDLFKE KAVASPEATVSQTDENKARAEKKVTL YSQNVKP |
| 6674 | 14725 | A | 7391 | 1 | 417 | MDSSRSVGNNGFTYQDKLSSSKLTSVLEA VAGEYALVINGHSL/ARHRY*LGQYLSS EHFCPGLLYLVLISPFDREDSQRGLGG AETPRCLLERLALSFGSVLQAHAALEADM ELEFLETACACKAVICCRVTPLOKAQV |
| 6675 | 14726 | A | 7392 | 3 | 700 | LVKSYLAQFAARAIISELVSIELAQPLER GTHFPLFLCLQQLAKLQDREWLTFLFQ QSKVNMQKMLPGKRKLTCLFCFFNIISR DFRYLEWYVGGTV*LSCSDNDKHYHRS HL*REIYNLTTFI*SRC*VFFICWVGSLLC YKDLKYLGDIIICEALLSGQDHLVK*TIR* CRWLCLESDQNKDRMLEILEGKGLSFL FPTPQLEKDLFEQIKLDPSPQTIYKWKD NI |
| 6676 | 14727 | A | 7393 | 83 | 3064 | GRPRLPPPSLPLFFVFRSPFSLPYPRRP DPEEAAA VAAAEFLGEGISFLSPPLTPS INIILLKILRCQAAKVESAJAEGGASRFSA SSGGGGSRGAPQHYPKTAGNSEFLGKTP GQNAQKWIPARSTRDDNSAANNANE KERHDAIFRKVRGILNKLTPEKFDKLCLE LLNVGVESKLILKVILLIVDKALEEPKY SSLYAQLCLRLAEDAPNFDGPAAEGQPG QKQSTTFRRLIPKLQDEFENRTR |
| 6677 | 14728 | A | 7394 | 259 | 1157 | EARWQDVGRQLTKTV*PWGRGWSRA SDPRLHAYFSYTAATGKAEPRAARTAPC KARERLGSCLWD*SPPPPGWRPLRYPT PRRAGPAQFGKKRSASARSTWP*/VMQ RLAPKKTRKEQSANDHPIGGPEGRLFTS QLQLKFRALSERISWLEVSRAVTPTSAA VTSTPSTSKPRQKRPTNSQSRSAAKPTPG RRCQPGGRCPTCTRSP*LR*ARGRRHGE ARRLPLREARRLPLREARRLPLRAPRSFR KVPSPGQGRSAPQAGVGAGTGRRRRSM DAWGRARSLAGSAGGVISLGR |
| 6678 | 14729 | A | 7395 | 3 | 432 | HIKRVKKNHMIISVGTEKAFDKIQHSFIIF FKFRKK*EWGHFFNLKSFS*KVRANITL SGDAFSLILVIRQGCLLLPLLFDKVLKVL DSAVKQEKEIRDI*VGKEIKLSLFEDDM IVYIGNNK*/SYRKLPEFINEFSKVAG |
| 6679 | 14730 | A | 7396 | 3 | 504 | AASTGGGWVSEFESVAPGSPDTTAAPTC PQRTPRSLE/LPHFQS*TGPCLNPISEPV EPGQNRGKPRPHYPGPNGWPGA/GGC WSKPGSTPALSDDQANTQVDRN/DLQV ASEGEA*PAELFPKKMKKRLGDLGPGF EGKNGLSTEDKNLIPQAWVPALCGYHV L |
| 6680 | 14731 | A | 7397 | 376 | 419 | VRKYSLCFYIL*NLQNIKAEGILPNSFNE ARITLILKQTRHSEKPKYRPISEMDRHA EILNKISAN*IR*RMKRIHHGQVRFS*/G/ MWGWFNIRKQINV/IHHTHSLKKKNHMI ISINAEKEFDKIRKLPKLNRNIYKQNI*LT VMVRNS |

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| 6681 | 14732 | A | 7398 | 205 | 1463 | VYKKVEASRNEKGWVCGTHAGAFDEG EGPEEAFLGAETAAGAP/GARDHPPFN HGYAGLLEGPDQVGSFSPGRRQA*VC G*RAPQSDCPGGSGRSMGEAGMPPR/Q GPGGLQPPQEGSVFAVMYSIGGQGA VR RIPVRPQPGREGVGQGSLLQPMKPDGEA ASIPTAGSRGRCGPAGRGRRALVGRSL RP*PPC*PSPR*SPPSSGASSPGHPRPAL AHNG*SGWATRGs**DTAPS*HLLVPKQ LAGTCLLCRCPKST**AKLEEIVPGSFHSP RGSYSRGLGAQHQLPSPASVAHPRCQPA PSAASHG*RRPRACLSLHGQLGMIW*S *APSGVQAQGHTHPPGPDISAERAPAGS* LSQLQGP*DSGGLGSGGCAVPVAAAGH PGSLAWQLPPPR*SPAPGSGSPAGRP |
| 6682 | 14733 | A | 7399 | 2 | 680 | |
| 6683 | 14734 | A | 74 | 743 | 1233 | ECGVFSFPFLRQCLVLSQAGVRWPH LGSLLQPDSPGSSRPSHLTLLSSWDLTGT CPPCLANFRIFVETGF/TCFRLVLNS*G SSDPPTPQSVGDCRAGSHHTLAVFSFCF EMGPCSITRAGVAR*HDHSSLQ*NPGLK RSPCLSLPSSGDYWSMPCLA |
| 6684 | 14735 | A | 740 | 15 | 239 | |
| 6685 | 14736 | A | 7400 | 658 | 1657 | PGILSLRNALLTGVDCKVVVPVPPGHTH PQLRLFHFKTCSGWGEWGDHGVVW AGPAPAIYHLHRDVQALWTNDHALAW P*AMTSERTLWPGHELARSFGRSWRISC PTGLPQGGDDRTRGHWVTATCCSADGL RLCRYGDVGRGGLPTVAWP*LTGSCSL RYGSGQCCYTADGTQLLTADSSGGSTP DRGHDWGAPPFRTPPRVPSMSHWLYDV LSFYCCCLWAAPDPGKDRAGLGCTPT*P STLTLASAFGDPHFVTFDGTNFTFNGRG EYVGMG*NQGGRLPSGSRAPTTAGTE TRGTGLTAVAVQEGNSDVVEVRLANRT GPER |
| 6686 | 14737 | A | 7401 | 1 | 422 | RPKPKNSF*LGGEKANKIPHMLMIKTLTK LGIEKTYVNIKVIPIRPMACHINGTKVK AFPVRFERQRCSPSPLLFNIGLKVPARAIE KEKEMKI*IGKKEIKLCLSGNDMTLYL KQPKNSPKTIRTDTFKVAAGYKN |
| 6687 | 14738 | A | 7402 | 247 | 660 | NWSGRRLRMWPSAALSPAVSSPALALTS PPKPLVKGRDGGKPPAGRPREGPGAW R*GPSPTTLGPAKAGSGQRRGRCQP*GP GWRPAASQPLSGCPWCPGITELLLESSE TAEQDRGPGSGEDS*TPDFYTPTRP |
| 6688 | 14739 | A | 7403 | 229 | 1047 | HSVQKAKADKTGVDGGSECGPPLLSLL QSHPRP*P*PLPQKPPEREVWPKDGKLL ASRAGGLVCISLL*EPRVHSGTGPLPVK AELGLLRAQGLPHPASPARLGNTG/VGL ATE*TGISEHKLGPLGN*GVMGDAVR*G LCSEGLCPPSRPWGPMGVCGGLAAKAR PH*QG*VCAPGTHLEGSSVWSLPSQLFP TPGPPAVCSALAPATPARTDGTIONHL WPVTRKSALPVQEWGGDSWGTGQAQE EGPSVGYPGCP*LPGEGRIPPL |
| 6689 | 14740 | A | 7404 | 595 | 626 | CPMPLVPPDISLINEQTEKEAGDLVCPs/A GPVPDSFPLGSEPSHGVSELKTRAKRQR ERHKKGGTEKDRKAERGT/PPGPLPLFLF VH*SG*COVAQGALDIISWLKIIVPKSVFP GCPLKSAAAAATPCSPCHPSHCSPVGV PGRASKFCACPLECP*SPPSPLSLQGPHL CPPPFHASPPDGNPGGQGVPLCLRGSPG HLCAMSRCLRWNP |

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| 6690 | 14741 | A | 7405 | 1 | 603 | EMESRSVT*AGVQ*QDLSSLQ/PLPLHPG FKQFSLPPVSPSKLGITRHTAYLNFFVFL VGDGDFAMLARLVSNSSSQ/CDPPSSAS QSVGITGVSHCACTCSLCCQTMCFLLVA SRYF*FWDGNLFCYNLQIGDVYFIFIYLF VMRPSYSITQARMQWCDLGLSPSPPPRF K*FSCSLSPSSWDYTQHAPPCLANFFVFL AEM |
| 6691 | 14742 | A | 7406 | 211 | 387 | PNLG*LNPPPPGLKNFSCGLP/SKWE*K GQCLPPGPVNFGLTKLGVFPCGPGWLE IYN |
| 6692 | 14743 | A | 7407 | 3 | 326 | LSGVMLSPGFPGYLFT*CIMDNKATH RYCVYISS*IFLQK/HHDYLEVRRGSSE TSTGIGRLNGPQIPCFLLSTHETSLYFHS DYSQNKQGFHIEYQGERSNKK |
| 6693 | 14744 | A | 7408 | 1 | 553 | SDPRTEESHKMLTD*RSSYLSLTALFP/P LPKSEAITRNRASRAASLVRITPSKKDV GFLQKPRLRSCSPSSRCPPGSAARST*AA GTACGCCGTSPRQR*APGALGLRRPPQS *GRRSSPRSLTHPSSALPPPPTSPRTR YRG*SRAAPLLSLRLPSGKLFQPTCRPV SLR*RPSQORVE |
| 6694 | 14745 | A | 7409 | 3 | 377 | KLSPSKPILASTLMGPIYHSHKVKF/PGMK GQFNIQKSIIMTYHINITKNKNDMVISSS SSSSSSSSSSSSSSSSSSPIEGNYFPITKE/Y EKSIANIILDS*KLKAFS/LRSGKRQGYLL SLLLFN |
| 6695 | 14746 | A | 741 | 2 | 311 | FQLDTGSRAPML*CSGVIMAHSIKSLQ TPGLMGSFNLSLPSRWYRHHPPYLANF LIFFIEMGSCYITQGSHPFTLNLGLSLSSLA NKIQGNIGSDLVEDTG |
| 6696 | 14747 | A | 7410 | 1 | 409 | NKVFHNNKRSIHQENKTILNVHVPNNKD PK*LK/QLTKLTEDTDSSIIIVKDFNNPLS/ TL/DRISTQNIS*DLENLKNMTMNQLDQINI YRT/LMPSNTKIEHMMGHKISFIKFQRIKI IQNTFSENGVTKSNNRYLENPKL |
| 6697 | 14748 | A | 7411 | 3 | 414 | KGQDLYGEV*KVLLKVIKQVLNKKWD MSCSNN*HTNFISN*NCIKVFF*LDEI/CSF V**NKC*RIAKEVLSSSQ*CLGGHL/TSPH IRRSYNTTFSQSIWCCYRTKQID*WTRTQ NPEKDLRI*GDLIYDLRCCSSRA |
| 6698 | 14749 | A | 7412 | 3 | 333 | LIKEGQIQKLSAKNGTPQDRHLFLFNSMI LYCVPKLRLMGQKFSVREKMDISGLQV QDIVKPNTAHTFIITGRKRSLAELQTRSSR ATIEKHKQNSSETFKAFGGRLLRD |
| 6699 | 14750 | A | 7413 | 3 | 391 | EEDIVNPANDLIKEGQIQKRSKNGTPQD RHLFLFNSMILYCGPKLRLMGQKFSVRE NMDISRLQGQDIVKPNTVHTFIITGTKRS LELQTRTEEEKD/WIQIIPATIGKHQNA GETFKAFGGPLNQGW |

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| 6700 | 14751 | A | 7414 | 3 | 1811 | RYIDVLGRRYTAPGLG*LWRHPAQS AVP TAHCGDPVSLAAAGDGSPDIGPTGELSG SLKIPNRDSGIDSPSSSVAGENFPCEEGL AGPSPTVLGAHAEMALDSQVPKVTPEE ADSDVGEEPDSENTPQKADKDAGLAQH SGPQKLLHIAQGFAPAEETYVVKRLHL DQVFCTRG*RMRGIPPERSSWGHNLSNI FLPFQPAHQFLLPELKTRITEEWDNTP RLGDILQKLAPFLKMYGEYVKNFDRAV GLVSTWTQSRPLFKDVVHSIQKQEVCGN LTLOHHMLEPVQQRVPYELLLKDYLRKL PQDAPDRKDAERSLELISTAANHSNAAIR KVEKMHKLLLEVYEQLGGEEDIVNPAHE LIKEGQIQKLSAKNGTPQDRHLFLFNSMI LYCVPKLRMLMGQKFSVREKMDISGLQV QDIVKPNTAHTFITGRKRSLELQTRTEEE KKEWIIQATIEKHKQNSSETFKAFGGAF SQDEDPSPDMPITSTSPVEPVVTEGSS GAAGLEPRKLSSKTRRDKEKQSCKSCGE TFNSITKRRHHCKLCGAVSPGRGGQGE ATLSSALTEQLSPHQHTSHAHQPCTEG LPDPGSI |
| 6701 | 14752 | A | 7415 | 189 | 392 | KQKWEKKQLKKSPPGAAAHTCNPSTL GG*GGRITRSNDRDYPGAQHSETPSLT*N GKNLGRGMVGG |
| 6702 | 14753 | A | 7416 | 2 | 325 | SHAGCLIRFWRKSMTPHSLPLTPTFLGT CEASFLEPRASVPPQCSMALRRYRLDM GQSFWGGLPSSHPPDPSRPGFV/PGVGHV PGQEGPGGKPADSS*H*DPTGG |
| 6703 | 14754 | A | 7417 | 9 | 1430 | NDNASFGEVYYHPYPPVGSQCHDESGA GFPPGSPCPGTWPTPALKPREGSGGWL LGQASPVTTPACPAF*VPCCTGEGQG WLGAPGKDASH/GA*KM*GVKGRLCVG APEGAG/PSQGI*SFFTEP**AHPQNGLYE DEHKNSRWGHPHPI*QWNWDRTS*CN PSRP*VHPWVRACGLEPAGPGHRT PSQVGVLFLQKRIKQACEPYALFTPLSP HSS/PASARPGSPD*MCRAPEDESCPEMA LLPGMGPPGSGERCSRAPSGAQVTGGV PGPFTWGSGESRCFRAPSPGASGEEAKC SRSPFTGSGESRCSGAPSGAQVRAGV PRPITWGSGESRCSRPPSGAQVRTGV GPFTWGSGESRCSGPLHLRPGSYVPFLA PERKGPQQRSEKQGHKRGGSQAAPKPS R/PQESPSPLTPSGGPGS\GRNGA*GVSEG *SAPGSGGEEEDVFGC*GPPALGPEG |
| 6704 | 14755 | A | 7418 | 1 | 389 | HLTFCHHHYDDRVRGLYKQKECPGIPR VYRIRHIGEGRLHYVLQFKDHPGIHQPLE PQVKYVGNMHSNKAFFGR*LMLQLSEFL CEEIRNKNQRIVQLIQDTRIHLPSMNPDC YQGGVAKGPNKPWLC |
| 6705 | 14756 | A | 7419 | 31 | 392 | KHNRA PPPS*KKSSSPVTTKGRYTKTP HTDVPQG*QPPYKQRGTTSSSPFSFISY SIVLSSSRPPHPGPTSPRLHPSRSHLSEV PPLTQVPPLQGPVPHDPDTPSWLYLSPSS YLY |
| 6706 | 14757 | C | 742 | 398 | 574 | |
| 6707 | 14758 | A | 7420 | 2 | 704 | TDSKCPFLVHQAHAAAM*KERHFLTANG SCIKFHQDINRLSSVFLP*ELVVRHCRG HQKRVD EIAKGNRLADQRAKSAVRRPQ GPKTLEAPLIWEGYIREIKPQYSP/DRDR MGHLSRYTFQPSGWLQSEDCKVRLPASS QWKILKILH*AFHLGKHKTSVHPKIVLRR KSTKNGQIGC*YS*NPLKNPNFNR*LLPH HNQRMGSYSGEDWQIDFTHMPKINGIQ LLEWVHTFI |

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| 6708 | 14759 | A | 7421 | 2 | 705 | FSRDEVSPSWPGWSQTPD/LRDT/CLGL PKC*DYRCGPPHLAESKFYFPII*KL YHSLMLCL*ADSKS*KPMSLFLFLFL FTQN FALVAQAGVQWHGFGSLQPLPPGFKRFS CLSLSSWDYRCLPPRLA*/FFVFLVQMG FTMLVRLVSNS*AQ/CDPHALASQSVGT IGISHCSWPNVYIITM*IFFSIPSPLLIR HLFFLFFFETESRSVA*AGVQWHNLGS LQPPRL |
| 6709 | 14760 | A | 7422 | 33 | 775 | VMGPAPAGEQLRGATGEPEVMEPALEG TGKEGKKASSRKRTLAEPKAGLLQPVK LSRAELYKEPTNEELNRLRETEILFHS SL LRLQVEELLKEVRLSEKKDRIDAFIRE VNQRVVRVPSVPETELTDQAWLPAGVR VPLPKCPMP*RACFRFLAPKPRITVCEA SYLSGQPSIRPDJNVDAITMPREILQDK DGLNQRYFRKRALYLAHLAHLAQDPL FGSVCFSYTNGCHLKPSSLLRPQ |
| 6710 | 14761 | A | 7423 | 74 | 576 | LCWQPIRWWSPTLRANGHQK*/SGVAILI SDKTNFKATAVERDKEGHIYIMLGLVQ QENITILNIYAPNTGTLTFIKRLIDLRNEI DSNTIIVGDFSTPLTALDRPPRQKVNET MDLNYTLEQMDLIDYRTFHTTAEYTF YSTAHGTFSKIDHRIGHKISLNTFK |
| 6711 | 14762 | B | 7424 | 158 | 346 | XLSQGEVVVPQIPVKSGPHGAGVLGLHL EGPFISREKRGAPHAHLRSFEADAFQDL LATQGQX* |
| 6712 | 14763 | A | 7425 | 1 | 1768 | FFVTVFVMYFTTIFKKQTKTNLKSASPTP QNHP/GSSSLAQ/PLSHDPGPLSHNPGLA LWDQPSLPAPPRSSQGGGALCGEWQ/ PGPKAGPGLTSS/GDWGVPSEVGDDQHA SSGF*/P*GWGTFKH*QPASLGTGRCS TS NTSAENLTCLSLPGSPGKTAPLPGAQA GAGQPLPKGCAAVKAEVGIPAPPPPGG QDPHPSPAFLGSPGACGLRSTPCALPQA LPQARPCPGRWFFPWLPFQTGGAPDHP ISLDPGDISFNWALQQEGKRTSARA/RGA YLLCPRTAP/GKQGGREPPTPELKWRESQ DNHP*RGAAPIPDV*PHCGCPQSQEGSRS PPASKLFQGESRPVFATWVCSRAKGTQK MAG*H*WGEQGTLPVPRHTALQHAGSP QPASTGPGDV*RDRVIEKRKQNAHPW HSGLGSPGSKNRGPGSLPPGGQSGAPG NCALAQEPGCGF/TRCTPQTQEQKANP*L STLPVTGPLPAGSSPPAHGGFTPWAPAT* LPAPPSH**HFPGVCRSPV/PSCRQALSP TGAQGP*TTAQPSHPRP*MPSPGGQPG WCHM*AQAKPGAKASPAGCTFSQPPPP GRR |
| 6713 | 14764 | A | 7426 | 36 | 620 | QHLKLLNIKNHTGEKS*KCKECDKAFK WLSHFIIKIVHTEENFYKCEQCGKTFNE CSHLIAQESIYT*KKMYKYKDHEKAINIY SHL/NHWRVHT**KEYKCNVCQKIFQ/INI NL*SEEGIFYFEDEHYKCEEGCSTFICITDFI VHILY*KKTLKCCSNFVQHQQIYIEKLC KFNF*KTLFQKVQLRRHQSSY |
| 6714 | 14765 | A | 7427 | 3 | 276 | PKKSTEKLLEVISNNSKFTROKANVQKSI TFLOYSNEQVKFKM*NTLP/YKMKYLG ISVTKHMQDPYEEKYKTLMKDNKEEQN K*RDIPCL |
| 6715 | 14766 | A | 7428 | 125 | 456 | LADWAHRAPASQQRNGADYAVYINTAQ EFDGSDSGARPDEAVSWGKIRVDAQPV K/VKRWLGA*GLWDDCGSHGLPRFPP TQVYAAASLVFPLLEAETFAQKMDAFT HEK |

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| 6716 | 14767 | A | 7429 | 1 | 571 | LSGKEVRENGIHRUGNLLVPMENYCKF EDWLMPILOQMVMEQNKRGGFGLKKW TPSKMIARLGKEINNPEVYYWAQKNHI PVFSPALTDGSLGDMIFFHSYKNPGLVL DIVEAERG/ADYAVYINTAQEFDGSDSG ARPDEA/VPPWKGIRVDAQPVKVYANAS LVFPALLVAETFAQKMDAFMHEKNED |
| 6717 | 14768 | A | 743 | 3 | 862 | RNERHAYDKGTWKTRRAIMTVQ*SGET NVDRAYNLLYQTLTDWTSYVTC*ENKEI AAGQRNESHSDWTKYQVWEWLQHL DTNQLDANCIPFQEFDINGEHLCSMSLQE FTRAAGTAGQLLYSNLQHLKWNGGHTG ISKSCKETRHLFPFFYLGPGLTLATCRAV SKRLQPKLQCAVHSFVTPGIPYLDEIGYR ARDLREPQQGVAALLPLSSDGNRRRPG LPKLKAQRRVRFPSPNKGRGGPSSPPFHS AFLNWQHKNVWMVKELSSYLGPLQY YPGSFGGAI |
| 6718 | 14769 | A | 7430 | 1 | 311 | RRVSSESRWRSLESRGRSLEIQGRMERPR CQRFRENSCVAPRHCKGPGGKGLQALF* VPVAQLGEPGAQLGDPGAHGEATVPEV QGE/PAALLPGTAKVPGGEGSPGFIPPRHC RGTGEEGSPGFTQGRETSKAQRTGCLL SCRGCLCLSVSGDS |
| 6719 | 14770 | A | 7431 | 250 | 503 | DDEKKSKEIEVWVGSDEEEDNGKDKKK KTNKIKEK/YIDWEELNLIKNIWIRNSDDI VTQEEYREFYKSFTSD*EDHLAVKHFSVE |
| 6720 | 14771 | A | 7432 | 3 | 540 | KRRGSFKMAELYQLPDESSAKALVSLK EGSLSNWNEKYSSLQKTPVWKGKNTS SAVEMPFRNSKRSLFSEDDDRQINTRSP KRNQVRVAMVPQKFTATMSTPDKKASQK IGFRLRNLLKLS*RH*WGIL/AKWFYSNI DKPLFEGDNDFCVCLKESFPNLKTRKLT RVEWGKIRRLMG |
| 6721 | 14772 | A | 7433 | 3 | 322 | FFLRWTL/DTVTRGGIQWCNLGSPQPP/P PRFKRFSCLSLSSWDYRPPPCANFLY F**RRGFTMLARLVLP*PRDPPASASQS AGITGVGHRAWPMPIFENRFDL |
| 6722 | 14773 | A | 7434 | 22 | 475 | PRMISCRPTRPPTRP*SHSAFRRHFLLVHP VKAKYFLSAVMTTHHLASASHFPFAA* SATFPAAPQPMWTSDLPPSTCLPLGTS PLPSRPLLVPSSCS/SFPDPTQMPPLPSTFP GLPFL*PHSSALSLPLL*LPHGFALSPSSV PFPT |
| 6723 | 14774 | A | 7435 | 14 | 362 | LFYQTFNSVN*KT/RHKMNK*TEDFNNTI EQDLDTVTFISLHSTVEYAILLITHATIFI DHLLS*KTHLSK/CSADGITQIPNYDTIK QEVKNTNMSKNK*KLNNKFSNTLLFKR L |
| 6724 | 14775 | A | 7436 | 1 | 440 | SPFPPKNFYFSLRPLIFLRGVGPKLPPPKK RVFSKNPPEVFKSPPLKKNFSPPPVNL GPPKDLLKG/PPSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSPDREPPPTI*N*PTRP |
| 6725 | 14776 | A | 7437 | 8 | 487 | DEVSLVAQAGVQWHNLGSLQPLLPGFK RSSYLSLLSSWDYRCPPLANFIFSRD GGFTMLARLVLS*PQ/CDLPASASQSV VITGVSHCARVAPSF*MSAGVTICVGW ELFGMSPVAEANDHLSGALVPFSALFS HFMPGLLPTMFCPLRGCE |
| 6726 | 14777 | A | 7438 | 1 | 445 | IDCWHKCQDMSMGKDNLFN*SYWDYWI SI*KKRTSNLISPIHKIES/RWIINLVNSK ALFRRKQRKTLHDCGLGNSFVEETQKAL TN/WDHKLQ/SFCSSKYTTKKLKR*ATD WGKIPTLFAKNNDKICEHTHNKRRYM FGQMHVKWWA |

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| 6727 | 14778 | A | 7439 | 131 | 763 | PGISADSRGQQLS*WGPPSHQPPPGPLKG SAPGGLVCLVGPAAKHALRPSFHSGA PSAGNLGCFAAWASSLNSNQSPSSKG HIPKDRGEPRGTVP SLRKATATGRKAER LSDEGRSSVHG*AGIPGHEGNAKENRDR HPWQLPGIASAAVVIASGRGALPPGGQA GPQKLAPPFSSLSVPGGARWG*AEGAPS KQRGKVTGEPGRQC |
| 6728 | 14779 | A | 744 | 15 | 404 | RNFRVDDLVSPPCCGILWFFTQGGQASCW RPLATLPSRQKPGSSPGKAGCWPA/WDL GLVPHGVSGVSIAASSTPQGGAVCSPSV AAPSTLLLRTHLLGAASLQGCQHQILL HHLIGMDLYVAASPSHRFW |
| 6729 | 14780 | A | 7440 | 47 | 265 | |
| 6730 | 14781 | A | 7441 | 1 | 330 | HHHLAPFSSLPFNIVL/EEVLARPINKEAK *KAP*LERKEVKLPLFAEEIQEMIWIYDN SKESTKEVLELINKFIKATRYRFHIQ*LVF LYTCNNLK*KLKYLINLTKV |
| 6731 | 14782 | A | 7442 | 3 | 423 | NNALLNNPWVKGAIPKEVRPYLD/TREN KVTA*QNLWDALKK*/CSGKLIALKE*C QINNLSFPLKIKEK*EQIKSPVNIKNVIFK KLKIKKGLKV*KK*RKISETKSWFLEKVI KIY*SQGRHARKKNEKSGITRDSRTRG |
| 6732 | 14783 | A | 7443 | 1 | 689 | YIYIYSYINIQFVFL*EHLLINKFLSFVYQ LMLKH*KKRTTNTLFTLIRTM*AFLFYY QIICISYVIAAVLFCI*IFFP*HLCLLVVLF MYFFNILRFIPLLRSDITSFHYMPLFGRFL SC*SKQEHHLNHCQPGIYFINLLVWKHFFL DVIFTLVYFVG/FALLIYDFLIMSVC*TF YLSLFISR/ACLLFYPHI*LIFIWAYISRLEH SFHTF*GIYTFASEIVFIIF |
| 6733 | 14784 | A | 7444 | 3 | 545 | TMLLFTLQNRCTSSHCMPAPALCPGK LTVGTGSMGPRISPWPSSANA*PVDKP SGQEG*GQCTAAAPCRVAVSLSKVRAP GDGLSCGSSCPPG/RQGRGVPCPAAGER REGREDLKPRE*IGSCIKNKLGISPAK*D* KNSQDKSKKNPIGDRTSLAVGTVPQSTR PRVPLGYHYCY |
| 6734 | 14785 | A | 7445 | 243 | 768 | NLPNK*QDEGRGGGAEPWPWP/SLPPR DVEAPSPRLGAPAWPPAGRWPPREG AWLG*VLCFRKRSPVPLGVAGA*ASVG GGCVGRCPVSGAWPPPGVGDKPSPYCSE RPAASFP/PRTCVPFNAEGGERAPRDSR GEGSLPCCRGEERGQGLKTTRINRFVY QEQRDFTS |
| 6735 | 14786 | A | 7446 | 596 | 1335 | LEQITFSVATAMDSRFPDFQDLLEPERA CHDAAGTLEVDFFLNFGTVDLARKE TTTEQALPPALLGIRPEFLSRPSVQTED APSKVNYVLCLLIAECSPGSDYLP CAIP SAYR/RWYLD FCPR*FLPPYY*RRHPFQW TTVTQEAFFSHHDVAFTSTPVLFPYPSAQ PFIVKSESSQIAKAALSQQRPSLIYERL HFFS*SLQRHTIDLQGF*ILMLSEERQH LFESSIGPHPTISKD |
| 6736 | 14787 | A | 7447 | 199 | 450 | ERSFSKKMP*NPPGGGEPP*PTLGIPSSPP PHLLGPKFLEKIFGLPGLPGGKIFP/P/GFA FGPNLGSNGEIPGGINPRSLPLGER |
| 6737 | 14788 | A | 7448 | 154 | 695 | GLLSNLLISIFFIPPKKSAPKYQHMKHSQS FHFYCFNTHFNFLNKF/FNELQ/K*HEL KLE*SKIILYNQNKPSV TYREIMQLRAQL KKIIDSVKHKRTWQGLKQGV/YWGFYV NVIGKSFFYFWDKYFIFIDWAKNTLRN MGPERPTVFLPNFIYSQSTKLALNWVINI MGQFIPSYVSA |
| 6738 | 14789 | A | 7449 | 203 | 443 | FFVKGPKNTHW/RKDSIVNKWC*KN*IST CRRMRDTCLSLYTKIK*KLRIPIESGTE PR |
| 6739 | 14790 | A | 745 | 1001 | 1459 | |

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| 6740 | 14791 | A | 7450 | 8 | 312 | QTLALSPGLGVQWRDLGSPQALPPGFMP FLLP*ASQISRDYRRPAN/LMPGPNFFIFQ AETGFSTVLAPGWCDLPDLVIHSASASP SAGITGVSHRCPARTF |
| 6741 | 14792 | A | 7451 | 1 | 2554 | MKVWLLLGLLLVHEALEDVTGQHLPKN KRPKEPGENRIKPTNKKVKPKIPKMKDR DSANSAPKTQSIMMQVLDKGRFQKPAA TSLLAGQTVELRCKGSRIGWSYPAYLD TFKDSRLSLYNSRGLLREGQAGPMGSQP KVNPTMARVPQVEPPVGETWESSTLLA DGAVDKRSSFALCSSFISTWKLATLNDP VHLLSLVCTWTLRTAGRSRTARHVAVA ASRCGHLTFAWQNQYISLERLSVYMCRF VTWVNCMSRFGFVDYFIQVLKLIQVLP PDSVHPRSHKHLLSLRSEIAKTTSYCPKH SSLSIPLPRNQMRSGVSVTLEQRSESTSSP FPVTALLFVNLTSLWLGKGPILPKYVAVS VQLSRAGACFSDVTHREVLMSFCYMVV GGDFLLGGSLVCQVWFVFWVSRGYTLI FSESREYLKEEEELFLCKGPGYAGQRVK KNDDPSSVKQNERYGQLTLVNSTADT GEFSCWVQLCSGYICRKDEAKTGSTYIFF TESGGRISVLVNLVLTAEQELLAHEPFDD VSRNSAPNLKHHLTVTQRRQVGKKAKK NYLFQEHCGENTRKHVIRIGVSLALKISL CKYCNIPSONDPEKQRIQCTMPKKKSHQ HQQKYPQKPSPEFLACPKDRIEKGEFVFP SPSYFDVVYLNPDRAVVP/PGDRAVG QSHAPQGIPSQGDPSQWNGHCL*HEAGL CVSATSFRAPGCGLLQGGGRGQISDLRQ VPAALRGGPNSSKPAFCSSCHMQAPW* V/LAALSRRPQFPPLPSPLSLGHQVTG IPSGPPSTTILASSNKVKSGDDISVLCTVL GEPDVEVEFTWIFPGQKPPSRVTGLWAG TWWCLYRVL |
| 6742 | 14793 | B | 7452 | 1 | 2586 | MKVWLLLGLLLVHEALEDVTGQHLPKN KRPKEPGENRIKPTNKKVKPKIPKMKDR DSANSAPKTQSIMMQVLDKGFQKPAA TSLLAGQTVELRCKGSRIGWSYPAYLD TFKDSRLSLYNSRGLLREGQAGPMGSQP KVNPTMARVPQVEPPVGETWESSTLLA DGAVDKRSSFALCSSFISTWKLATLNDP VHLLSLVCTWTLRTAGRSRTARHVAVA ASRCGHLTFAWQNQYISLERLSVYMCRF VTWVNCMSRFGFVDYFIQVLKLIQVLP PDSVHPRSHKHLLSLRSEIAKTTSYCPKH SSLSIPLPRNQMRSGVSVTLEQRSESTSSP FPVTALLFVNLTSLWLGKESREYLKEEEE LFLCKGPGYAGQRVKKNDDPSSVKQNE RYGQLTLVNSTADTGEFSCWVQLCSG YICRKDEAKTGSTYIFFTESGGRISVLVN LVLTAEQELLAHEPFDDVSRNFAPNLKHH LTVTQRRQVGKKAKKNYLFQEHCGENT RKHVIRIGVSLALKISLCKYCNIPSONDPE KQRIQCTMPKKKSHQHQQKYPQKPSPEF LACPKDRIEKGEFVFPSPSYFDVVYLNPD RQAVVPCRVTVLSAKVTLHREFFAKEIP ANGTDIVYDMKRGFVYLQPHSEHQGVV YCRAEAGGRSQISVKYQLLYVAGWMFS FLVMTLTENPSSPFQPNPSIVHSGAASVL DQSQQFIQACFLFLSHAGSMVSAAL SRRPQFPPLPSPLSLGHQVRGIPSGPP STTILASSNKVKSGDDISVLCTVLGEPDV EVEFTWIFPGQKDERPVTIQDTWRLIHRG LGHTTRISQSVITVEDFETIDAGYYICTAQ NLQGQTTVATTVEFS* |
| 6743 | 14794 | B | 7453 | 520 | 600 | MIDCVFGAELAESLSFILGILGFTFLL* |

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| 6744 | 14795 | A | 7454 | 78 | 624 | TNKSQGSQGLCVAGPRACPQSSPVQQR NVPPLSILSAPFSGS*GL*PCGGVLGATG GAELMGLLRSWCPPGVCTVSLGQQVGS LSLESEPPASSLNNRGLLREGQAASVGG QPKVTSPTMARVL*VEPPVCETWGPHP WQMGPLPRG/VWAGPPQTPCGVTQLA ANGKQPVRKPGSYP |
| 6745 | 14796 | A | 7455 | 3 | 369 | ISQPPKNLGPPEKTYKRPPSSSSSKKEFPF FFPGESKGGVLSRKGSSSRVKPFSAPT PKKGGPRSSSRGGKSSSRNFKKGGFP G*PRRFFFGPGKPPRPPKAG/H/YRGK PPGPGPK |
| 6746 | 14797 | A | 7456 | 2 | 648 | QTLPFKGRLPQEDGLGIRRPSCRPALPWL CQGAACPLPASLQVVPQHMDPIQLVP PFLSPARLLEL*EGRQKGRWGRPSQAG GQEKQLSSSSASPTAERARPPRAGTYG* CLALP*VTGGVGPMASTLPVTTGMGQD SRGNR*EGPGVR*/DWGCSPRER*EGGTG VALEERGLLQREQTSVGVSSEPGFVF QRPALPGPWVCPRLHKRLA |
| 6747 | 14798 | C | 7457 | 89 | 376 | |
| 6748 | 14799 | A | 7458 | 3 | 864 | MNFSPLFSPNFGDFSQNIPTSEQQQPLA QNSSGKTEYMAFPKPFSSSSSIGAEKPRN KKLPEEEVESSRTPWLYEQEVEKPFIF TGFSVSVEKSTSSNRKNQLDTNGRRRQF DEESLESFSSMPDPVDPPTVTFTKTRKA SAQASLASWKDKTPKSKSKRNSYSSWK SRVKNIRYESASMSSTCEPCKSRNRHSA QTEEPVQAKVFSRKNHEQLEKIICNRST EISSETGSDFSMFEALRDTIYSEVATLISQ NESRPHFLIELFHQLQLLNTDYLRLRAL |
| 6749 | 14800 | A | 7459 | 2 | 743 | KASQASLASKDKTPKSKSKRNSTQLK SRVKNIRYESASMSSTCEPCKSRNRHSA QTEEPVQAKVFSRKNHEQLEKIICNRST EISSAHARRILQSNRNACNEAPETGSD SMFEALRDTIYSEVATLISQNESRPHFLM ELAFHELQLLNTDYLRLQALYALQDIVS RHISESHEKGENVKS VNSGTWIASNSELT PSESLATDDDFIQEK*KYASQKHLHINV HSIFSHDSLKLKHQEING |
| 6750 | 14801 | A | 746 | 3 | 357 | |
| 6751 | 14802 | A | 7460 | 1 | 336 | IYFPTPEKFGPPKETLKKGAPSSSSSKQKF PFFGPGGKQKGGFGLQLTPPS/RSSPFP QPPQEKGFQGRSSSSG*ICIFKKKGGFPG WAGGVQNPKNPKGFGPPGPLKPWG |
| 6752 | 14803 | A | 7461 | 1 | 3010 | YRIPGGGTWQSARPRVGSRAVDGEGA RRGLCSPSSRRWRPGPPQPHCPGRAPA LSCAAAAPARRPRGHAESRRDGGGLGSAE EEESWYDQDLEQDLHLAELGKTLLE RNKELEGLQQMYSTNEEQVQIEIYLT QLDTRLHVNEQHAKVYEQLDLTARDLE LTNHRLVLESKAAQKIHGLTETIERLQA QVEELQAQVEQLRGLEQLRVLREKRERR RTIHTFPCLKELCTSPRCKDAFRLHSSSLE LPA |
| 6753 | 14804 | A | 7462 | 2 | 190 | SSNKKKPPKNHPEPDSFKTEFYQTF/INT P*IPILKLFQKTELQEILPNSFCEVSITNSS TRR |
| 6754 | 14805 | A | 7464 | 359 | 1095 | PKGNGNLWCGASLLNARMRAGNKSPP LRLPPGATKSLPQALQFQPLLAEPDSA AGLGTGGTPRLTEVGGAL/S**RSGSGFP ENQKGPPDPASGYLDLMHTPPFSQDPIS PASHMPIPSWSTLFSVEDRRSRQKTTGR WGSRCGLPHTCSILVGGVTREGVEMLP MGTCGKCAPFAPHLAASSNSVLTAGDP APGAGRLGSAAQEAALGQGGGRRSQAP PRRALQRPHAWVETTSQWRSAG |

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| 6755 | 14806 | A | 7465 | 16 | 405 | VGAIQRAPPAPPSCARCLHTPDIRATLTQ TPGGLTPQEKDHEHGHGDRAGHS VWVLDPGTCSRRRR/WFSPLYLELRSS GECRG*SPASPSLSHHTAHVTPKAFIEHL LCARCKEDSGITGQGAF |
| 6756 | 14807 | A | 7466 | 16 | 255 | ARPCPCSWSFSCCGVSPGA/LVTEAAIF YETQPSLWAESESLKPLAKLMTYFKNS TYLIRLFMIYRCKPVKSKKKKRNN |
| 6757 | 14808 | B | 7467 | 1 | 1026 | MRARRLPWALTTLVAELGWDTOGGDQT SPGGNDRMSMEAECESTTVSPLSCSIPTG CGQTREEVSARATPPPSLGASLLQTLTPD THCTGVSAITMSMLVVFLLLWPFSSST LAKHKRIHTGEKPYKCEECGKAFFRSST LAKHKRIHTGEKPYKCKEKGAFROSST LTKHKIHTEEKPYKCKECDKAFKRLSTL AKHKIHHAGEKLYKCEECGKAFNRSSNL TIHKFIHTGEKPYKCEECGKAFNWSSSLT KHKRIHTREKPFKCKEKGAFIWSSTLTR HKRIHTGEKPYKCEECGKAFFRSSTLT HKTIHTGEKPYKCKEKGKLLSTPQPLLN K* |
| 6758 | 14809 | A | 7468 | 1255 | 2710 | ARPCPCSWSFSCCGVSPGA/LVTEAAIF YETQPSLWAESESLKPLANVTLTCQAR LETPDFQLLKNQVAQEPVHLDSPAIAHQ FLLTGDGTQGPLPLPLGLVHRMDPAEQAP WS*QGPKALFNSTPPTESLPAPWLSMAP VSWITPGPETTSRCRGVLRGVTFLRRE GDHEFLEVPEAQEDVEATFPVHQPNYS CSYRTDGEALSEPSATVTIEELAAPPPP VLASTMESPPRCTLGNKVTLTCVAPLSG SGISSLRGGGERAAGNPGGSTSPDRIFH LNAVALGDGGHYTCRYRLHDNQNGWS GDSAPVELILSDETLPAPEFSPEESGRAL RLRCLAPLEGARFALVREDRGRRVHRF QSPAGTEALFELHNISVADSANYSCVYV DLKPPFGGSAPSERLELHVDGELAGHQR GRARVQCPSGPPVFPLFPWASDGGALGL GSAPIAYPGGEQAIGGRGSGDAWNFLGF PTDASP |
| 6759 | 14810 | A | 7469 | 3 | 1312 | GEAGRGGSTGLGAGQGCATSQGLAARS SWGHRVGHQLGSRGPTRSSAQ*GAAA ADLQAGRHSNDHNPPPT*AA*G*NLPAE E*GGPRAGAPAHASCPTDPSAGEPGTGA GAARRWHQGLCSPSGV*PQASPGSSPR AQTSQPGAAQEHHEPRE*AAQAGERPA GGSEVGAGASGGPAAGTGACGNPGPA AAGSPRGQGSRAATGHTGCGAVQLPR PAPSGRG*KCPAAAAAQETEG*VRPTAA TLRLAGSGARRWCRPSASHHGPPDIPGG DSGGHPGSAPQP*AAAGPGCPQLPQEAG GSEPQA*RATGCLQGPGRCILGPDPEAP GLLPQHPRAGTGAGTAAGPGHDG*RA TF*ATGVRGPAP/EAGTSTKS*G*GSWQV QGTGPKWGLCLOPSPSIQGPAATRPSPK GRAEQSSASTEPSHPAPRKT |
| 6760 | 14811 | A | 747 | 461 | 791 | ESLQTGLTFKSDMDLLPHIGPCR*DG AVSGAPSSNSFPTSVAGSTRLAKERGDH HLRKQPRWEVHGAVRRRAVHRPFIFHLR KEAACCLFPPPTLLPSRQQTLLPSK |

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| 6761 | 14812 | A | 7470 | 1 | 1987 | MWEP CGS QGDT/GVFGCRDR*GG*GAA GCAGRPS PGDRGQWPHACGGGGRGHPS TSTGAPAGHGEEAASEQRLLSGGPLRPP GPH*AH RHVGP GAGRLC*LGRREPQHR VPSRSAPAAPGRLPALPFLDEDKG*AEPR EAAPRRPRAAGHSPGHVSHCGEAPGGL DHLHL PQ/SPAGMGSEHDGRSGQC*PSR HTSP\PTRLQPSPPDTHPGGSSLPAPRPAL SCWARVFASLGDQPAFLGGHTGPPDAS GEPQHKH*PS/GPLSSSFFGAPIQGRQRNT ESLPGTC*GMEWPTAALG*RGPRPVTAT PGTPGGAPTS\GFP\GCQAQKPEAGLVVA NGTMCCPAKHTWRSGPKIPTLISILPLLL LHGGAVSLGSP PQGSALRPAPASLGPCV TDKSIPSLAQNTKYSPDLP*ET**HLPECS RGWGSPLLVLHPLLGHILVSAHIPLPGYK ACPRPLNLLGRFGA\QGPRGSLSRSSRG */PGPAPSALGVSGSPSSHPPN/GLYAEAH RMGFLPD SKSKNGLISKCKLTFHPQTSK PPAPISP*SKTSGGRKNRLPGLHSQQSFG RMPPGMP*APSVYLLPLSHPLPLRTAG KPSSLPQPRSPSLVSSHTRAQQLSLV*G QPCVPGHTSTRQGLPPLHSILPAELPQSSF ANRGIKASLRIRK |
| 6762 | 14813 | A | 7471 | 2 | 353 | DRKEERLRSRSGAAATRSSGKGVAE WDPLPCLDPELWDQFDNLKNHSEKFI SAKERTIEISYTKQLRNLLKTCQPKRN WKEKEYIT*NSPSLPVNKMSDHARQH*V ITLGSIKLSSLRS |
| 6763 | 14814 | A | 7472 | 2 | 390 | PLDPQRVKIEDKVNKSRSS*KN/LGLEDL GTYSVIVTDAEDISASHTLTEEELEKLL KLSHEIKNPVIKLISGWNIDILERGEVRL WLEVQKLSPAELHLIFNNKEIFSSPNRK INFDEKGLVEVIIH |
| 6764 | 14815 | A | 7473 | 3 | 223 | DAWVTSTNADKEFEKIQHPLMIKLSK* VYNMSYIYPLFKIIGIYDKSLVNIILNVE KLKAFFLRTGTREER |
| 6765 | 14816 | A | 7474 | 3 | 1033 | CPLPFSL*YSTCGEKQPMQSWRASAASP GQSAPSSSAVGCWKASCKQYVWGTPSY SYTNRFPRRTPHSPGVWKACISRAG*PA RKNSLICLAGKTGALKDTSKGAPVFPL CHRHSDPGGGFHCAELGTGNSPLGRLL KGLP*PAAVPCPPGAPHLPQRRPAGRPT *FPPAQSSPPQSVWSRSRCTRMPGTGPG RWGPAAGSWPATSLASGCPSEVCGAT NP*APRLSTALGCCPSPPEGKRRPNTPA TRPPCVPAG*APPPGHSRGNGGLEKSSSF \PASCGR*QSGAGPSRLDFPSSPSRLHSVP PGPFRFTSHPVQASSVSEKGEKPLRSYD PRR |
| 6766 | 14817 | A | 7475 | 63 | 389 | KNQEQESEETLPNLFYKASITLIPKLDTS SSSSSFSSSSSSSSP*KPITHRNIPSSSSSS SSHQIQYIGKIIHHDQVGCIEHLIKFNI AA**EPSKNGDRRNT |
| 6767 | 14818 | A | 7476 | 3 | 335 | HASGKDRHTDQRNRIKNPETDT*YSTF* QKC/RLI*WRKDSL VNKWC*SNWA\SPM KKIKLDLSSSSSSSSSSSSSV*NVKLL GNNVGGNLQYRGLRVHTVDVKAQHI |
| 6768 | 14819 | A | 7477 | 50 | 378 | LEAWAGLSQVQTPSKFLENPSQSRYLTV PLRKHVPRPKQHEIRRLA*VGNLSDFT G*/HPGCIRGLRPG\HLSRLMDLGLGLMV KSMERDQRLVERAQLDQELLQALEK |
| 6769 | 14820 | A | 7478 | 62 | 389 | KRDPRKTFITPPPVSGERQIRRGPTCKWG FLGLVGRGGPPEGEKSNLLWNPGPPLG PNIKKGPRLTTPSSSSSNFQREKFHPGGG APP*NPT/ILGRPGGNKLGWGV |

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| 6770 | 14821 | A | 7479 | 18 | 373 | RGEPPSPAPIGIFKSPKRGFPKTFPGGF LPKGKKKPGPIPPGFLETKEGGTTPPNPF KK/ARVFLVFKPKAGSSSSSSPNYKPIYL NNTDTKFFNNMLANRI*QCIKEVMQYDR TRG |
| 6771 | 14822 | A | 748 | 40 | 317 | LRVTAQWASHTLPDPVVGPNPGSGWKEK DRDSEWGWRDLKSKTWVEVEAEGGLS GDTFQWLPQGSSQRPGLPLVNQAGVQ ETKGAGPL*SPAPLPPGSPEGAQASGCSP VGAIGMYPLTGPLPPPPQPRSWISGPSTPI LSLCPSPTRSQGFPPQGLEVCVTPIELLP EVRLKIRECFPSFL |
| 6772 | 14823 | A | 7480 | 2 | 1288 | FFFFFSCYAVNAAGNEGNDTALSFPERS QSRLCGFSQNTLCLLPAPTRSNFPGSCR RQPPGSLPALALAAGDSPGEAGPPGEGS RGIQHTFP*IPRPRRVQGSQSSPSTSHQ QFINGEGQTS**QNLGLRTQEFECNRLIS RL*VVRFRSLFAFFPLFAFHSPSPFF*GN V*ARLQGQKMESLGAEGLHHRPRQGW RKTQKQAPSAYVGKNGNPAP/PWFPPKV FRTGAAP*GFNPISP*RHSLDLAKG RGPDPARTGTLSCLAFWPSRELITPG CHVLIGLSRLRGALFGG*GTAKRLSHK GRQSGP*N*PGRHTAPLIPSAASGRVRV GLQRNEPLPQNPTLRLSSPLLPGIKVKE TVGI**GVGMR/DLGS*NEVSAFIGN*ESR GSGSSNRMVFLPLPNARESPPSRFETVN |
| 6773 | 14824 | A | 7481 | 3 | 352 | QFSIE*KKRKIFPTQA*DKQRLNVQKYKI LLVTRKEGPNKGRGKPCS*IRKLNIVKTS IFPKLIDSYNKFNPY/LSASLLELTSCILK LIWE/QNPFMKMQRARTVKTLSSKKNK VEK |
| 6774 | 14825 | A | 7482 | 2 | 253 | SMKKVERSKISILSFHIREKLEN/QLNPK*IR RRREIKIGAEINEIENRK*IEKINETKSYF WKISKPLAKLIKEKTQITNTRRAY |
| 6775 | 14826 | A | 7483 | 2 | 1114 | WSHRDWICPASGFQMLNVGSGVQILRK KLMTYAL*LLQLTVWRDSRLLCREGAP K*SL/SSLPESRRQSSEFEKAKTCQLFNA AVDSPADYHISLAQSALQICLTHPELON EICCQLIKQTRRRQPQNPGPLQGWQLL ALCVGLFLPHHPFLWLLRLHLKRNADSR TEFGKYAIYCQRCVERTQQNGDREARPS RMEILSTLLRNPYHHSPLPSPVHFMNGI YQVVGFDASTTVEEFLNTLNQDTGMRK PAQSGFALFTDDPSGRDLEHCLQGNKV KPSPFQEPSPTNSKEATLYKSKLCKKFN SGVFQNFNQSNLHDKKKKMQDFVKPIEF LIHNLIIYTFHIKERKGVSNNGNDTSLIRII RVDM |
| 6776 | 14827 | A | 7484 | 4 | 252 | GDVEY*SIYSLAPIRHWLRNGPRASTLW LFFFFFFF/ETQSCSVTRLDNGMISAH CHLRLPGSSDCPAS |
| 6777 | 14828 | A | 7485 | 95 | 670 | FLEGGWAHFFPPPKGSPKIPKEGFKTP PKRKKIFPSHPPLNLGPPRDLKGGP/HSS SSSSPEVINIYCSPFREGHGRR*SKVSSW STEVENKPV*DKFPHTPSY/ATPCPLPQGY RTAVFSYSPPK/HMQSLPTFQKACSPYS FSHHSQSPTLVAPFFPCLMRSSDKLM NDVPAPVFLPSFKGNHACSSR |
| 6778 | 14829 | A | 7486 | 2 | 338 | ENGWCWIATYGRKTGFLSLTCKS*LK RDLDLGTETMEILEENLGEVLLDIGLK/ NFMKTPKADSTEIKINR*DLIKLS*CTA KKS*T*/SNRQSTEWKKIFGNYASDRTS |
| 6779 | 14830 | A | 7487 | 117 | 334 | LYAHKFNNLDEMDQFLQRHNTPKLIQEE /HRLTVIK*IKSIVINLPKQKA*GPDGFSGE MYQLLKEEIIYNVF |

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| 6780 | 14831 | A | 7488 | 325 | 353 | CILKDRCR*LYAHKFNNLDEMDOQLQRH NTPKLIQEETDLL/SIK*IKSIVINLPKQKA *GPDGFSGEMYQLLKEEIIYNVF*RTDVE G |
| 6781 | 14832 | A | 7489 | 3 | 458 | KSREITTLANNQCMATESVDHELGRCTN SVVVKYELMRPSNKAPLLVLCEHRGRM VKHQCCPGCGYFCTAGNFMECQPESSIS HRFHKDCASQFNNASYCPHCGEVSSK AKEVTISLKQTPRPWPVPVPGQE*GSSLV GRADTTPGSGAR |
| 6782 | 14833 | A | 749 | 2 | 333 | QKRGKTLPDF*SDFG*QLNGRHTHFQ/HP VVGNGPGSGWKEKETKGAGPLCYPPSHS KVWGRGATSSVSEGGSQRAGHLP/TSPA AQQGLECRNTRLPKVRAVAVRLCYPPPL GG |
| 6783 | 14834 | A | 7490 | 49 | 457 | MHNPDGSASPTADPGSELQTLGQAARRP PPP/PRGTRRPPQDTPISPETPAGCFSSRRPM PTREPPKTRGSRGHLHTHPPGPGPPLQGL APRGLKT/RRPPSVPAAGTPQGGKDQED CV*G*VALPGPPGRQEAYWSHP |
| 6784 | 14835 | A | 7491 | 1 | 816 | MDEAQPQEALGASDWQTCSTQCLQRC KARSQSDHFKGELGVSSPRVHPQAARRP PPP/PRGTRRPP/PGPAHQPGNP*AASPGG RCPPGSPQRLAAP/EGHLHTHPPGPGPP/P PAGTPQGGKDQEDCV*G*VALPGPPGRQE AYWSHP*GA*A*APPSARL*A*VPASEQ* EGTEPLCRSVPGPVRRVLGAPARGGVCT GKAQAAGGPAELPAPTPKPEGGPGSCSPG LEGV*DEANGSWLPGQAGSLPLPEG*TE ASQSDPEIR*PRRTRPSARKPLSCFSRRP MPTREPPKTRGSRGHLHTHPPGPGPPQP GPHKAKTKKIVFEDELLSQALLGAKKPI GAIPKGHKPRPHVPDYELKYPPVSSERE RSRYVAVFQDQYGEFLELQHEVGCAQA KLRQLEALLSSLPPQSQKEAQVAARVW REFEMKRMDPGFLDKQARCHYLK GKLR HLKTQIQKFDDQGDSEGSVYF |
| 6785 | 14836 | A | 7492 | 27 | 445 | MHNPDGSASPTADPGSELQTLGQAARRP PPP/PRGTRRPPQDPPISPETLSCFSRRPM PTREPPKTRGSRGHLHTHPPGPGPPVSLD REGVPRPGL*AKDLAPAV*GTPVFPTPRF NSRPRFVAAAGTGAPRPNQRP |
| 6786 | 14837 | A | 7493 | 1 | 368 | FQQNLTLISAHCNLCRKF*FSCLSWDDR HVPTCLDNFLYFW*RWGGFYHVDQAGL KLLDSSTPSAS/SFPKCWDYRHEPCTWP* KYSFLTEH*LLPVY*K*IAKPFPGPKQIVKT FS*GCKNI |
| 6787 | 14838 | A | 7494 | 10 | 504 | EGDKGTPVLRGFSSVSGWSRRMPFLL LTCFITGTSVPVALDPCSAYISLNEPW EGTIDHQLDESQGPPLCDNHVNGGWYH FHGHGRGDAMPYLSFFTRKPLWEPTAPV WLNQSHPL*GDGIVQRQACASFNGNCL WNTTVEVKACPGGYVYRLTKPSV |
| 6788 | 14839 | A | 7495 | 84 | 250 | NRIENPEIKLNTDSQLILPR*FNWER/DSL FNKCWWNWIFKCKTMKLDPPFIPDKN |
| 6789 | 14840 | A | 7496 | 63 | 743 | SSCLLAAFRGPAHASHCP*SPAHSKRPI HAQLFPLVASPGPEIPQGFAR*SCCLPVP SPGPVLPSPVWYSPIS*LKTTYFGSAPAQ HLAAVGLKLPQVKRSRPRSCCPGAFTG PATA*RWLPQAQVLPSPSLPRPCLTVA FPVHVTACYPTALTQTLPSHWTV*DKL IRLPASPGQSSCLTLASIGPGAESAMVCL GPSHAFLKTLQATIWPDTFCGPM |
| 6790 | 14841 | A | 7497 | 340 | 368 | VPTICQVMS*HFHPSSSSSSSSSVINY*/ FGLLLC/QVAHFYNSIDQMIQSQRPMM LQSALAFEQIIKVNGLLI |

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| 6791 | 14842 | A | 7498 | 2 | 826 | LVKKTCEVPLQAGRLYLDHHQSKPFLKL HSKTHV*RCPLGIQTTGPVTLRR/AFNLR PVLSPQQRVPVEARPRKCETHTESFKNSE ILKPHRAKPYACNECGKAFSYCSSLSQH QKSHTGEKPYECSECGKAFSQEASSLIQH QRIHTGEKPYKCSECGKSLSARNANLTK HQANPHREEEALTGCSECEKAFS*LLSL VQHRIHTGEKPYECSDCGKAFRHSANL TNHQRTHTGEKPYKCSECGKAFSYCAAF IQHRIHTGEKPYRCAACGKA |
| 6792 | 14843 | A | 7499 | 64 | 372 | KLFFFHRESVNEIKKKTIDWENICNTYE* KPVTYK*FLQIN*KEIN/DQIEKWTKATN RQIAEEIIVNKHKRYCSASFRKKQIKT KKRCHFSITGKNYKE |
| 6793 | 14844 | A | 75 | 3 | 298 | |
| 6794 | 14845 | A | 750 | 444 | 999 | HSLTATALTLGSLVFLHSSPPCAAGLWA SDLPSVSLPLTQRRWLPFPKP*KWLGG* QRGPAPLVSCIPAPWFTQRRMKDGSIS HAPSPTLRHPGVGGRSPRPLAWSVPGAI GMYPLTGPLPPPPQPRSWISGPSTPILSLC PSPSTRSQGFPPQGLEVCVTPIELLPEVRL KIKECLSLVSVKK |
| 6795 | 14846 | A | 7500 | 2 | 414 | RQGL/DSVTQARVQWSDQ/GSLQPRSPG LERSSHLSLLSSW*FEISFRTLQQLVITGN ILGHQKITGTNHR*FMLYSSVCLFFEMES HSVQAGVQWHDLSLQPPPLGFKRFSC LSLWSSWDYRHPSSCLAYFCIFGST |
| 6796 | 14847 | A | 7501 | 18 | 73 | SYPGAAVSPAPWSPGASPLRSSPELHLRL SSSASSLALAKNALSRA SPSPAAQ/ALPSP SPLLWPLTSSPGRQASPVAPPSASNGT*W GTC*PEAILGLQSAQPPGAPGPPH |
| 6797 | 14848 | A | 7502 | 3 | 363 | KTASPVQVKFCAGVALPNLKQRPLREK AQQCI*PLLMAFRNTGRIPCFSCNIPVLP GQKHGTEDYWFVQDLRATRQIFKAIYLV IPDAYTLFMTLTSELYW/WSVLNLKDIFI CIPSPES |
| 6798 | 14849 | A | 7503 | 47 | 231 | NCSSVFCFPGSQRVGSILGKSW*GWVVA TGVWLLNPLKAVGQEEYSKMEGPRPE VTCRHL |
| 6799 | 14850 | A | 7504 | 1 | 3099 | MGSCSGGERLGTSPKYSMGKWEFVAKE QCGVPCPVQLGTLRNDLSLEAQLHEYVK QGNVYVKVKILKKGSQPHSPRVHSLFTE GTLDPAQDPCLMARETONQDAPCPAPF MAEEASSPSTGQPSLCSFEINEIYSGCLIL EDDIEPPGAASSLEADGPNQVDELKSM EEELDKMEREACCFGSEDESSKAETAY SFDDWDWQNGSLSSLPESTREAKSNL NNMSTTEEYLSKCVLDLKMOTIMHEN DDR |
| 6800 | 14851 | A | 7505 | 2 | 707 | LTTH*IIHAGEKPYKCEKCGKAFNQFSNL TKHKITHTGEKSYKCEECGKAFIQSSTPS KQINDGEKPYNCEECGKAFNQASNLY*/ HKIIHTGEKPYKCECDKAFNQSSIFTKH KKIHTGEKPYDCEKYGKGFN*SSVLNTH TIILTAEKLYKPVRCDSASDNISNFSNHK RNHIGES*KCGECNKVFKWLSHLIIGNI HIGKISYK*EQCGKVFN*YTLHRKSFIFE KNCRN |
| 6801 | 14852 | A | 7506 | 1 | 681 | IVTADQLLGMGQWAAIRNQTMLNDEVI EQLWKCCLDADWDKIQDDDKLPCPF*QP SDGAQT*NRIPHFNCPFKDAAEKSYP*IA RANDLL*NLMAEQVNPRL/CQVAICPIK GKIPPGDVLTSYIKVCEGVRGTLRTAM VMAQAMVSIRMPGQFPKCFCSQSGH SKRNCPPWHTDRCSFQHQQPKFFQQA LSTICPRCQKGNHWVAQCHSKFDIDGNP LRSLP |

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| 6802 | 14853 | A | 7507 | 2 | 342 | STVKGPCSMCRTIHHVPHIMGFIFGVQG WHDM/C/KSINVNHSVNRMKNNHMI/S NDAEKAFDKT**SVSIKT/L/NKLEVKG YLYIKVAYDRLPARIIADD*RAESFPLRL GKR |
| 6803 | 14854 | A | 7508 | 1 | 358 | VFQSFFKHRNQKVPEPPPLSKT/AKNLFA QLAENIASCLDDSSCYGYKKANIRDQWP *EAKELMPQDNFN*LFPQTDATRSSIW/L LKTSIIKKYHVTHYEKALKTHEKELTCLR HDRVGTC |
| 6804 | 14855 | A | 7509 | 2 | 681 | |
| 6805 | 14856 | A | 751 | 172 | 431 | IGRPTKQGLGQWTAVWERMERTNKSRA WPNACEGPGAVGNIAWASGLP*MLKT RAARTWVQAGVRESAQGFLNKNRRILE MGLSR |
| 6806 | 14857 | A | 7510 | 670 | 1466 | KKIRPFFQIFDGFISNVLVFAQSGFPCLP VAPSVTS**LKA AVTAGLEVPSDVSDRA FEWLSAFPLADSPYSIHHPRIQVFLKRE GSSRRWVLEPITADSDPAYSSKVLLSSP GLEELYRCCMLFVDDMAEPRETPEHPLK QIKFLLGRKEEEAVLVGGEWSPSLDGLD PQADPAG/SWVRTAIRLCAGPELGIDLS AVTKWWRFAEVSVAAGDPPGGLQTVV VYLPGLDHHAYFGRKWEVPGAKQKA ARGSSPNPGRHKG |
| 6807 | 14858 | A | 7511 | 155 | 359 | VNSSHRDQWNRIGGP/ETNAYIYGQLVF GKEAKFI*WRKNSLFNKWCWET/WISLQ KRMELDSYLTAYVKI |
| 6808 | 14859 | A | 7512 | 2 | 495 | RKDILYSWARRFNIVKMLMLLPKAIYRF TVIPIFLLQND*TAFFAEMEKPVLFKI*SY RRP*IAKQS*SSSSSSSSSSSSSSSSSS SSSSSPVNSSHRDQWNRIGGP/ETNAYIY GQLVFDKEAKFI*WRKNSLFNKWCWET GFPYKKE*SVDSYLTAYVKI |
| 6809 | 14860 | A | 7513 | 155 | 359 | VNSSHRDQWNRIGGP/ETNAYIYGQLVF GKEAKFI*WRKNSLFNKWCWET/WISLQ KRMELDSYLTAYVKI |
| 6810 | 14861 | A | 7514 | 2 | 495 | RKDILYSWARRFNIVKMLMLLPKAIYRF TVIPIFLLQND*TAFFAEMEKPVLFKI*SY RRP*IAKQS*SSSSSSSSSSSSSSSSSS SSSSSPVNSSHRDQWNRIGGP/ETNAYIY GQLVFDKEAKFI*WRKNSLFNKWCWET GFPYKKE*SVDSYLTAYVKI |
| 6811 | 14862 | A | 7515 | 1 | 399 | NVLIWEDCIAGQAEVLHDSYGIIDWSPK GMFSMNCTSSQSCPWPHYVQLV*TERSD SRNDKKYGKSSYYLETWQYSGPQPQMI WPAVGAHKDLWKLIIAFDKIKIWEK YTMSQYNPNYILELVENNTIW |
| 6812 | 14863 | A | 7516 | 10 | 225 | YCNIHVGDFNTPLSGMDRSSR*KT/NKE TSELNYTVDQRSLTDIYRTFHPNLMHIL KELEKQGQTKSNIN |
| 6813 | 14864 | A | 7517 | 37 | 348 | WKMGQLPGRPQLPQLSQEKILSLNSPNV FSSSPLK***NILPKKKRPDCFTHKFYQTF KEEIIFLKTTHQEFEKKEILLKSFYEGSV V*AAKLNADINKKTTH |
| 6814 | 14865 | A | 7518 | 3 | 353 | CRLGGLKGRSREQGA VIREGEDTLG/SET EAGRPAGSLRQQRRGRPWLPVPVKH GVPTGEEHWAGEPAGWGGSVSGQAG*A ESRLSSSGHSGQKGGAVMLLAADRRRG QRRRGSG |
| 6815 | 14866 | A | 7519 | 54 | 284 | NHKTPEENIGEKL YDIGL/NDFLDMTPK AQAMKAKVDRWYGKIL*NLCTSKETIN RI/NNRQPMELKKL MANHISDKR |
| 6816 | 14867 | A | 752 | 253 | 428 | QASGVSDLQ*KLCAC*AQSQDLRGGGFR EARKTST*QPGFLLFCLLYSANKLQESV TFKDAIDFSWEEGQAESAQRMTVYGE VMVENYQEPGFLGKYLFTQTRGGPL |

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| 6817 | 14868 | A | 7520 | 29 | 261 | NHKTPEENIGEKLVDIGL/NNDFLDMTPK AQAMKAKVDRWYGIKL*NLCTSKETIN RI/NNRQPMELKKLMANHISDKR |
| 6818 | 14869 | A | 7521 | 5 | 2088 | LSSPSQGRGADSA/PGEFSGTQLPPQGE LVPQHLAQPHAVPAA/EVGPAWWPAG P*TSPSGRGRPRLCPPAPGPPLPLAAGPG ISHGQPPFMLLDGLAPGPPGGSGASGLPG SSALPRPRGEGVTPGIRGEGLRHTGA/G APSHSHSTCPSRRWQAGCPPTLTAPPPG WATSPPPESRCRVSGTSR*A*NPGHAA ASSGRWDRGPGAAAGPRPG*AHPA*GS GASGSSPGEGRARGT*PCSTEPSPGH* STGPSPCPAGGPRGRLLLPLPGPDQGRW APTSIGPLRTG/PKLQTPPTSCPR/KLAEG EAPGLMGVQVRQCEAQHTQRPVWL LQEGQDAVCVELEPVRVPAGPRGAADG RGCHRRQA/P*RAGPGRRLCSCTAGAA GSFPPAPRSGQQGGLGLAPGTAAEQAA HRAEPPRCKMPA*/PGPCVSTTCPCVSAS ELGTPGSEPLAGR WREAGSSQAVGLAA GGGGC*DQRTPAFGGS*GAGKGLRGPPG LVTSLSAVGRCASEPGGASGAAGRGRS GSPREPRVSGASRSPCG*AGCRRASSA GCRPRPGRA/GSAGEKADTYSCCRAAS/G RPERPSRPGARS*TPVRVYTA/GMVGGQ GLATPGSPCCCP/GPPGGRPRSRPE/SFPR ADPSGYRGLPADRHWSKGP*GPALPGPG RSQAWALLGPQHPRSPAPAGAGRGRAG HRRAR |
| 6819 | 14870 | A | 7522 | 45 | 301 | AGHHHWKRGPEAPRHEMCPGSSKNQGL VQGLAGGWGKKGKILKGSSTSPGEPGS GQIHLKKAGTCCGSSKDRGVRNYSGR LLRR |
| 6820 | 14871 | A | 7523 | 453 | 704 | AGHHHWKRGPEAPRHEMCPGSRSGSEG ATCFARGR*RPPGNLSNVSRMGTRSSYS CRRHSPAFLSWGKGRCHLCNKAHLLAG A |
| 6821 | 14872 | A | 7524 | 3 | 543 | TCCIQAAAGTGGSGAPGLASVVGGAAPL WSSF*NSLP*QIRFALVPLPGCRAPGTFFA PLYSQWPFPGPQWARSLARGEEGVG LAPHPQPPTWGRHGEQSPRRHHGVGH HHQHVMALGADMRRGLAAVAALVAS* AGRVLGWCGRPARRAAQLGQEGAQGT VLALNGLFFPSRRHGC |
| 6822 | 14873 | A | 7525 | 218 | 533 | AARRAGRPHHPKTRPAQLATSATAASP RR*GRPWGRGLGPAWRPGRGAALGA QRCGHGVRAVPVARAELGAAGFGGA GPGAARGQCPALLPGRVEPRAARGVRT TPRPGQLSSQQAQPQRRARAAYPRREP* HADDDDLHGADRSSRFGEVEHPVQGH TANPSDGGPVQHQHGLPHRYHLHLV *HSRPSGPPGATG |
| 6823 | 14874 | A | 7526 | 3 | 1185 | GP RR*GRP WGRGLGPAWRPGRGAALG AQR CGHGVRAVPVARAELGAAGFGGA AGPGAARGQCPALLPGRVEPRAARGVR TTPRPGQLSSQQAQPQRRARAAYPRREP *HADDDDLHGAGGVSVPRGAPARWA AGGVGRGRRRLLPWGCERSFSSSL*I* HSQICFF*SSLEQCGEWEGVYGDPSDGG PVQHQHGH/PASQPLPEWKVAEVTGGA RSTEDTSWGKAGGSS*EGGPSGPPGP GAGGLPGHNGLDGQPGPGPKGEKGAN GKRKGMGATG*L*RYGWHLGASGALL *AGHHHWKRGPEAPRHEMCPGSKGSFR ENGHTPSKPAQSSEGG*LPSPYQSGRW QKLLMGQGVQRTTHHGAREQVAVPRKV DLLDHQDLREPAGCQDTTDWMDSLVL AQKEKKEQMEKEEKWGLQDNYEDMAG ISEELPLCYEQAITTGEKAQKHQGTCA GADAAEFKTTTTRRSQVIRKACNVH |

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| | | | | | | QGARAASEKTGTHRPSQLNPQKASNYH WNYTAAMDRSYRIIIIIHEHRCRIMMPIG LSWEVLQKCDSVLRPRQWA |
| 6824 | 14875 | C | 7527 | 35 | 217 | MXDSRGRXPGARTYRESPGPXXRMXGR SREIARWPRRRPLAPLLHRLLPSPRPGIC GGAA* |
| 6825 | 14876 | A | 7528 | 2 | 342 | RALPPPDKPSLLSSIGSYRVPAPESVEGPL /SPWERKQPGERPLSCMS/GLPQLRVGGV RG**EPQGLPQDGDPAHTRCGAEPSSL SLPQDGVQDAAAASFLHTPSQTPCVQRE |
| 6826 | 14877 | A | 7529 | 2 | 440 | PRVRPRVRQSSHLWRCRVPPPPPTMCL SAHPAPGPDGTSCESHRVIPMTSIAQWG N*V*RGEITCLKSQE/GKS*GHGASCPMT GELKCPHCWG*TGPHQLPG/MSHMFVCI LRGLAGSPARTAARGFLEVAFFKGTIPE RKPLM |
| 6827 | 14878 | A | 753 | 963 | 1497 | NTALSNEEILVMALVVISFLSLTFFQLME GTRLNKLWGFIPRTL*FSE*TLSSIKAKL LTILTPSLKFNREVKNEVCHFVEWFSY HNNLIKMPFISMFTPLNKMKAFTFICK MTVNNNNMHQSTIYAKGEEHLMGCYVN CKLRTACFMAFAVKKLLAFNMYFKIY SCLGENF |
| 6828 | 14879 | A | 7530 | 3 | 471 | RALAAERPLAPLLHRLLPSPRPGICGGA A*PWERKQGERP/FPVSQYLPSAC/GASP PG/PLGTGRGHGADDAPRRTS*ISEVGSV SVRDPG*IEQGS DGRLPIGHSRWDERGLR GLGFVTGK/PWIKGGAILPVGPSKVVLG YTGRGAGLARSQGY |
| 6829 | 14880 | A | 7531 | 2 | 1021 | FFFFSCETTIENTLIFFSGEVSNLILPIPVGH K/GL*GGVKEEGCGCVLGLRPAVGSPAG MAQPSAPGVQAGSSILEEGLEVLSQPR PSRGSQGPVSPPSWKVLQQPVRRTPTPH ASWGKPTHASSFVGGLGAQGGKRMPLG GPGCRPAPGLGAHLYVVCPEFSAPIRGL RSGMVPLKKAATS*DTSGSSPGLGEPASP QLHLFN*SLRGASSVPLSTASPPPEGGLR TQALGRY*ETGKWPFTGLLPLRLSGPST DSGAGTR*EPMEERSEGLG/ERPARDPP GSVPTCGWRGRGSPGTCG/LPGQRPLGR ALRAAKTRPGTCRATDRGVPPGLPRLCR |
| 6830 | 14881 | A | 7532 | 40 | 403 | QWHRLAACSNLASAVSFRIFLYYGERRP SGGARPMILTSPSLTAWIINPLSQLL*YL AAEQQLHRGPRTAPVSGAE*RWTF/L IARTHCLRRGQGRQPPVSGATGAPSFPL QQMPRR |
| 6831 | 14882 | C | 7533 | 182 | 289 | |
| 6832 | 14883 | C | 7534 | 50 | 223 | MEQLCTKVRRFKITTLALILXXXXXX XXXXXXXXXXXXXXXXLFSILYEWYPCH LK* |
| 6833 | 14884 | A | 7535 | 3 | 398 | SNLASAVSFRIFLYYGERRPSGGARPLT SPSPATAWINPLSQLL*YLAEEQQLHR GPPRTAPVSGAE*RWTF/LIAHTHCLRR GQGRQPPVSGATGAPSFPLQQMPRFT |

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| | | | | | | PGASSSHQEATKSSTREF |
| 6834 | 14885 | A | 7536 | 287 | 568 | CLRDGSPPEPSCGLHCHCPACQ*PTPHPHY KHRPAGESIPGNTTPMSASRKRPASTSR RAPPALILSFLCKMGTLPASRGCWKE RSEIVLK |
| 6835 | 14886 | A | 7537 | 574 | 1266 | SIPCPSSSFSTWLQSSRNFTEDILASVLISA STQSAQSRSPQNQNLCKGGSQAAPPASS HPISSHWGLCLDDPPAKDIIDFPLVLP PYAVSHQCRLQYGAYSACEDMDGDSS LISPWAKYPKQRPQGQVFIRVPKKHMQK GSACPLWPVRGKSLPVKMHNPGLAGR WKSS*STWT/IQS/RSCGLHCHCPACQ*PT PGPHHKHRPAGESIPGTPNFCFEKEACV PYFM |
| 6836 | 14887 | A | 7538 | 1 | 785 | NRQLSCGTALSTTGGIYIGERSVRVWGH RFHCLGNEILLDNCQMTVLGAPPCIHGN TVSVICTGSLTQPLFPCLANVSDPYLSAV PEGSALICLEDKRLRLVDGDSRCAGRVEI YHDGFWGTICDDGWDLSDAHVVQCQL GCGVAFNATVSAHFEGSGPIWLDLNL CTGMESHLWQCPSRGWGQHDCRHKED AGVICKFTAFRLYSETETESCAGRIEVF YNGTWGSVGRNITTAIAVGLCCRHLC GGRNGC*PCIHGNTVSVICTGSLTQPLF PCLANVSDPYLSAVPEGSALICLEDKRLR LVDGDSRCAGRVEIYHDGFWGTICDDG WDLSDAHVVQCQLGCGVAFNATVSAHF GEGSGPIWLDLNLCTGMESHLWQCPSR GWGQHDCRHKEDAGVICKFTAFRLYS ETETESCAGRIEVFYNGTWGSVGRNITT AIARIVLQATLAVGEEMDANPSPL |
| 6837 | 14888 | A | 7539 | 1 | 1113 | |
| 6838 | 14889 | A | 754 | 1 | 363 | WRESPHSARPRLEPQCYDLSSLQPPGLK* CSHISLPSSRDYSCCATMPS*IFCVFFGVE MRFHVAKAGLKFPGSSNPPASGIPKCW DYRCILGQFSSFEAKPRMLIFLFIICSGH VMMS |
| 6839 | 14890 | A | 7540 | 1 | 214 | VAFFKSAGASVQEKQAQLQEQVKEQRV CCQRLAHPVASAQKEPEAARGPGAP/WA WGRV*QLYGPPEGEGRP |
| 6840 | 14891 | A | 7541 | 3 | 141 | |
| 6841 | 14892 | A | 7542 | 39 | 210 | |
| 6842 | 14893 | A | 7543 | 72 | 353 | QRCPPGGHIYSHKFSNPDSVLPPTVVCESP QPNPGFDPTVWQWGRPIYPHRSALRL QS*RQSGSP*VCLAGSLCCPWRLGHG LCQAHPGQ |
| 6843 | 14894 | A | 7544 | 5 | 726 | AAILYSGRLSSQPVVVEIHPYTYDTSTS GTVKIPGAELRVEFDRQCNTERRHDPL TVMDGVNRIVSVRSGREWSWSELRI GDELKWKFISDGSVNGWGWRTVYPIM PAAGPKELSDRCVLSCPMDLVTCLLD FRLNLASNRSIVPRLAASLAACAQSL AASHRMWALQRLRLKLLTTEFGQSINIR LLGENDGETRALSFTGSALAALVKGLPE ALQROFEYEDPIVKGA |
| 6844 | 14895 | A | 7545 | 441 | 1009 | GLSHGRNTGPLTTSQASTSPRGNNPRAC VARTRVGVPATELLWMEEMRCVQLFCY SKARSQCSHQ*DV*VFYQACWVSDT WHYLQPLTDSG*YA*KLS/D*VMSPILA TGPCTSHLA*LLDSEPLERSVSSFCKWDV RLLGKTSLLCCVGLAALSSEIFNCLLGVF VWNLASCLCGSACCRVFLRDT |
| 6845 | 14896 | A | 7546 | 59 | 378 | |

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| 6846 | 14897 | A | 7547 | 31 | 302 | KGRRVLWWGDKNHERSWHKGVMGQR VQDRQKRKLCQLMGKKRSQRA*ILSGTE HLHVHSHLLACQQQVSTGRALHLLP*RI WRARAKNEQ |
| 6847 | 14898 | A | 7548 | 1171 | 1731 | SPRWSAPRSPSGAPSDASCDGLVPMNGR KMACWPVDIPKTDWSPNPWQEKREIVS SEDAVTPSAVTPSAPSASARPFIPVTDDL GAASHIAETMTKTKEDVESQNKAAGPEP QALDEFTSLLIADDDRVRVVDLLKLSVCS RAGDRGRDVL SAVLSGMGTAYPQVAD MLLELCVTEL*NPRSRTP*CFSCRADEE VSLALECWEPEELPRTQSPALTTQRAQN TMNKLNFHNRVMQDRRSVCIFLPNDESL NII/DKCLVFSWGDGDFGKLGRGSEGC NIPQNIERLNGQGVQCIECGAQFSLALTK SGVVWTWGKGDYFRLGHGSDVHVRKP QVVEGLRGKKIVHVAVGALHCLAVTDS GQVYAWGDNHGGQNGTTTVNRKPT LVQGL*GQKITRVACGSSHSVAWTTVDV ATPSVHEPVLFQTARDPLGASYLGVPD ADSSAASNKISGASNSKPNRPSLAKILLS LDGNLAKQALSHILTALQIMYATDAAV GALMPAAMIAPVECPSPSGAPSDASA MG*SP*MGEKICLLAC*YSENRLSPNPW QEKREIVSSEDAVTPSAVTPSAPSASAR FIPVTDDLGAASHIAETMTKTKEDVESQN KAAGPEPQALDEFTSLLIADDDRVRVVDL LKLSVCSRAGDRGRDVL SAVLSGMGT YPQVADMLLELCVTELEDVATDSQSGR |
| 6848 | 14899 | A | 7549 | 2249 | 5398 | KCHLRAGRCRDVTAIFWLQSSFMQLEE KADLRKSITFYQNQGGRAKDAALGGGH HQAGAQQGDEGEAAGAAADGVAAYSN YNNGHRKFLATAQNPADPGPGAPAPQ ELGAAGKHGGLPNLRLSFKLALIRDMAI LPFQWNLLISFNAVGLVFSWGDGDFGK LGRGGSEGCNIPQNIERLNGQGVQCIECG AQFLLALTKSGVVWTWGKGDYFRLGHR SDVHVRKPQVVEGLRGKKIVHVAVGAQ HCLAVMDS |
| 6849 | 14900 | A | 755 | 1 | 433 | FFKNFYRINRDSYYKAAKFFPVLCISSFH SYCSTLPQAPLPQAWNLRRSSGVFLLLI SIVRADVPTPFQILGLILEAPPSQSYFLPFS SMDGLMLHPNRKVGQLTFSRPGVAHT CNPSTLGGRGGRIA*GQEFETSLGSLIS |
| 6850 | 14901 | A | 7550 | 1 | 609 | AAATTTTKLAAARQPLPGGGGESAVGA GAGREVIYLFATASAKRGGGRKRTPG AQSSGR/AVLPSLGPPGRFLAGVC*GSGG PSPFSSPPNHSG/Q/PGAGGEPGNRGPKM GVLAYSLHL*VPCGVSRNTLPAGDGNPV P*SPFLSFTWSP/VP*PWG/ANGPWWADP PPSTHTVP*PSGPPGASGAGPPPSWPRPA KGFAPPRGL |
| 6851 | 14902 | B | 7551 | 222 | 360 | XAVLALRPWDVEAEQFLEVSFLLFFLFS DPRPRDRLRLRLREPT* |
| 6852 | 14903 | A | 7552 | 1 | 601 | RDTSRNCSASTSQCRKASTAPGAEG/DGP QASGRGGAVTTRGSRASSGRGRSVMPL CSRA*DVRARRRRSQARGSSGKLHLCSG KPLRKRSPCSRVPAPGQSRGRRFTSSPP GFPASPCITERSRQKARRRTRSSSSSS SSSSSSSSSSSSSSSDGRKKRGKYKDK RRKKKKKKKKLKKKGKEKAHRSQSIIR |
| 6853 | 14904 | A | 7553 | 42 | 384 | LKSAALSHGGAKQAGDPLHPLPLRRD WAGPETNPRGKGHQHPSGFPLAP*NLP LGRQRSSTGLGQRGPSGKQPSSHLEGQA VPSGRLAGEESTQDGRGTSQTDAGGWM AGM |

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| 6854 | 14905 | A | 7554 | 1 | 713 | AKGAGLEARGAMAHVGSRRKRSRSRS RGRGSEKRRKKSRKDTSRNCSASTSQGR KASTAPGAEASPCITERSKQKARRRTR SSSSSSSSSSSSSSSSSSSSSSSDGRKKR GKYKDKRRKKKKKEEESLKEEGQRKKA EAQ/RGRASSASVVD*DGHAQAY*REM /DEGPKRKS*PKNDTERSTSQTQRTAD GHCQMQSDGYASREGPPHGGQPDGRQL AAQPGQVSGCQWEA |
| 6855 | 14906 | A | 7555 | 2 | 642 | HALTTAFNIVLEVLVSAVRQEKEIKSVI GKKEIKLSLFTDDMIVYVEYPKIDKNA/L LEIISNFTRVVGYKVNTQNSVTFRVYHQ *AS/EYLKLLKILFALEPPKVEYLGSNLTK HAQDLYEKNCKTLIKEIKELNKWREILC G*KYSVFKMSVLLNFVYRFNAVPIQIPVS CFVGI/EQT/SLKFIWKAKRPRIANSILIEN NKVTGLTLPPFFKA |
| 6856 | 14907 | A | 7556 | 3 | 577 | TSNECGKTFRHNLSVLVIHKTHTGEKPYK CNECGKVFNRAKAKLARHRIHTGKKH* KYEECDKVYIVNQVLKDRRIHTGEKAY KCKS\CDKNLGRDShLAQQTRSHTGEKP YKCTECGKAfSGQSTLIHHQAIHGIGKLY *CNDYHKVFSNTTTTVSNHWRIHNERF*K CNKCGKFFRHCSYLAVHR*THAGE |
| 6857 | 14908 | A | 7557 | 286 | 336 | GL**NTTS/PKISTEYISP*AKPPVMRGQD SVLYHSDYDEEEWNRVWVANVGKSLSCS IAMVDKLIERDGGSEASGGINDGEKERSL TDAIPSLPREDWYEQLYPFILTLKECV |
| 6858 | 14909 | A | 7558 | 2 | 246 | RPLKHTLVTCDKGGL*FEPsfVSG/PPRC A*GDGTKPEVPFIGTATFYHYLPTAYGC MLTST*RKVEETELDDFYDGNsRRGR |
| 6859 | 14910 | A | 7559 | 3 | 348 | GWRLVRPLFMGHRQPVISGLQPEQLHL KL*FLCSGVSDCASFVPV/QSPEPKVFFAK EQLARRKLQAEAGASATLSCEVAQAQT EVTWYKDGGKLSSSSKVCMEATGCTRR LVVQQ |
| 6860 | 14911 | A | 756 | 362 | 567 | PAPTPGTWDYRHKSPCLANFLYFY*ROG FHHIGLAGLELLASR*STHLGLPKCWDY RCEQHVOPIENIF |
| 6861 | 14912 | A | 7560 | 16 | 220 | HREMTGNDLKILQKVNKLWHLYTTAY *KRAIKKSKLLVHTK/TWVNLKGVVLSE *SQSQRVKYWSTRP |
| 6862 | 14913 | A | 7561 | 204 | 868 | KGNQVSHEYSWKFRTLSLS*KQF*VLKRV YYRAVKLVNMSNIAEHPGFMKTGECL RCMFWNNGCIHFAMSKHNLGIFYFKK ALQEE*QCLCTAPVQVALIQVKNFQGRP MCTLLNPIRGYELLYNCGISLLHIGRPL AAFECLIEAVHVVYHANPRLWRLAECCI AANKGTSEQETKGLPSKKGIVQSIGQG YHRKIVLASQSIQNTVYNDGQSSAIP |
| 6863 | 14914 | A | 7562 | 1 | 1047 | MVSISWPRDLPASASQAGITGLIGALVL SVGIYAEVER/HEI*NP*KCLPGSSHHPHP PGRRHVHGLLHWCAGVPP*QPELLASL RLSRGYGLVLSWLEPRYEKMISGMYLG EIVRNILIDFTKKGFLFRGQISETLKTRGIF ETKFLSQIESDRLALLQVRAILQQLGNS TCDDSLVKTVCGVVSRRAAQLCGAGM AAVVDKIRENRGLDRLNVTVGVDGTLTY KLHPHFSRIMHQTVELSPKCNVSFLLSE DGSGKGAALITAVGVRLRTEASS |
| 6864 | 14915 | A | 7563 | 77 | 2246 | |
| 6865 | 14916 | A | 7564 | 1 | 475 | HIKNMTFIYFSSFICFPWRSL/DSVAQA GVQWRDLGSLQAPPPGFTPFCLSL/LQS SWDLQAPRRARLIFYFFLVEMGFVTL ARMVSI*PRDPPALASQAGITGVSHRA RPETYNFCSFIHSSLPVEPEARKMTKNSD IGEWINLGTCLIV |

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| 6866 | 14917 | A | 7565 | 3 | 362 | SAIIV*DINTPIMGTTTRQMINKEIEDVNS AINQEDLLVIYRTLHTAAAEFTFFSSLHE VSSSDMMMLGH*TSLNKF*SEIIQNNSDH KGIKFEINNKEI*KIHKYVEISSTLLSKQG |
| 6867 | 14918 | A | 7566 | 188 | 1055 | VIKAAEGDSGSAWVLDEADPTGGPGLG CRGTKYLLRSGAGGLSD/GGPCPGPTDL ALSPKPPGLHGPPSPALAG*DLSRLPR AHSENWPGAAGGGSHRA*VGS/ADQAD NDTEGNNKDPGRPQAQPSRGS LGPATG RSGWPYGPSP*PTWGGQGPVSTPREGPAGV RIEAKGKS/NVGGTGGMAPSPSRTCNLLS LPKLSGVV*EAWNPGRADVHIMHAVGLI KTSHEWLDPPADSQAQSGCAGSGQEPQPA ASGSAAWRRCSQGGLGRLRHQQQEEGP SSQHVGVGCVPCGG |
| 6868 | 14919 | A | 7567 | 2 | 380 | AR*LFSRVNHMVGHKLSLNR*F*KIDIIQSI FYDHNSMKLENNNNKRKTGKFNLWRII* IIYL*THK*KKKITREIEKYLEMTENRNRK TYRNLWDAAKVVPKGVEFIAIGASL*KG GKSPIQVS |
| 6869 | 14920 | A | 7568 | 1 | 370 | GTSAWPQYKLDNDSK*PENGTFEFSILQ VLDNSCHKMGK WSEVPDVQAF FSHWS LPSLCSQC/GLIPNLSSFSFWSFG/PPPQV PSP/TESFFSMDSSDLPPSPQAAPRAEPG PNSHLASAPPPY |
| 6870 | 14921 | A | 7569 | 3 | 369 | HEVKTMKILEENLGEYLLDLVGKDFINR T/PETIS*NKIYKFNFIKIKNFCSLKDILKEI NRIDWEKIVTKHSDKGLVSRICKFHDSV /YKMRTQFFPPKDKDLGRYFTNKET*MV ASGHLKMC |
| 6871 | 14922 | A | 757 | 204 | 389 | DMGYDVTRFQGDVDEDLICPICRGVLEE PVQPCQTKVICILGQV*GEAHDYHAPYC EHAFC |
| 6872 | 14923 | A | 7570 | 1 | 2722 | MGSAPVPSQACLEALLLIVPWGACGVSQE EEESPAEGSKDEPEGEQVELKEEAEPVE DGSQPPPEPKGDATPEGEKATEKENG KSEAQPKSEKAEAGPEGVAPAPEGEKKQ KPARKRRMVVEIGVELVLDLPDLPEDK LAQSVQKLQDLTLRDLEKQEREKAANSL EAFIFETQDKLYQPEYQEVSTEEQREEIS GKLSAASWLEDEGVGATTVMLEKELA ELRKLCQGLFFRVEERKKWPERLSALDN LLNHSSMFLKGARLIPEMDQIFTEVEMT TLEKVINETWAWKNATLAEQAKLPATE KPVLLSKDIEAKMMALDREVQYLLNKA KFTKPRPRPKDKNGTRAEPPLNASANRA FPSPLTPWADQNVLSTVSPYKILGKGET MVVPRVFGRMVGKSREAVAQAMVLEM FREEDY YNDDVLDQMGASILGVEGPRR HPDEPPEDEVFELFPMFMGGLSAHNRA VLAQLGCPKINLDALENAQAIAKKLGLK GRQVLPPSELDDLHFFHYEFQNRFSAE VLSSLRQLNLAGVRMTPVKCTVVA AVL GSGRHALDEVNLASCQLDPAGLRTLLPV FLRARKLGLQLNSLGPEACKDLRDLHL DQCQITTLRLSNPLTAAGVAVLMEGLA GNTSVTHLSLLHTGLGDEGLELLAAQLD RNRQLQELNVA YNGAGDTAALALARAA REHPSLELLHEVQRNLNSWDRARVQRH LE/HP/SCGIWKIAGVPLILGARPSCEW RARAPSKSPLRRCPNSHPASVM*PA*T NLSIPWCCVASSLLRRCGSQSL*PSS/HPA AVSMETYHVTLTLPPTQRGEEQVELSTIE ELIKVP*SAPSQP*WSTSGLALPQEA WY PVRSH*CPRLSQSPDLTGYSYSGFGL TWEMSWKAPRNCV |
| 6873 | 14924 | A | 7571 | 2 | 394 | |

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| 6874 | 14925 | A | 7572 | 1776 | 3257 | TNLSIPWCCVASSLLRRCGSQL*PSSPPL PSPWRPTTSL*HCHQHREVKNKWSSPQL RN*SRMP*SAPSQP*WSTSGLALPQEA YP/REKPPMMPQAQPAIPRNRLFLRQLR ASH/CGK/WSWKAPRNCV*LNSTTPCS RSGPSPRGDPRWSGQKTWHLLGSQA* ATTPGPLMEL*/ELFNPDACGRRVQTVVL YGTVGTGKSTLVRKMVLDCYGRLPFAF ELLIPFSSSLCQLVAQRYTPLKEVLPLMA AAGSHLLFVLHGLEHLNLDLRLAGTGLC SDPEEPQEPAAIIVNLLRKYMPLQASILV TTRPSAIGRIPSKYVGRYGEICGFSDTNL QKLYFQLRLNQPYCGYAVGGSGVSATP AQRDHLVQMLSRNLEGGHQAACFLPS YCWLVCA TLHFLHAPTPAGOTLTSIYTS FLRLNFSGETLDSTDPNLSLMAYAART MGKLAYEGVSSRKTYFSEEDVCGCLGG WASGRRRSFWSLHIFRSGWP |
| 6875 | 14926 | A | 7573 | 201 | 1436 | PCDPREYP**ATSPTRRSWPWSISHPRPG S/HPLALSQLFNPDACGRRVQTVVLYGT VGTGKSTLVRKMVLDCYGRLPFAFELLI PFSCEDVSSVGRAPASMCQLVAQRYTPL KEVLPLMAAAGSHLLFVLHGLEHLNLDL RLAGTGLCSDPEEPQEPAAIIVNLLRKYM LPQASILVTTRPSAIGRIPSKYVGRYGEIC GFSDTNLQKLYFQLRLNQPYCGYAVGG SRVSATPAQRDHLVQMLSRNLEGGHQA AACFLPSYCWLVCA TLHFLHAPTPAGOT LTSIYTSFLRLNFSGETLDSTDPNLSLM AYAARTMGKLAYEGVSSRKTYFSEEDV CGCLEAGIRTEEFQLLHIFRRDALRFFL APCVEPGRAGTFVFHRRARHAGIPRCPLH CAGFAQDDPAKGGQGGSG |
| 6876 | 14927 | A | 7574 | 1 | 376 | PFLPPYMKINSR*SKDINVNFKSGSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSPL*KKNTPIKKVVKMDMRPRA |
| 6877 | 14928 | A | 7575 | 288 | 468 | KAEAGGWLEPRSSRPWRREAGAGQSP GPG\GRGCSEL*LCHCAPAWTTE*DLASK KKKQK |
| 6878 | 14929 | A | 7576 | 1 | 378 | YRKP/TADNIINGERLDAFPLRPGTRQG/T PFLLLLFNIVPEVLVRAIKQDLAETIIIV*IR KEEGKLSLCTDDMIFYVENPKEFIKILLE QISSQVAEYKINIQKSVVFLYTWNEQSK YEIKIISRA |
| 6879 | 14930 | A | 7577 | 840 | 1093 | QHKNLVL*SGRR*LLSQEES/GIFFTLVI TTFCWER*NRRILSI*RTMGARIHFQEP VIPAPWEAKAGGSLEIRSSRPAPWPTW |
| 6880 | 14931 | A | 7578 | 254 | 701 | KTGKEGPVRWLMPIVILAPWEAKAGGSL EVRSSRPAPWT**NPISS/KNSKNIKISLA WWCTPVVLATEEAET*ESLEPGGRGCSE PRSCHSTPAWVIGAPSQKKKKKEKQARR SWLAGHSGHLHYASYAGRCGRVGGLE PRNSRAAWAT |
| 6881 | 14932 | A | 7579 | 12 | 154 | CLCMSTCMCACVSVCMHICVDCVC /CVCVCACAYI*LRVCVLVCVFLYVCIFV SVIVCVMCMCVRIYLAFFPKSLLK |
| 6882 | 14933 | A | 758 | 381 | 1335 | DMGYDVTRVQGDVD*DLICPICSGVLEE PVQAPHCEHAFNACITQWFSQQQTCPV D\RSVVTV\AHLRPVPRIMRNMLSKLQIA CDNAVFGCSAVVRLDNLMSHLSDCHEHN PKRPVTCEQCGGLEMPKDELPHNHCIKH LRSVVQQQQTIAELEKTSAEHKKQLAE QKRDIQLLKAYMRAIRSVNPNLQNLLEETI EYNEILEWVNSLQPARVTRWGGMISTPD AVLQAVIKRSLVESGCPASIVNELIENAH ERSWPQGLATLETRQMNRRYENYVAK RIPGKQAVVVMACENQHMGMVQEP |

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| | | | | | | GLVMIFAHGVEEI |
| 6883 | 14934 | A | 7580 | 139 | 350 | AIMAPNFPS*VKT*SQEDGQTPNRIKLKK STSRHII/IAEN*/LAK*NILKAVREKWLIT CRRTVISMTMDF |
| 6884 | 14935 | A | 7581 | 17 | 245 | GG*GCSCSEL*SCHCSPA WVTSTKLTQK KNPQF*QVV*NI*IPCLLDSEFGLFLPKS YCYQCKVTLQCSKSL |
| 6885 | 14936 | C | 7582 | 82 | 300 | MLGIFEGQLQINQLVETGLKRWLRLRNSF LKRFCYLLKSLSRSTTTTTAFVCDGR WIMQIPGSVLPFPQCW* |
| 6886 | 14937 | A | 7583 | 1 | 772 | KENLITFPRIQISKDDFRRYRGAIARKRI RLGRKYVISHKEEVPLCIHWDISKQASLS DSNVEALKKLAARGWEVSTVEKIKIY TLEEHDVLSVWVEKHV/VEVQHI*LIRLL SDFTKRPLWDPHFVSL*SHRLG*VKDDQ LYHITCPILNDDPKDLVVLRIHEGKPLK DGNTYHS/VAVKSILPSVPPSPQYIRSEII CAGFLIHAI*QQFMHSYLTLTICLLGILPY FGWEILGGLGPKSIGRKQOPLVYSS |
| 6887 | 14938 | A | 7584 | 3 | 307 | RFTEHHRILTGEKPYECKEKGRLSSNT ALTQHQRHTGENPFECKE*GKAFNQKIT LIQHQRVHTGEKPYECKASGK/AFSWCG RFILHQILHTQKTPVQA |
| 6888 | 14939 | A | 7585 | 1 | 374 | TGVTPAATQASWTPPIDGPTTQEKLS*A NTAPGTEGEQQVHGEKKEDPAVPSAPP* YEESTSGEGRKAWAFPPAPTGEFPHPNW AYVDPNSNSRYDNGVPTGDHEL*TTFS WDDQKVRRVFVR |
| 6889 | 14940 | A | 7586 | 1 | 512 | |
| 6890 | 14941 | A | 7587 | 1 | 399 | FFFFNYITRYNKHRYYKMSKKRCHKIF QMIDMLNAASCAALGRHSRWVVGGAH PTTP/GSAQAPAPWSHAMGARTLPPRPF SVFGHSSATPKVSPSAAMPTEAQRPLPGC GPGSDFAGHPQC*PPQVQIPTSC |
| 6891 | 14942 | A | 7588 | 49 | 430 | KWWKVDCVGDMLECASIGRSEAFKTSS FQFSLATSEVCGHSSATPKVSPSAAMPTE AQ/QTPPGCGPGSALLGIRSADHPKCRSP LRVPPPRSTSKVLAPFLASSDHLEHTCS SQVRLPAAVRGAST |
| 6892 | 14943 | A | 7589 | 467 | 1518 | LANCRCVPGGHWQMVMRELWMWNV EEEEHEVGICTWGGQHCGCPAKSLPGPH PGGVSA PQSASQLMVKLLVWQKSVHKL RKVSATSSIAVYPCPGQSSGGAESPAPGP GLAGWSHLCGAALAEVQAAPVSQAAYS DASLGPEWSQEGCRPGLTSGQHGRDG R*RGSRQGDPIQSPSPGIPASSAAL*VGL VLVKWRPVHKAYDPVPEASPLSANFRN PGPAEAPGPMGKTKGRGSAGGA/GAGS AGLAPPPRSSQGAAGIGQ*PGLPEEAVHP CKGSCPASSLSAGTPRAPPPHCPCLGPRR QGPCSHGVTGCRSLG*AGGVG*APPRT QREWRPRAAQEAFAFNMSII |
| 6893 | 14944 | A | 759 | 1 | 1236 | |
| 6894 | 14945 | A | 7590 | 296 | 423 | MVI*KL/PYKKSQGLGTFTDEFYQILKEE LISILLTLFQKIQKE*VTYKKSQGLGTFTD EFYQILKEELISILLTLFQKIQKE |
| 6895 | 14946 | A | 7591 | 3 | 167 | VYTKILRADRDMLTGYPCCSTGLLTADD ***DNTLEV/IALRRGPFFYLEGLDLSPK |

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| 6896 | 14947 | A | 7592 | 19 | 406 | PLQELGGQSLSLHYVGGRAPGPPAPGHP PVQSLQRPCVPTQQLLTPEFWCPAL/RQQ Q*GHRQGTGPVPTPGPLKGQWQQGPP QKEWQMRPKAFGHHPGGLCQSLGGAPR RWNRDTYQAGPRQGCGALM |
| 6897 | 14948 | A | 7593 | 2 | 3532 | |
| 6898 | 14949 | A | 7594 | 3 | 300 | KGPWKQENVEAEASMVIAVPEPFGGAIH GQESITYHNGDKYLAIAPIIKQSTIVCHN RVDP*WPQDTLLGDMEGRLFTALQKNP TEKKIPQALQQAN |
| 6899 | 14950 | B | 7595 | 1 | 819 | MARGSAGLVLGRGRLHDWQLGSGHSAP GMLGQVALAGRTELAVPSLDTPGGGEQ RASDL SRLTSSSHESDHTVRAAHSPLPAE ALTRSLPCLQNVAVHRLYIKCQLDFGGD SIAVGTWPYPMVWIPVWVWIPVWVWIPVW WMEHTVLIHLPVGGHVGGSHLSAPVNN VCGNVAEPPALCGTKASKPPLTPPIRS KAKFLGGSVCLGRHNKLSQTRWLKQQT FISHDPGGWKSNIKLTRPAQDLLMSVCM NCNTHGSEDMDVISHLIKIRLKP* |
| 6900 | 14951 | A | 7596 | 2 | 3235 | SPASPAGRSAAHGSASPSGSPHPSWCTV GRSSCWSSPSP*ASSGSGTPPTQPGRCSL G*MRRRPAGGAQAFQLKGKKWRRFGG W*PRWEAGCFQGEW*GATDSRTASNQL GPPHLQHLHINPPARQPPAFNRVVKQAP WRPQARAGAPGKPDQDAHQRLVQNG HLGAQTQEEVAVTLGWPVPLVVGRL LCGTAPCAGSARSPRGELADGGDHSVE PPDGIPLDG/EQSGSGMSGALPGSSFLCP RRCRP |
| 6901 | 14952 | A | 7597 | 2 | 1065 | HMILCVENSKDSTKKNLLDLINEFSKVA GYRINIQKSMALFTNNNLAESRKQCPF /TDNIKHLRIHLTKMKMVHQYSLHTENH KTLMKYIEEDTNK*NDIPCS*IGRINVVK VSILPKAIYRFNAIPIKISSAFFEIEKVIQF LWIHKRSQITKAILRKKNPGGIILPNLNY YKTRVIKTIQYWHKRYTGQ/WK*PEINPN MYG**IFDKSTKKT\WEKGSFNK\WC WDF\TCRMLKLGPIYITPYTKINPKWIKD LNVRT*SHKSRKENIRGKAPWTLGFGQC FLGYHTKTSGYKSNNK*MKLYQSKLL HRTKTINKMKRQCTDKEKIFANHISGV LIFRI*EELIQLNS |
| 6902 | 14953 | A | 7598 | 3 | 333 | TLLPEIQAYTQEQWLGSPPEATALAERL QQESAGPGLQMNGGLVLGAWVCLPP/SS RPPAEPSTGAQSWVGG*EGPGGCGKVM VTGGLSVLAWTAESEISSHTCVLRIVS |
| 6903 | 14954 | A | 7599 | 252 | 684 | HLFRQLFLEVLMSLQSPCLVAHSASRWC TAPVTADAPSLWRALALWLWLAHQGP GTGWPVLSLRRRSASRLAASPSNPSPR NIH*SPQRPVCSRGPSGPATCPLGLPRTSP GATRPGPVSPSPRSGIAAAPGLAPAST PP |
| 6904 | 14955 | A | 76 | 189 | 442 | KTMRSIRSFANDDRHVMVKHSTIYPSPE ELEAVQNMVSTVEALKHVSDWLDET KGTKTEGETEVKKDEAGENYSKDNG*R TL |
| 6905 | 14956 | A | 760 | 55 | 792 | GRAGACSLIDTAMSIESSDVIRLIMQYL KENSLHRLATLQEETTSLNTVDSIESF VAELKSGHWDTVLQAIQSLKLPDKTLID LYEQVVLELIELR/ENLGAARSLFETRPDP MIK\KQTQPERYIHLENL\LARSYFDPRE AYPDGSSKEKRRAAIAQALAGEVSVP SRLMALLGQALKWQQHQGLPPGMTID LFRGKAAVKDVEEEKFPTQLSRHIKFGQ KSHVECAPRAEFVQRRSN |

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| 6906 | 14957 | A | 7600 | 156 | 888 | FRSSVSPGSGPPFSVSVTGSGCPS**HSGR PGVLVLKLPQGS*ASLPPAFPGGSDVAA GRGLSSAADCFSLTGLGTLATPVLF LTSN LKLLQESVPK*LNSASS/PGVPRP*LQMH RLCGG/PRSLAVVGTRPGARNWLASAFS/ VGGGQLLGLQHPLQKIPPSRNIH*SPQRP VCWKAGRRKTKPRVDLQALETCPLGLP RTSPGATRPGPVSPLPSRSGIAAAPGLA PASTPPLSPGPTPLPP |
| 6907 | 14958 | A | 7601 | 231 | 457 | QWLSLLPLGLGEDTKSLRANTSNELEHS QATIWEEGGPTSSSLWRPFNPGSPTNRN PKLMPAVQPPHPSG*TPSVTWLHISWR WSP*GOSKASLPLPWNSTCYPQTNKE TKTQSALSTPSTNCNQPKERRPVCLPWV PPTSCSSTDREPPAWAHSTDPSCDGTAK VPSSAGSKLGRKHHPRAAVGS LGASSHN LKAMGEEPTL/VTALRGSKVTTV/SETTR PRKKLSTDQYT*APPTGSHPKASTPKIRC CVSPFSRCYEEIPETG*LIKERGLIDSQFH MAGEPSGNLQPWKAKEKQAPSSQSGR TE*VPAGEMLDITYKTIRSHETHSLSREQH GENHPYDPITSTWSHP*HVGIMGITIQGEI WVGTQSQTISLTYPSP*NQTKEVSNK*RP PYGRREDQPLPPCGGLSTSLVPQQTGTPS SCQQCSRPIPVAEHPQ |
| 6908 | 14959 | A | 7602 | 2 | 289 | LACYSPFPFGGP/PSSPPPRAGGSNPPGPPG LTPFPKK/AKKLL/RPSSSPPLFPPLGRVG PGDSFYPPGGEFP*PRVPIT*NWGFPPPR GTKKKLPF |
| 6909 | 14960 | A | 7603 | 3 | 805 | DRVSLLLPRLECNGAISPHCNFRPGSSH SLASASRVAGITGVCHHA*LIFVFLVEME FHHAGQAGLELLTSGDPSPPWSPKV/YRI TRHGATATWPYIFKNFYPTRPS*NSLSLK RTS*IQMPAL*MERLQFVCPS/LAEDLTK F*EKQDSKFTSQNRN*AFSRRS*GMLEK D*KWTTSDIV*VFVLFKSHVEMLSPVLE VGSSRRFLGHGGRSLMNGWVLSLW**V SSYSISSCESWF*KESSVFLTFLLPFWPC DMPAPPLRLPP |
| 6910 | 14961 | A | 7604 | 75 | 484 | EIQLVLSLKTSLNKFKKIEIHSILSDHSGI KLEINSKGLQNHANTWKLNNLLNEH WVKNKIKMEIKTF/FELNDNNGTAYQNL WDTAKAVLRGKFTALNAYIKKYERAQT DNLRSHLKELEKQQT KPKSSRRKKK |
| 6911 | 14962 | A | 7605 | 3 | 1105 | |
| 6912 | 14963 | A | 7606 | 802 | 1204 | VLEVLTRAVRQEKEIKGIQIGKEEVKLLL FADDMIMYLENPKDSSKLLGLMNEFSR VSGYKINVHKSVALLYTNSDQAENQIKN SAFFTUV/SKKN*LND*IKYLGHLTKEVK DLYKENYKTLKESIDDISK |
| 6913 | 14964 | A | 7607 | 3 | 419 | RVECVVGLEYDRSAAASNTITQVVVTHI QALSHEQ/SAAYTSFSNKHESFSRIHLL GHKLGLNHF*NVGIM/PN/IFSNPNRITLEI NTRSKTEKSTNLWKLNTLLNSQQSREE IPREKENT*NENENAAAQHLQDAAKAA |
| 6914 | 14965 | A | 7608 | 1 | 341 | RMGTVCVNPRSLKGFGRPGGKKKPKQSSP LKS/SPKMALMGGNPGGAPFFRFLFFNF RFPGPKSSSPAPIFFLKKGL*INFGPPREP GGFNQKPQFPSAPGFEPWNPQGP KP |
| 6915 | 14966 | A | 7609 | 1 | 409 | |
| 6916 | 14967 | A | 761 | 85 | 379 | KKPKTKKRTGPVRQNVWRGRLSPGRA PAEGPOGGSTESPLLVGRCLILGLREPG VPPAAYGRFLRDYMNISIQGKLEKQRPQ* GLPSLTGAELIKH |

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| 6917 | 14968 | A | 7610 | 3 | 644 | GDQORDLISNNEQLPMLG/ERPGAPESQRP AOPSRDTRPPLPSPKIASPMCSLKKG*KA ITPMPLLPQSPKTPKP/VSKMRMATPLLM QALPM/DALPQGPMPQATKY/GNMTED HVMHLL/TVLTKC/QEEVSHIPAVHPGSF RP/KCDENGNYLPQCYGS/TGYCWCVF PNGTEVPNT/KSRGHHNCSAPSPSPISHL LIP*DPGAWLFRHPGQDKPSRNSR |
| 6918 | 14969 | A | 7611 | 1 | 1032 | MHRRRSRSCREDQKPVMDQORDLISNN EQLPMLGRRPGAPESKCSRGAlyTGFSIL VTLLLAGQATTAYFLYQQQGRDLKLT TSQNLQLENLRMKLPQASIKPVSKMRM ATPLLMQALPMGALPQGPMPQATKYG NMTEDHVMHLLQAD\PLKVYPPLKGSF PENLRHL\KNTMETID\WKVFE\SWMH WL\LFEMSQPLPCSKSPLDAPP\KVLTKC Q\EEVSHIPAVHPGSF/RGPKCGRTGNY LAIPVAYWGASATC\WCCLFPNG/TREVP NTRSRGHHNCSSESLGTWKDPSFLGLGV LTK\QDLGPVPIVRASRGGLQHPASPTQL QLSCSLQPPAPPPSPTL |
| 6919 | 14970 | A | 7612 | 59 | 321 | LSGSPLVTATSQVPLSRGKTGGPDPA/ SALPAPTSPISPPPSRSLRRPRAPSGCP WGCPGSLQAPGLHWQDYRPGVRVRL PG |
| 6920 | 14971 | A | 7613 | 1 | 464 | DEEDGENAHPYRNSDPVIGTHTEKVS ASDSMDSLYSGQSSSGITSCSDGTSNRD SFRLLDDGPYSGPYCDQATLHTDFTSP YDTSLSKI*KGDIIDICKTPMRMWTGMV NNKVGNFQFIYVDVISDEEAAPMTIKAN RRSISILSKTLQ |
| 6921 | 14972 | A | 7614 | 1 | 2119 | LSFLDLNENDFLSNNIHTYQGKTLQGT YQAIKSGSDPVESMGTLLKRLQKLWTK KARVQNLDEVKPTLINLQDEDDTLISCL KLTKSREKKVNSVSTRKEEMEIRLDTL SASLGRSSTLNNCNLEDKLAWEYGEAY MWHHWKPPENPLWTCLDFQIAQVGPW DHCSSCIRHTRLKSSCSMDLLHSWVTL CRQESSNITCWTKLREKRGDLFCILFVCF IDRKTPRKFSDDQALEILKIGRKQKVHSL GVVRIQNAQEKAIQCFREGETSKTKEYE SVIKFYKQORSSSGNFDRFRNNSLSKPD DSTEAEHGDPTNGSGEQSKTSNKEAVW GKKMRAISWTMRKKWGKKYIKALSEE KDEEDGENAHPYRNSDPVIGTHTEKVS KASDSMDSLYSGQSSSGITSCSDGTSNR DSFRLLDDGPYSGPFGRARVHTDFTPS PYDTSLSKIKVIGEQQCLVTWKGDIIIC KTPMGMWTGMLNNKVGNFKFIYVDVIS EEEEAPKKIKANRRSNSKSKTLQEFLE RIHLQEYTSLLNGYETLEDLKDIKESH LIELNIENPDDRRRLLSAENFLEEIIQE QENEPEPLSLSSDISLNSQLDDCPRDSG CYISSGNSDNGKEDLESENLSMMLTDP LQLSPQLPQRGAGNINRRKTGFSLGHGK LNKEQRKDKRLIQGWEVAELGPSAAF G |
| 6922 | 14973 | A | 7615 | 3 | 452 | |
| 6923 | 14974 | A | 7616 | 1 | 475 | PDSSGPHRLRENPPMVAVSCPTKTNVKG PPGGKVGAAHAAQYGAALGRNLSFPT TKTYFPHFDLASHGSAQV*GATGKKVAD ALTNAVAHVDDMPNVAVRP*SDLHAHK LRVDPVNFKLLSHCLLG*PWPAPHLRPS FTPCGGTPSLEQSSWASC |
| 6924 | 14975 | A | 7617 | 26 | 461 | WESCGPHQRTG*AGSSRCGWRRRAAGP GCHQPRAGVPGRTRCAGRSPAADAAGR CWLGGPPPPGCGPRCLR*CAGHPPAGSA RVWSVVAGASTGLGRLWGRRWSPSCH RCQSPGCQAGRRGTARLSWPLSRRTSCR |

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| | | | | | | IPAARVYPR |
| 6925 | 14976 | A | 7618 | 3 | 419 | LLDPSDGKSCGPTSKDCRRRIRQYSVEA LPRPALPHTRGSGRKEARGEQSGAGA PADPDKLEAAVAVGEDVQQAPGCHQPR AGVPGRTRCAGRSPATRGTRDGT/QGR AGPATVPIPPGPWGGFTCRRCRTLLARR S |
| 6926 | 14977 | A | 7619 | 2 | 227 | AGVFCDAGLTFTSSSGQQTAAQRAELLC QPAALRRRSEPFVHLLDISGEYLLGTFY YCVENLRDGPCVVADAV |
| 6927 | 14978 | A | 762 | 209 | 393 | WAVYCTSFMLS*CYKI*CKPALSLGI*T TEVKTYVYTNRCCEMSTSALLIVAKN*K HSKC |
| 6928 | 14979 | A | 7620 | 11 | 394 | SEFCDWVADLDVQKYEQPS/HEALTS MGSTEARVDYMGSSILMGIFSNADLKLQDE WKVNLNTLDSSITDKSEIFVHGDWKWD IFQVMISRSTTPDLIKIGMKLQEFFTQQFD TSTRALSTWGPVPYL |
| 6929 | 14980 | A | 7621 | 3 | 185 | FFFFFFER/CPTLAQARVLWCLHSSPQ PQS PW/VSSNPAS/ASQAAGTAGMCHRA WLLKTEVGDL |
| 6930 | 14981 | A | 7622 | 1543 | 1744 | FVKSKALAFFLSFFFFFFLQSLSVTQAG VQWVPVDSLQPLPRFRKRFSCSLPSSWD YRCVPQCPAN |
| 6931 | 14982 | A | 7623 | 1 | 259 | SENQEQUEEVITVRVYDPRVQNEGS WNSYVDYKIFLHTNSKAFTAKTSCVRR RYREFVWLRKQLQRYAGLVPVSELP GMPTLYGLY |
| 6932 | 14983 | A | 7624 | 3 | 265 | CCHPRLACSGMILAYCQSRLPGSKRFP CLSLPSSWDYKQPCCHTRILVFLVETGF HHVGQTGLE/MLRNSGDPPTLASQKC WDYKA |
| 6933 | 14984 | A | 7625 | 2 | 375 | RAALTPTSTYKGAPSPK/GAPHSTAGV TSA SPKEAPTPPAVTPPSPEKGPATPA PKGTP TSPVTPSSLKDSPTSPASVTCK MGATVP QASKGLPAKKGPTALKEVLV APAPESTPI ITAPTRKGPQ |
| 6934 | 14985 | A | 7626 | 2 | 425 | IFPPPKRGFFSKKKGVVFNPPASSSR FFARPPPGVGPPQVSSSSSPFYFYASS SSYSSSNFPS/HSSSSSSSSSSSPRQ QHPLYPHCLRGLWAERAW/PPGTPLY HYKTQRKQGT SASPGRGTTCHTPQSP PLPGHHRCPW |
| 6935 | 14986 | A | 7627 | 3 | 253 | |
| 6936 | 14987 | A | 7628 | 48 | 557 | AGLGKARLAPGTPLYHYKTQRKQGT SA SPGRGTTVTQRGHYQNA PGRTLQPPPGGQQTSGH*GPGW PYESQRLWKTPQRS*Q*FLHPP PR/HCHTPACGAASAPCVGRY CPRCSCAPARSASLAALTRETAP LLSPSWAPGDPTLEGWPGNGSPL PPRGM*PHLYPHCRLGWAKRA WPRGHHCHITIKPRGNKEQVQ VRGEGPLSRKEVTVIKTLV VHF SHHLAASKPAAIEGLDGL MSLRGYGKLHKDLDNDFCILL ALPHSCLRSSFCITMCR ALLPEMLMCSCSLISGRSD SGNSSSSSFLGSRPHVGG LAREWFTPTTEGDVTGI EDGL |

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| 6937 | 14988 | B | 7629 | 122 | 1028 | MENGQSTAAKGLPPLTPEQQEALQKA KKYAMEQSIKSVLVKQTIHQQQQLTNL QMAAVTMGFGDPLSPLQSMQAQRQGA LAIMCRVYVGSIIYELGEDTIRQAFAPFG PIKSIDMSWDSVTMKHKGFVVEYEVPE AAQLALEQMNSVMLGGRNIKVGRPSNI GQAQPIIDQLAEERAFNRIYVASVHQD LSDDDIKSVFEAFGKIKSCTLARDPTTGK HKGYGFIEYEKAQSSQDAVSSMNLFDLG GQYLRVGKAVTPPMPLLTATPGGLPPA AAVAAAAATAKITAQEAVAGAAVLX* |
| 6938 | 14989 | A | 763 | 348 | 638 | VQGKWPWGMGRAVCPAGPVRLEERPVC GTPCLCLHPARMTPAWGSIHCLPSHGGC PCLPVNAPSWLGGQSPWARALLQ*WVV LGAEGHLPTLRITTVG |
| 6939 | 14990 | A | 7630 | 3 | 407 | KSMTEAEQQQLIDHFLFDKPVSPLLA SGMARDWPDARGI/WIETLFKSKDYEFM WNPHLGYYLTCPSNLGTGLRAGVHIKHE KFSEVLKRLRLQKRGTTGGVDTAAVGGV FDVSNADRLGFSEVELVQMVVDGVN |
| 6940 | 14991 | A | 7631 | 1 | 170 | |
| 6941 | 14992 | A | 7632 | 1 | 411 | SYEVFKELFDPIISDRHGGYKPTDKHKTD LNPNLKGGDDLDPNYVLSSRVRTGRSIK GYTLPPHCSRGERRAVEKLSVEALNSLT GEFKGKYYPKSMTEKEQQQLIDHFLF DKPVSPLLASGMARDWPDARGI |
| 6942 | 14993 | A | 7633 | 2 | 1250 | LPTDGAPPPPPGRPPAAAMPFSNSHNAL KLRFAEDEFPDLSAHNNHMAKVLTPEL YALRAKSTPSGFTLDDVIQTGVDPNGH PYIMTVGCVAGDEESYEVFKDLFDPIED RDGGYKPSDEHKTDLDPDNLQGGDDLD PNYVLSSRVRTGRSIRGFCLPPHCSRGE GRANEKLAVEALSSLDGDLAGRYAL KSMTEAEQQQLIDHFLFDKPVSPLLLG LGHGRRNWPDARGIWHNDNKTLVWV NEEDHLRVISMQKGGNMKEVFTRFCT GLTQIETLFKSKDYEFMWNPFWATSL PCHCNLGTGLRAVGLHIKLPNLGQGM KFSEVLKPAELSKSRPPGGVEHGLR WAGVDFVQTLNRPGPSQSVELVQMV VDGVKLLNEMEQRLEQQQAIDDLHAW PKK |
| 6943 | 14994 | A | 7634 | 1 | 175 | EQLPYFVTFISMPATT/EGRRGFSLSVESA CSNYATTVQVKVVRNMHISPRALGTLH HN |
| 6944 | 14995 | A | 7635 | 1 | 83 | |
| 6945 | 14996 | A | 7636 | 61 | 2028 | |
| 6946 | 14997 | A | 7638 | 517 | 1038 | NKRIYNMMISSRRVISLSPVLLQIFDCP RLKFSEIPQRLTALLPPDPVINVHVSEV APACFSDQGMISFLPSLPLPLPSLLPP CWICPSGALGPVWGHRGHEGLDFPGSV DPSDQKKTACYDIDVEVEEPLKGQMSF LLSTANQQEISALDSKVGPKPRAGVGH |
| 6947 | 14998 | A | 7639 | 154 | 1594 | LSRCRTLPSMTPLGHPPTVVQRPMP GARMPHQGRPWAPRAPRTWAAPPCDPA WPPRDGARQASSAPARQSQAQSQGQP EPTAPARSRSARRKMAKILPQRIRELV PESQAYMDLLAFERKLDQTIMRKGVDIQ EALKRPMKQKRKLRLYISNTFNPAKSDA EDSDGSIASWELRVEGKLLDDPSKQKRK FSSFFKSLVIELDKDLYGPDNHLVEWHR TPTTQETDGFQVKRPGDLSVRCITLLM LDYQPPQFKLDPRLARLLGLHTQSRSAIV QALWQYVKTNRQLQSDSHDKEYTMDGK YFPQNFDCPRLKFT*IPQRVTAFLMPP DPVINVHVISVDPSPDQKKTACYDIDVEV EEPIK/GGQMSFLLSTA/NNQEISALDS KIHETIESINQLKIQRDFMLSFLRRPHKL CARTWLRSEQFGTSR*LTDVAGNPEEER |

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| | | | | | | RA\EFYHQ\PWSQEAVSRYFYCKIQASA GKEAW |
| 6948 | 14999 | A | 764 | 746 | 1280 | ISHMELQFGAIFAEILFRGPFHHLHNINFT WASCCPHASQPGRQRGSSWNEYHSFRE FNQEKEIWRAGESAPLPLAGAAACPW RGGASNICVTGASAAAGGRAGGSGEET GSAPGAACSST*ESYEAFGFSSSPGNSV *TFSTSSTYTASPPTSPSPSVSPSPPCYYYS SSSSL |
| 6949 | 15000 | A | 7640 | 256 | 426 | HPICPQTTKAFLPRMLELQNGHIVCLNSV LALSAIPGAINDYCTSEADFGFMESLT |
| 6950 | 15001 | A | 7641 | 1 | 985 | RIARPGEFRPLPGSAARRMAWKRLGALV MFPLQMIYLVVKAAGVLVPAKLRDLS RENVLITGGGRGIGRQLAREFAERGARKI VLWGRTEKCLKETTEEIRQMGTECHYF ICDVGNRD\EVYQTAKAAREKVGDITILV K\NAAVV/HMGKSLMD\SDDDAFLKAQ\ NINTLG\QF\WNHQPFGSKLCWKQONGP H/LVCLQLPLLGVLA/LPGAIDYCTSKA SAFAFMESLDPG/VLAGTCPGV\SATTVL ALSTTSTEMFQGH*EFRFPNLFPLK\PET VARK/TQVEAVQLNQALLLPWTMHAL VILKSILPQAALIEIHKILKETYNLE |
| 6951 | 15002 | A | 7642 | 1 | 376 | KQAASNQLDSLMGLG/DSHPVEERGILC EFCGVQLFYDVLVHYQDQWDLRPGTAF FRVTEGIPRLHSQAQETWPEL/PLRRVRR QENLSSGYLDDTLLETANGPTFCLPARPF WNNMTATYNQLSRS |
| 6952 | 15003 | A | 7643 | 1 | 2753 | MKEFSSTAQGNTEVIHTGTLQRHERHHI GDFCFQEMEKDIHDFEQWKEDERN SHE APMTEIKQLTGSTNRHDQRHAGNKPIKD QLGSSSFHSHLPELHMFQTEGKIGNQVEK SINSASLVSTSQRISCRPKTHISKNYGNNF LNSSLLTQKQEVHMRKESFQCNEGKAF NYSSVLKHKQIHLGAKQYKCDVCGKVF NQKRYLACHRRCHTGKKPYKCNDGKKT FSQELTLTCHHRLHTGEKHYKCSECGKT FS |
| 6953 | 15004 | A | 7644 | 1 | 149 | DSFGASRFLRIHAENTYFTLRAVFAESRCI EALDELASLQVTMHQAQKHT |
| 6954 | 15005 | A | 7645 | 81 | 331 | KGARFLLILYLDAFLFNLDLFFLEYPS YFLLCFCSLLFFFCFCHFSLYFFVCRPSSS LFSSSILLILLFVLVRLLFCFL |
| 6955 | 15006 | A | 7646 | 701 | 1114 | ATRHSMLSCHYTYTYIKHTHTHVFIIYIT YTYIHTHIYTYTYICHTHIHIYIYIYIHT FFFFFFFFFETESRSVTQAGVQWHDLGSLQ AASWGHA/DSPASTSQAAGTTGAHHHA Q/LIFFFFVFLVETGPHRASQDS |
| 6956 | 15007 | A | 7647 | 1 | 207 | RSVFRERGGKLSAG/SLVERLYRVRFRDRF ERILKMARKAVETHVLRSPHLVSDYRDS IIPSESLALPC |
| 6957 | 15008 | C | 7648 | 244 | 432 | |
| 6958 | 15009 | A | 7649 | 898 | 1144 | IFQLLMEGPANIIGNTGSSNTGRSNTGP SNQSSYLISFLFLFCFFETESRSGRPLGV QWAWISGSLQALPPGSTPFSCLS |

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| 6959 | 15010 | A | 765 | 1 | 493 | KGPVSKEPRSGMNRNSALRVNVRPLRPC PQEGGLPLQSCVPPLGLCRVPSRGKQPK HLLPTG**AIAGLPNLHVIDFIPLKLSFGL* GVPQGGPPLGRGPQSQGLVTQAPMGG GPRKGLPIDRPE*GACTLGPWAAPVPLS SKGPFPTVGPRLSDSFSAR |
| 6960 | 15011 | A | 7650 | 1 | 476 | ATRELVTSSGLRRKTGLWARPKEKPTA WHLASLSRPDELVRNPQEPQGPREEGS LGHVARTPAPGGGGQRHLSRAGHSRPG RRFKATLWLSEEHPLSLGDQVTPHIDLM AISNAHFAKLRFITLRLPPGFVPKIEIPL FHVNLARIHLSGNLCGC |
| 6961 | 15012 | A | 7651 | 1 | 1071 | |
| 6962 | 15013 | A | 7652 | 2 | 240 | SCSIGSFQFG/YYPGVINAPETIIKKFINK/S LTAKANAPPSEVLLTNLWLSVAIFSRRG YESASLFPSGLFVNRFQVLT |
| 6963 | 15014 | A | 7653 | 2 | 391 | QTGRGMWCSLVFLILPATPRKQSEPK TTDAAAPGTADTAGPGTMDTAVPRKAE TAVPGKRNTAVPGTADPASPGTADTAEP MRTTTPVLAWSPLTQSTKAPSPRLLP APSPGSCSATSTSCSRSP |
| 6964 | 15015 | A | 7654 | 1 | 200 | |
| 6965 | 15016 | A | 7655 | 3 | 416 | CLFPVQLLLDHGADPNQRDGLGNTPLHL AACTNHVPVITLLRGGSGFFPSLSSFP SPPECSPQLVPAGARVDALDRAGRTPLH LAESKLNILLEGHAQCLEAVRLEEKHHH MLKEHLELLGRHYQLINAWMTLD |
| 6966 | 15017 | A | 7656 | 1 | 395 | KVQSRCSSKENILRASHSAVDITKVARR PRMASFALTSMDKAFITVLEMTPLVLTGTE IINYRYGMARGLVQYVVSDDIVFSFLSL LYEYFIRSFHLSLFIYLSLRSFFKLRESF FCFSSIFLSSTFALS |
| 6967 | 15018 | A | 7657 | 210 | 441 | LNPILYSPGRDHRVQNFHLPRLCIQKLP KSKCFIYELPAHRKKLVQLEPLTDDLE PDFVRQVTEMSYIFSHSMI |
| 6968 | 15019 | A | 7658 | 8 | 399 | RVGVAGPAPWWLRVSLGGRDFHTPISV TKVAERGKAEDADLRPGDIHVAINGESAE GMLHAEAQSKIRQSPSPLRLQLDRSQAT SPGQTNGDSSLEVLA TRFQGSVRTYTES QSSLRSSYSPTSLSRA |
| 6969 | 15020 | A | 7659 | 2 | 260 | WEPWPWGPVLGLPLPPLPPSPSPPLPPP PRGCSLGASSA/WTAWVSSPKEPVRPQE PPPGGEGSNENHRRKWHPPFSVMLKSCY |
| 6970 | 15021 | C | 766 | 82 | 201 | MKSKHFINLISRQHKNYNLIYTFIRSRDF KTAIFLSILS* |
| 6971 | 15022 | A | 7660 | 2 | 442 | PRVRVYYFRQGHEAYVEMARKNKIYSI NPKKQPWHKMELREQELMKIVGIKYEYV GLPTLCCLKLAFDPDTGKLTGGSFTMK YHDMPDVIDFLVLRQQFDDAKYRRWNI GKGE/CSDRFRSVIDDAWWFGTIESQEPL QLEYPDSLQ |
| 6972 | 15023 | A | 7661 | 965 | 1232 | TGVQWPDLSLQPLPEFKQFSCSLLR GWDCRRPLQLADFCIFSRDGGYCYVG QAGLKLLTSN/DLPASASQSAGITGVSLC TQPKSS |
| 6973 | 15024 | B | 7662 | 111 | 374 | MVAAATGSEILLWALQAEGGGSEIGDSG NWIEIAYGTSLGGVRVIVQHPETVGGSP QLLQFTTVHRSPVTKIMLWEKHLISVCA DNNH* |
| 6974 | 15025 | A | 7663 | 387 | 545 | |

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| 6975 | 15026 | B | 7664 | 181 | 4716 | MGRPAPAVPRPARPATPPAWTAALPAG RPRGDPGFRAFLCPLICHNGGVCVKPD CLCPPDFAGKFCQLHSSGARPPAIPGL TRSVYTMPLANHRDDEHGVASMVSVHV EHPQEAASVVHQVERVSGPWEEADAEA VARAEAAARAEEAAPTTLAQSA GYSDASGFYCFRELRGGEASPLPGLR TQEVCCRGAGLAWGVHDCQLCSERLGN SERVSAPDGPCTGFERVNGSCEDVDEC ATGGRCQ |
| 6976 | 15027 | A | 7665 | 209 | 1288 | EEKNERRDRDTERKGEARTSKTSQKRET KETTGGKTKQKRKKEKTTDKKTKRKKR TSKTEENKKRKQEKEDRERDESTKRRKE GERERRGNARRRKKGGEHSKKRGERRN NSKGEGEEERGRKTKAKTRRTQATNT DSKNEKGRKGKGQTRARRPAETGRRRR KRRQRKAGETTPGETGRWCASVRSVD GSPTTAFTVLECEGSRRLGSRPRRYLLN CQANGSLAMWDLTTAMDGFQAPAGG LTEQELMEQLEHCELAPP/R/CASSLNG AVSPSPSPRISLT/NASTQASSNTSFVWPT VGSPKPPARLKARRRGWGEALWKAAR NWCVGQTS DGHQPAPWPSKRSRHS HTFQE |
| 6977 | 15028 | A | 7666 | 3 | 1703 | GGRAAALGVAIGAAGAAARAAAWTGP ARRASPRALHPGRVPRALRPWADRLPLY PDLRAPQRHQRGQRRSRRGGPGGTRLPR LVPSEAAEPAQPSGASARRTAQPLSDG ATRCPTLAMHGCWAECWMRKPLPHQP VRFYLVGQPEEPGMVRLVCGHHNWIA VAYTQFLVCYRLKEASGWQLVFSSPRLD WPIERLALHARVHGGALGEHDKMVAA ATGSEILLWALQAEAGGSEIGVFHLGVP VEALFFVGNQLIATSHTRIGVWNAVTK HWQVQEVQPITSYDAAGSFLLLGCNNGS IYYVDVQKFLRMKDNDLLVSELYRDP AEDGVTALSVYLTPKTSDSGNWIEIAYG TSSGGVRVIVQHPETVSGSPQLFQTFTV HRISPVTKIMLSEKHLISVCADNNHVRT WSVTRFRIGMISTQPGSTPLASFILALES ADGHGCSAGNDIGPYGERDDQQVFIQ KVVPASQFLVRLSSTGQRVCSVRSVDG SPTTAFTVLECEGSRRLGSRPRRYLLTGQ ANGSLAMWDLTTAMDGLGR/SPAGGLT EQELMEQLEHCELAP |
| 6978 | 15029 | A | 7667 | 8 | 566 | TLVTVGNSQGREGLAFLVSCPEGRADCA SESACSSDSLDEARSSGSEGTADTGDLS PGHGASAPSVSREARQTVPLTVRLHTQ SVSECITEDGRTVAVGDIVWGHRR*GRT CWPGASDLCSGTL*AFWPAACRAHWA WSAWCEVPRGPAVCSGRGT*AQRLLP LSVFVPTTQMAALAHEAV |
| 6979 | 15030 | A | 7668 | 2 | 610 | SPEILVDPRLRPRVRLAFLVSLVGRADC ASESACSSDSLDEARSSGSEGTADTGDLS SPGHGASAPSVSREARQTVPLTVRLHT QSVSECITEDGRTVAVGDIVWGIHGF WWPARVLDISL/WPEGGRRAVLARVKV SWIGSPTTSFLSISLSPFSEFFKLRFNRK KKGMYRKAITEAANAARHVAPEIRELLT QFET |
| 6980 | 15031 | A | 7669 | 3 | 392 | ADAAVPTRCVTSGHSLPISGHAAESELFH R/P/AGIILPSRRNVLPARGASSTRARPLE RPATPVVAPSSRAARSRHIDPLLQSSSPT PPGPTGSAAVAVPTPNSSSPGPAGRPA GAMLYHSWVSEITE |
| 6981 | 15032 | A | 767 | 88 | 372 | QGMDSKRRGVKLNDDGQFMPVLGFGTY APS*VPRSKALEVTCLAIEPGFRIDSGH LYTNEEQAGLAILNMIADGCVKREDIFY TSELWATFY*PE |

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| 6982 | 15033 | A | 7670 | 5 | 393 | GFRNPPRDSHHPHSTRRRRAFLRRWEKD PGRGKGRAPEPAQQRDASPPTRRPLEGP/ PREHLRQWERLPFPKSPWKEVFAFVSAN KACSALSGPVAPVETAAEPSPPS/PRVRG RSGPRTKGARPRNRCCDD |
| 6983 | 15034 | A | 7671 | 2 | 399 | ARTNTGGRPYCFIRMSNLHRTQQGYN NPRPLSTNIILSDIQTETKLRPYQISMCE LGSAGVTSAFSADCKGAEKISSGHQRL EPATLSGIA\GFILSLLWGALNLIPGFHAI QRLQREGDDFNSFIALF |
| 6984 | 15035 | C | 7672 | 151 | 339 | MSTFPIHISPKLRGDDVGRXLXWRWPL RGFCATVRWCPPGAAGWCAXPVRAESA FXRPAKS* |
| 6985 | 15036 | A | 7673 | 19 | 443 | SVRWNSCRAEAPQWPAPAAAPAAHSPH LSLGEGLGKLILINSLFLTDLYSPEYGP SQRIKKPVQVYILVFLIDDKLE*Y*YTQST CCNFHYAS\QSWQPAINYIDSKFEDYLN ESRVNRCQMPGNRVQGCPLYFIAPSGH |
| 6986 | 15037 | A | 7674 | 152 | 532 | QALRANRPAPVAEGATDRTVAQKLLNG QRQLQPRPPTLJ*AWVEQSKVLIDGG VQLLLTIVDTPRFGDAVDNSNCWQPVIN YIDIKFEDYLNESRVNRCQMPGNRVQ* *LYFIAPSGHGPHN |
| 6987 | 15038 | A | 7675 | 1 | 627 | GSARSAAEERSVNSSTMVAQKNLEG YVGFANLPNQVYRKSVMRGFEFTLMVV GESGLGKSTLINSFLTDLYSPEYGPSPH RIKKTIVQVEQCGVLIKEGGVHLLTIVD TPGFAGDAVDMSNCWQPVYIDYIDSKFE DYLNESRVTRRQMPDNRVQCCLYFIA PSGHGLAKPLDIEFMKRLHEKVNIPLIAK ADTLTPEECQQFK |
| 6988 | 15039 | A | 7676 | 2 | 371 | VLELEERALLREARLGRARSSGGMQATP ATEGLARPQAPSSAFRCPCYCKGKFRS AERERHLHLHRPWKCGLCFSGSSQEEE LLHHITCQVCGQSFTQSWFLKGHMRKH KASFDHACPVCGR |
| 6989 | 15040 | A | 7677 | 44 | 983 | RGSMEGSRPRAPSGHLAPSPPAFDGELD LQRYSNPAVSAAGSLGMGAVSWSESRA GERRFPCPVCGKRFRFNSILALHLRAHPG AQAFQCPHCGHRAAQRALLRSHLRTHQ PERPRSPAARLLLELEERALLREAPTGES PKLRGHAGHPLPLMVW/PRPQAPSSAF RCPCYCKGKFRTRLERERHLHLHRPWK CGLCSFGSSQEEELLHSLTAHGAPERPL AATSVAPPPQPPQPPPPQPEPRSVPPQPEP EPEPEREATPTPAPAAPEEPPAPPEFRCQ VCGQSFTQSWFLKGHMRKHKASFDHA CPVCGR |
| 6990 | 15041 | A | 7678 | 1 | 582 | GNAGLSSLTEGVLDLFAVKAVYMGHPGI DIHTVCVQNKLGSMFLSETGVTLTYGLQ TTDNRLHLHFVAPKHTAKMLFSGLELTR AVRKMRFDPDQRQQWLRKQYVSLYQE DGRYEGPTLAHAVELFGGRRWSARNPS PGTSAKNAEKPMMQRNNTLGISTTKKKK KILMRGESGEVTDDEMATRKAKMHKEC R |
| 6991 | 15042 | A | 7679 | 2 | 428 | SVGSESDSSKEGPSMTRSGPLRRRAVP G/PEESQGNLTVIRVVIHDLQQTCKIRFNP DATVWVAKQIRLCTLTQSLKDVLYGL FQPASNGRDGKFLDEERLLREYPQPVGE GVPSLEFRYKKRVYKQASLDEKQLAKL HTK |
| 6992 | 15043 | A | 768 | 177 | 311 | WFQNPCYYYLFFLETESLSPRLERSGTVS AHCSL*LPSSSDSPAS |
| 6993 | 15044 | A | 7680 | 1 | 248 | VIFLVNSGSEANELAMLMARAHSNNIDII SF/RTMCPDVFRGPWGGSHCRDSPVQTIR KCSCAPGPTGQGGCQWSVGSWKGHE |
| 6994 | 15045 | A | 7681 | 1 | 501 | |

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| 6995 | 15046 | C | 7682 | 60 | 380 | |
| 6996 | 15047 | A | 7683 | 3 | 649 | LSPSYFHSISFPHSLFLPLEGTVTRNRELW GLLQAMGVHHSRIPLAPPHPHLNLKVQQ DSEQLEPGLQSASMGVGFSLGRNDSNLE TFAETLVPGSIPLPGILEMHPFLSLGTSRT SVTKLSLHIKPRMPPCDFMPERYQVIFLV NSGSEANEALMLMARAHSNNDINSFR GAYHGCSPYTLGLTNVGTYKMKLPGG TGCQPVSLEIFLLFL |
| 6997 | 15048 | A | 7684 | 27 | 211 | FHIVQYFNFFVCLFVCLFETESTLSPRLEG SGVISAHCNLTLPFGFNNSCASASRVAG TTQ |
| 6998 | 15049 | A | 7685 | 1 | 310 | RPRRRGDHREVKGGRGGKGGEGRPQGG QRWAVGKGGEGRPQGGQRWAVGKGGE GRPQGGQRWAEKGKGGEGRPQGGQRIGQ WGKGGEGRPQGGGERPGPGKGGE |
| 6999 | 15050 | A | 7686 | 2 | 320 | KYVFTDISYSIPHRERFIVREPSGTLRKA SWEERDRMIQVYFPKEGRKILTPHIFKEE NLRFEPDSTEYIKVHHKTYEDIGKRKGY DLLRSTRYFGWEWVWVFC |
| 7000 | 15051 | A | 7687 | 22 | 1071 | GVLRAWNGSVSGLESSPGTVACSNRYL ALSRWGCHSRINSYGAESGSPETKKPT FMDEEVQRVLTKMTGLNLQKTFKPAIQ ELKPPTYKLMTQAQLEEATRQAVEAAK VRLKMPPVLEERVPIINDVLADKDFWK GTETTKYVFTDISYCIHRERFIVREPS GTLRKASLEDNRMIQVYFPKEGRKILP PHIFKEENLRTMYSQDRHVDVNLCAQ FEPDSTEYIKVHHKTYEDIDKRKGYDLL RSTRYFGEMVWYFVNNKKIDGLLIDQIQ RDLIDDATNLVQLYHVLHPDGGSAQGA KDQAAEGINLIKVFAKTEAQKGAYIELT LQTYQEALSRHSAAS |
| 7001 | 15052 | A | 7688 | 2 | 383 | FSAPAASEPLPFGPPPPSEPLPFGPPPSDP LAFAAPPSEPLTFSGPPPPSEPLTFSGPPP SDPLCFTAPPSEPVFSGPAPSRLPFFG PTTSEPPNR/PGMPTQHPICLSKNTPLPE PTRLHP |
| 7002 | 15053 | A | 7689 | 3 | 2484 | PAIKIRRRRVRDLQDPPPPQMAPEIQPPSH HFSPEQRALLYEDTLTYVLHRLGHPEPN HVTEASELLRYLQEAHFVEPEEHQQTLO RVRELEKPIFCLKATVKQAKGILGKDVS GFSDPYCLLGIEQGVGVPGGSPGSRHRQ KAVVRHTIPEEETHRTQVITQTLNPVWD ETFILEFEDITNASFHLDMWDLDTVESVR QKLGETDLHGLRRIFKEARKDKGQDDF LGNVVLRLQDLRCREDQWYPLEPRTNES YPDRGQGHLLQQLVHKRRATSASRSQP SYTVHLHLLQQLVSHEVTQHEAGSTS/W GRVAESQAATVFLHATQKDLSDFHQS MAQWVAYSRLYQSLEFPSSCLLHPITSIE YQWIQGRKAEQEEELAAFSLLTYGL SLIRFRSVFPLSVSDSPARLQSLRLV QMCKMKAFGELCPNTAPLPQLVTEALQ TGTEWFHLKQHHQPMVQGIPEAGKA LLGLVQDVIGDLHQCQRTWDKIFHNELI SSTLKIHLFSMAFRELQWLVAKRVDHT TVVGDVVSPEMGESLFQLYISLKELCQL RMSSSERDGVLAALDNFHRWFQPAIPSWL QKTYNEALARVQRAVQMDLVLGELT KHSTSAVDLSTGFAQISHTARQLDWPDP EEAFMITVKFVEDTCRLALVYCSLIKAR ARELFFRARRTKARAANMLCVVNDME QLRLVIGKLPQALAWAELEQRVGAVLE QGQLQNTLHAQLS\GALAGLGHEIRTG\ VRTLAEQLEVGIKHIQKLVGVRESVLP EDAILPLMKFLEVELCYMNTNLVQENFS SLLTLLWTHLTTLVLEAA |

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| 7003 | 15054 | A | 769 | 193 | 363 | IPLALSTGNGTLLFFF*DRVSLLSPTLECS GVISAHCNLCPLGSSYSALASQVAGI |
| 7004 | 15055 | A | 7690 | 31 | 510 | GDHASDKETITVNIYAPNIRACSKYIKQT LTELKGEVDSNVITAISILRFQQLPTLIKT ESLRNRNNSSSSSSSSS/PSSSSSSSLKSLP TKESIGPDGFTDEFYQTFKEELK/PKSSSS SSSSSSSSSSSSSSSSSSSSSSPEKDATRE ENYRPISL |
| 7005 | 15056 | A | 7691 | 2 | 189 | TYHIDRIKDKSHMIISATEKAFDKIEHPF MIKALSQLEVVGMNTNVIKAIYKKS MANI TQQ |
| 7006 | 15057 | A | 7692 | 3 | 409 | NTANRAARVSASIEDSPDNSETLPDES RNGENAKRFAIDIGGTLTKLAYYSTVQH KVAKGRAFDHSGKDTERDTSRPMRVQF KKRALLDGTSLRRRKPTPKPAWTSSKTIS STORP/EVIQATGGGAYKVKDLI |
| 7007 | 15058 | A | 7693 | 88 | 480 | KEELYGDFEDLET/G/DVHKGKSGPDTQN EDIEKQDEIDPDEKKSAKKKHLDKRRKL KEMLDAEYDEGESTYFDDLKGEMQKEA QMRLLKNHRWYKKILKSQDPHFSVGVWR VHTILLYYIEDHNGRQRLKY |
| 7008 | 15059 | A | 7694 | 1 | 1068 | MAANRKDFIHRRCGPESQSEAVPQGLC RAERSSALAMLSGSPRRRTQLRPFCKGTQ RRCRRGGGEADSGGEAVGGGAAERRSAA ARRRGRRRGGEAVGGGAAERRSAA ARRRRGRRRRRGGEAGGGGAAEARR AAAAARRAAAAARRAAAAARRAA AARRIAESGGEAHSRGEAHSRGEAHS AGAERRRRLHSPALKTHPGQSSEGHVE YKLNHVEFEDQDDEARVQYEGFRPGMY VRVEIENVPCFVQNFDPYPIILGGLGN SEGNVGHVQMRLLKKHLWYKKILKSQD PFISVGGRRFQTIPLYIEDHNGRQRL KYTPQHMHCGAAFWGKI*LQ*LAYCRD |
| 7009 | 15060 | A | 7695 | 66 | 844 | KEELYGDFEDLETGDVHKGKSGPDTQN EDVEKKEEIDPDEESAKKKHLDKRRKL LKEMFDVEYDEGESTYFDDLKGEMQKQ AQITAYRFPPTPSCTLNHAEFEDQDDE ARVQYEGFRPGMYVCEIENVPCFV*N FDPYPIILGGLGNSEGNVGYVQVGPFA AYLVPEALWISPPSIILPSHPPQMRLLKH RWYKKILKSQDPHFSVGVWRRFQTIPLCYI EDHNGRQRLKYTPQHVHRG/AAFWDKI CLQ*LAYC |
| 7010 | 15061 | A | 7696 | 1 | 1177 | LRMRLGTRSALWACRGWGQHMMAW LTEQPLGVLPPEELYGDFEDLETGDVHK GKSGPDTQNEIDIEKEVKEEIDPDEESA KKKHLDKRRKLKEMFDAEYDEGESTYF DDLKGEMQKKAQLNHVEFEDQDDEAR VQYEGFRPGMYVRVEIENVPCFVQNF PHYPIILGGLGNSEGNVGYVQMRLLK WYKKILKSQDPHFSVGVWRRFHTIPLYIE DHNGRQRLKYTPQHMHCGAAFWGPIT PQGTGFLAIQSVASGIMPDFRVAATGVVL DLDSIKIVKKLKTGFYKIFKNTSFIKG MFNSALEVAKFEGAVIRTSGIRGQIKK ALRAPEGVFRASPEDKLLMSDIVLMRLS TCSIPA/FY/NPVTSC*TIGEKHLVRMRP P |
| 7011 | 15062 | A | 7697 | 163 | 371 | KGTTKL VVKLSDFKSYFKAIVIKTVRN/W HKYKHIDQWNRIQNPEINPHIYQGMIFK KRAKNKQWKDGL |

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| 7012 | 15063 | A | 7698 | 270 | 1479 | PGCAFSSSGTSRQLAPVLGYLGSROKHS LPDLPYDYGALEPHINAQIMQLHHSKHH AAVYNNLNVTEEKYQEALAKGRFQAER EKNVVCFTNF*GDVTAQIALQPALKFNG GGHINHSIFWTNLSPNGGGEKPGWIYCA PLSTTSCTVGIDVISWAL*QKIF*IHVI*HF TVIIGNLFICGWFWDFFFNRLELLEAIKRD FGSFDKFKEKLTAAASVGVQSGSGWGLG FNKQRGHLQIAACPNQDPLQGTGTGYI*IG LSVVPVWKTSPLLKNVDSKVKGKRTVY QGDGHYVNHHPNQVFWGRGAVKALNR NLKGAPDLELDGESRANCGEKGREESER SGR*AWQLCSVTGAPFFLTGLIPLLIDV WEHAYYLQYKNVRPDYKAIWNVINW ENVTERYMACKK |
| 7013 | 15064 | A | 7699 | 94 | 330 | KRSRYKKMCLHFNFSGDVTAQIALQPAL KFNGGGHINHSIFWTNLSPNGGGEKPG WYILVHPYLHFVHSNRLLIYWR |
| 7014 | 15065 | C | 77 | 183 | 350 | MYGLPGFFYAHXXXXXXXRXR HAPALRVNTRSHSPTGGRVALPQPWL MV* |
| 7015 | 15066 | A | 770 | 260 | 360 | SPN*SPNVIFDS*DSPEKTAATVRGDFYV TGDRGMMMD |
| 7016 | 15067 | A | 7700 | 33 | 807 | GPRAAQERHSWLWWLRQLQOIGGISG STSTSSMLSRVCGTSRQLAPVLGYLGS ROKHS LAPDLPYDYGALEPHINAHMHLH HSKHHAAYVNNLNVTEEKYHEALARG DVTALQALQALAKFNGGGHINHSIFWTN LSPNGGGEKPG/EELLEAIKRD FGSFDK FKLEKLTAAASVGVQSGSGWGLGFNKER GHLQIAACPNQDPLQGTGTGLIPLLIDV WEHAYYLQYKNVRPDYKAIWNVINW ENVTERYMACKK |
| 7017 | 15068 | A | 7701 | 2 | 436 | SGRGASLRPGVRPPSVSWEPYSGPGSTPP PPSSRSKDVGKPAQSWVRGGSTQNTGQ LPKEGLSTPHVPVPRAGIPSSRQALLSSGN PGTRAPSAPALRPEAQASPAEFGAP/SPE LGGERLGGARFQEPQPAAASFPGAAAT QA |
| 7018 | 15069 | A | 7702 | 1 | 389 | PGSSRQRCWHQPCFACQACQALINLIY FYHDGQLYCGRHHAELLRPRCPACDQLI FSWRCTEAEQQRWHENHFCCQDCAGPL GGGRYALPGGSPCCPSCFENRYSDAGSS WAGALEGDAFLGE/HWKVTHSLGRLDS TN |
| 7019 | 15070 | A | 7703 | 1 | 1217 | MGGHLANVPTGTSLQQTGLMEKHFTSG KQLLKTQNNIPQTTERTHNGWHQAWL LVFSCVRSFYVAALFAVGLCGIHWFC AVFSVCAGHSTAVVSLPGSQHLSANM FVALHSYSAHGPDELDLQKGEGRVVLG KCQDQWLRGVSLVTGRVGIFPNYVIPI FSTPSQLSGCREVGPTLVKPVVHKMGVY GWEEGSISEGD/HGKAVPSNPS/VVPTAIV NPVRSTAGPGLGQGSRLKGRSSMRKN GSLQRPLQSGIPTLVVGSLLRSPT/MGPS ASAVPILPATGDPLPLSRGGGDGVQA/S PSRGSPSRASAGAVRPGSTPRPAPSLWK TKKSPSRVS/LLPKPPASAPPSILVKPENS RNGIEKQ/DQNREISEIQALLPPNITLPYPT SGKPEQPSLPQCVPA |
| 7020 | 15071 | A | 7704 | 27 | 211 | FHIVQYFNFFVCLFVCLFETESTLSPRLEG SGVISAHCNLATLPPGFNNSCASASRVAG TTQ |
| 7021 | 15072 | A | 7705 | 27 | 211 | FHIVQYFNFFVCLFVCLFETESTLSPRLEG SGVISAHCNLATLPPGFNNSCASASRVAG TTQ |

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| 7022 | 15073 | A | 7706 | 1 | 514 | LSQSEKNYYSSRFSPDSQYIDNRSVNSD RASQ/ARERAPRLNHPPEQIDSHSRLPHS AHPSGKPPSAPASAPQNVFSTTVSSGYNT KKIGKRLNIQLKKGTEGLGFSITSRDVTI GGSAPIYVKNILPRGAAIQDGRLLKAGDR LIEVNGVDLVGKSQEEVVSLLRSTKME G |
| 7023 | 15074 | A | 7707 | 65 | 515 | DPRVRAAGILYEFTWNQFCDWYLELTGP VMNGGTEAKLRGTRHTLVTVLEGLLRL AHPPIPFITETIWQRVKVLCGITADTIMLQ PPQYDASQVDEAALADTEWLKQAIVA VRNIRAEMNIAPGKPLELLVAGICTRNPN TSVNNENRGFL |
| 7024 | 15075 | A | 7708 | 2 | 505 | EPVKKIFYNIHVFRNIMDFKLFLVFVAG VFLFFYARTLSQSPTFYSSGTVLGVLM TLVFVLLLVKRFIPKYSTFRALMVGCVF ASVYIVCQLMEDLKWLYDNRIYVLGY VLIVGFFSFVVVCYKHGPLADDRSRLLM WMLRLSLVLVYAGVAVPQFAYAAAIL |
| 7025 | 15076 | A | 7709 | 2 | 417 | EPVKKIFYNIHVFRNIMDFKLFLVFVAG GVFLFFYARTLSQSPTFYSSGTVLGVLM MTLVFVLLLVKRFIPKYSTFWALMVGCVF WFASVYIVCQLMEDLKWLYENRIYVL SYVLIVGFFSFVVVGTSMGPLADDKSRNL |
| 7026 | 15077 | A | 771 | 80 | 357 | GPPFFFFGDRVLLCHPRLECSGMITAHCS LKLLCSQ*PSHNSLLNSWEHRHMPPLA KFFFHQQTKL*KK*NKNRSLESAPLSVFI KKVTTT |
| 7027 | 15078 | A | 7710 | 14 | 426 | RPIRMAVKQKISMLCHVNPEQVICIHDVS STYRVPVLEEQSIVKYFERLHLPIGDS ASNLLFKWRNMADRYERLQKICISIALV GKYTKLRDCYASVFKALEHSALAINHKL NLMYIDSIDLEKITETEDPVKFHE |
| 7028 | 15079 | A | 7711 | 61 | 204 | GRYAYVWHCPQGPGLETPLVADTSGA YFRREGLGSNYLGGRSPTSVS |
| 7029 | 15080 | C | 7712 | 537 | 710 | MCHHTQPIFVFMVEMRFYVVGQAGLEV LTSGDPPVSAAQSTGITGLSHRAQPSSVR F* |
| 7030 | 15081 | A | 7713 | 788 | 894 | KHGWLGTVAHTCNPSTLGGQGGWIMR SGVQDQPGQ |
| 7031 | 15082 | A | 7714 | 1 | 452 | SPVPQLIVPTVLSVVLLEPFLGAPLPANR LWTHLWAPRAWKQSPWQAPGLGRPLS SLGIGSCGAPGAYTRPDIRLHDKACPAE HGGGRGPGEAASRPLTAPSPGGCPERGL GTTSPQSRTASSGGSYRSFTDPPPPPIC HHRFFLTL |
| 7032 | 15083 | A | 7715 | 48 | 421 | DLQSSQGGQPRVQSWSPGRGIPQLPC AKALYNYEGKEPGDLKFSKGDHILRTQV DENWYHGEVNGIHGFFPATNFVQIHKLP QPPPQCKALYDFEGKDKEADKDCLPFA KDDVLTVIRRD |
| 7033 | 15084 | A | 7716 | 2 | 492 | LTLLNTITPSLARGNFYPLEGGRVLLDGK PISAYDHKYLHRVISLVSQEPVLFARSIT DNISYGLPTVPFEMVVEAAQKANAHGFI MELQDGYSTETGEKGAQLSGGQKQVVA MARALVRNPPVLILDEATNALDADSRDL IQHALSIGNLRKHRDFLSPVWP |
| 7034 | 15085 | A | 7717 | 2 | 721 | EGKVEEPENPAAKEKCEGKEEEEETDGS GKESKQCEAEASSVKNELKGVEVGAN TGSKSISEKGSEEVKRKSWRMTNKSEES SQPEAGAVSRGNFDEESNASMSTARDE TRDGFYMEDGDPSVAQLLHERTFASF WPKDRVMINRLDNICEAVLKGKWPVN RRQMDFDQGLIPGYTPTTVDSPLQKRSF AELSMVGQASISGSEDITSPQLSKEDAL NLSVPRQRRRRRRKIGN |

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| 7035 | 15086 | A | 7718 | 111 | 381 | DRGLASFAQGLEVQWHNLSLQSPVPPV LRRF/SPCLGLPRGCDYRPVPPHQANFCI VSRDGFYHVQGAGLELLTSSDPPTSQSQ SAGITGV |
| 7036 | 15087 | A | 7719 | 1 | 190 | ENKEEGQLPSSFYEASILTLPDKDSTK KS/SYRPT/SLMNFDAK\IFNKMFTNRIQQ YIERIIH |
| 7037 | 15088 | A | 772 | 80 | 357 | GPFFFFGDRVLLCHPRLECSGMITAHCS LKLLCSQ*PSHNSLLNSWEHRHMPPHLA KFFFHQQTKL*KK*NKNRSLESAPLSVFI KKVTTT |
| 7038 | 15089 | A | 7720 | 1 | 2499 | MAAAVAAPLAAGGEEAAATTSVPGSPG LPGRRSAERALEDATGTLNLSNRRLK HFPRGAARSYDLSDITQADLSRNRPEVP EAACQLVSLEGLSYHNCRLCLNPALGN LTALTYLNLSRNQSLPPYICQLPLRVLI VSNNKLGALPPDIGTLGSLRQLDVSSNEL QSLPSELCSLRLDLNVRNQLSTLPEE LGDPLVRLDFSCNRVSRIPVSFCRLRHL QVILLDSNPLQSPPAQVCLKGKLHIFKYL STEAGQRGSALGDLAPSRPPSFSPCAED LFPGHRYDGGLD SGFHSVDSGSKRWSG NESTDEFSELFRISLAREPRGRPRERKED GSADGDPVQIDFIDSHVPGEDEERGTVEE QRPELSPGAGDRERAPNSRREEPAGEE RRRPDTLQLWQERERRQQQSGAWGAP RKDSLKPLRAVVGAAAVSTQAMHN GSPKSSASQAGGCSGAGSPAPAPASQEP LPIAGPATEPAPRPLGSIQRPNSFLFRSS QSGSGPSSPDVLRPRYPQVPDEKDLM TQLRQVLESRLQRPLPEDLAEALASGVIL CQLANQLRPRSVFPIHVPSPAVPKLSALK ARKNVESFLEACRKMGMVPEADLCSPSDL LQGTARGLRTALEAVKRVGGKALPPLW PPSGLGGFVVVFYVVLMLLLYVTYTRLLD PRSPQVAWEVAPSRMTPLAPWDPKYE KAGPRPVVWSWGQTCGTGWGAQGA WPEAPVLCPPHPRGPTVAQEPRSQAGRC VTPHSGRCMKQPRAGVSGPWPLPQGTG MDSRRPQMQGSRWCAVKMSSSRTLCCP GGSVFPCTCPRPPSR |
| 7039 | 15090 | A | 7721 | 1 | 647 | RPPVPVQVPDKDLMTQLRRVLESRLQR \PLPEDLAEALASGVILCQLANQLRPRSV PFIHVPSPAVPKLSALKARKNVESFLEAC RKMGMVPEESLCQPHHILEEEGAPGRGLR LIIAAVVQRPAGPALGVKVGAGGPPRPG PREQKTRLGSALSEKHVVVRVAWAWARL GLPRLAASGVEGLGGRTCGCRRRCRVSR NKQKPEALWKRGCIIKKL |
| 7040 | 15091 | A | 7722 | 3 | 450 | SRLVQRGGIPLGGWRMGVRRTGQVGP TMHPPVSGASP/PPPPPPPPPHHHPHL LRTSCVPSGLYAQSSSSSSSSSSSSSS SSSSSSSSQLNKLKPKFQVSSPNSPTLSSSF SFLPFFPASSLTRQFFIECLPGAGMSQVL GK |
| 7041 | 15092 | A | 7728 | 3 | 368 | LLGQAVKYGVNPGPYGGTT\RKLYEKK LLRLREQGPESRCSTPVPTISSAENARQ NGSNDSGRYSVNEEDSKIELKLEKRDPL KGRAKTPVTRKQRRVELSESYSQAGMD EGVWSSGSSKG |

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| 7042 | 15093 | A | 7729 | 1 | 1492 | ALMDEILMLQDEINELQSSLAEEVSESC EADPAEQALQSTLTVLAERMSTIRMK SGKRQLLEEKLNQLEEQRQEQALQRY RCEADELDSWLLSTKATLDTALSPKPEP MDMEAQLMDCQNMLVEIEQKVVALSEL SVHNENLLLEGKAHTKDEAEQLAGKLR RLKGSLELQRALHDKQLNMQQGTAE KEESDVLDTATQSPGVQEWLAQARTTW TQQRQSSLQQQKELEQELAEQKSLRSV ASRGEEILQHSAETSGDAGEKPDVLSQ ELGMEEEETSADQMRMKWESLHQEFS TKQKLLQNVLEQEQEVLYSRPNRLSG VPLYKGDVPTQDKSAVTSLLDGLNQA FEVSSQSGGAKRQSIHLEQKLYDGVSA TSTWLDVVEERLFVATALLPEETETCL FNQEILAKDIKEMSEMDKNKNLFSQA FFENGDNRDVIEDTLGCLLGRLLDSV VNQRCHOMKERLQQLNFQVSKILSKDT |
| 7043 | 15094 | A | 773 | 810 | 1075 | SLRSSKTQPROHGKTSSLLKIQKISR VW*RTLLLGKLRQENCLNPGGGGCSE PRLHHCTPAWATE*DSGSQKKKKGQ RKSCHSVRT |
| 7044 | 15095 | A | 7730 | 1073 | 1233 | PYSGLGFFFLRHGLTSPRLGCSELRL C HCTPAWVTSKTVSKNKKQKNSR |
| 7045 | 15096 | A | 7731 | 34 | 445 | STHASGDHSPICS/TG/SYFFANSLPS KGPTTILMPVNTAALTVPANPASVIT VPSKLP TSSKPPGAVPSNALTNAPS KLPINSTRAGMVPSPKVPSTMVLTKG CASTVPTDGSSI NEETPMAPTPAGA VGSSSLAWLDT |
| 7046 | 15097 | A | 7732 | 3 | 416 | |
| 7047 | 15098 | A | 7733 | 1 | 2115 | |
| 7048 | 15099 | A | 7734 | 1 | 662 | SLFASNVGSGHFIGLAGSGAATGIS VSAYELNGLFSVLMWVFLPIYIAGQ VTTMPEYLRKRFGGIRIPILAVLYL FIYFTKISVDYAGAFIQSLHLDLYL AIVGLLAITAVYTVAGGLAAVYTDAL QTLIMLIGALTLMCYSFAAVGMEGL KEKYFLALASNRSENSSCGLPREDA FHIFRNPLTSDLPWPGVLFGMSIPSL WYWCTDQGG |
| 7049 | 15100 | A | 7735 | 3 | 315 | |
| 7050 | 15101 | B | 7736 | 107 | 388 | SKKLLFAGSRSQLVQLPVADCIKYR SCADCVLARDPYCAWSVNTSRCVAV GGHFG SLLIQHVMTSDTSGICNL RGSKKVRPTPK NITVVAGTDL* |
| 7051 | 15102 | A | 7737 | 98 | 473 | IRGDTISYTVRSPPPRAGREYAMST AGPPSPFSPLTQFPALYREEGKYKI PLNPGAK/YVRAPPNPSPQTHSRLH FSPHPENIHRPWSRTRPTSPALPLK GHSTLSTPPPYVHRCPTFGSGG |
| 7052 | 15103 | A | 7738 | 2 | 433 | GDTGHRERSLGLLREKHTWGPHPQ ATPQAAVPSSRYTQPGPQGWVTVQ GQPPSRGEHPRPAAGLSLLHLGV PDIGLQSGLDCEVTPKPSYSFPGT SGAGPPGTMGSSLP GNGNWDEE AHTLPQGGQEGMNEGGVPWRLIFR |
| 7053 | 15104 | A | 7739 | 328 | 496 | HNTDLFIY/CIYEMESCSVTQAGVQ WRDLGSLQPPPLGCKQCSCSLPSS WGLQVPATT |
| 7054 | 15105 | A | 774 | 499 | 946 | LWLRPRGAGIAGAGICLRREGTWLL PLRSHGGKCEAASPWVSQRLELLQK PSALWWPLGLLHVHIFWKYTCAGS FLAGKLLRITFNFFLFFLPFISCIF YLFLLFFFRDGVSLCCSGWP*TPGL KQSSCLSLPSSWDFKCTPLCLL |
| 7055 | 15106 | A | 7740 | 1 | 372 | MEKEEPGVERKKENRVKEVIHKNR KGAEGPPAGAAALPLGGRGEGP/SP EPPGGAAAPRAGERCGLAGASPEA ETGTREPRRGASAARKLAAAAPVGL LRPGCPRAGR |

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| | | | | | | RAPWPGKRLSEPRV |
| 7056 | 15107 | A | 7741 | 34 | 366 | ERPGPVGTLTTPTQGPHPAGP/S/GRPGS LGFTWPYPGPCTWRPAWFPARPPAGSI TPPGFCTHTLVSLDPGRDCPSPTGDCDS LCPHPDASPGIKAFCAQGGKKKKKK |
| 7057 | 15108 | A | 7742 | 2 | 462 | IRARNYKLRKVMVDGDIPPRV\KKDAHE LILDFIRSRPLKQVSERRRLRRLPPKQSR HEKILEEIKQERRLRPVGE/ELGCPRVW LS/SPASSTPAPEMPSPPPASTCQSQMLGA APSAR/VPRVLLKAPTLAEMEEMNTSEIR AQGPRNVTAHNQ |
| 7058 | 15109 | A | 7743 | 2 | 1002 | TGPGVPMCQVGEDYGEPAPEEPPAPRP SREQKCVCCKEAQPVVIRAGDAFCRD CFKAFYVHKFRAMLGKNRILFSGEKVLL AWSGGPSSSMVWQDLEGLSQDFAKRL RFVAGVIFDEGAACGQSLEERSKTLAE VKPILQATGFPWHVVALEELVGSEGAY KAAVDSF/RPAAACAGGPGVVLARLKG RNSHPSP/SLDPQNLARPPAPAQTEALSQ LFCSVRTLTAKHEELQTLRTHLILHVARA HGYSKVMTGDSCTRLAIKMTNLALGR GAFLAWDTGFSDERHGDVVVVRPMRD HTLKEVAFYNRLFSVPSVFTPAVDTKAP EKAS |
| 7059 | 15110 | A | 7744 | 2 | 397 | APDTPDSSKFQRSK/NYKGPLDPQRGKIE DKVNKSKVILKEPGLDLGTYSIDIPTDA DEDISASHTLTEEELEKLLKSHEIRNPGI KLISGWNIDILERGEARLWLELEKLCPPA ELHLIVHNKEIFRLPNR |
| 7060 | 15111 | A | 7745 | 1 | 849 | QKKELGHVNGLVDKSGKRTTSPSSDTDL LDRSASKTELKAIHARILERRASRPGTP TSSASTETPTFEQNDVDEIHDVDEEPVA AEPDYVQPLRRPFELLIAAAMERNPTQ FQLPNELTCTPALPGSSKRRRKEETTGN VKKTQRELDHNGLVPLPVKVCFTCNRR CRVAPLIQRDYCPLLFHMDCLEPPLTAM PLGRWMCNHNIEHVVLNHNMTLSYRC QVFDRTQTVSQHVVKVDFLNRIHKKH PPNRRVLQSVKRRSLKVPDAIKSQNVSTP |
| 7061 | 15112 | A | 7746 | 1 | 201 | MKKKKKEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEE/EEEEEEEEEEEEEEEEEE EEEEKKKKKKHNIFKILSNLYIFIIFYCSKK |
| 7062 | 15113 | A | 7747 | 3 | 112 | KRTRLGMMAHA/CNLSTLGGQGGRVTR SGVRDQPDLK |
| 7063 | 15114 | A | 7748 | 1 | 1476 | LTVIRRVNENWAEGMLADKIGIFPISYVE FNAAKQLIEWDKPPVPGVDAGECSSAA AQSSAPKHSDDTKNTRKRHSFTSLTMA NKSSQASQNRHSMEISPPVLISSNPTAA ARISELSGLSCSAPSQVHISTTGLIVTPPPS SPVTTGPSFTFSPDDPYQAALGTLNPLP PPPLLAATVLAATPPGATAAAAAAGMGP RPMAGSTDQIAHLRPQTRPSVYVAIYPY TPRKEDELELRKGEMFLVFERCQDGF KGTSMHTSKVGGFPGNYVAPVTRAVT NASQAKVPMSTAGQTSRGVTMVSPSTA GGPAQKAIQNGVAGSPSVVPAAVVSA AHIQTSPQAKVLLHMTGQMTVNQARNA VRTVAAHNQERPTAAVTPIQVQNAAG LSPASVGLSHSLASPQAPLMPGPATH TAAISIRASAPLACAAAAPLTSPSITSAS LEAEPGRIVTVLPGLPTSPDSASSACGN SSATKPKDKSKK |

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| 7064 | 15115 | A | 7749 | 139 | 6503 | LSGITKMTLHATRGAALLSWVNSLHVA DPVEAVLQLQDCSIFIKIIDRIHGTEEGQQ ILKQPVSERLDFVCSFLQKNRKHPSPEC LVSAQKVLEGSELELAKMTMLLYHST MSSKSPRDWEQFEYKIQAEAVILKFVL DHEDGLNLNEDLENFLQKAPVPSTCSST FPEELSPSHQAKREIRFLELQKVASSSSG NNFLSGSPASPMGDILQTPQFQMRRLKK QLADERSNRDELELELAENRKLTEKDA |
| 7065 | 15116 | A | 775 | 56 | 425 | GQSPPGHVGHVAQARELLRPGRLPCWV PDGHIPVRPVSGPEPPTGSRILSGEESPR PPSSQAARPQPGQPRDPSSLRIPLLLPRP* LSQSGLASSGSLRAGALPRRPPGPALLS PTPCTSI |
| 7066 | 15117 | A | 7750 | 1 | 5290 | MTLHATRGAALLSWVNSLHVADPVEAV LQLQDCSIFIKIIDRIHGTEEGQILKQPV ERLDFVCSFLQKNRKHPSPECLVSAQK VLEGSELELAKMTMLLYHSTMSSKSPR DWEQFEYKIQAEAVILKFVL DHEDGLN LNEDLENFLQKAPVPSTCSSTFPEELSPS HQAKREIRFLELQKVASSSSGNNFLSGSP ASPMGDILQTPQFQMRRLKKQLADERSN RDELELELAENRKLTEKDAQIAMMQ |
| 7067 | 15118 | A | 7751 | 241 | 6574 | LSGITKMTLHATRGAALLSWVNSLHVA DPVEAVLQLQDCSIFIKIIDRIHGTEEGQQ ILKQPVSERLDFVCSFLQKNRKHPSPEC LVSAQKVLEGSELELAKMTMLLYHST MSSKSPRDWEQFEYKIQAEAVILKFVL DHEDGLNLNEDLENFLQKAPVPSTCSST FPEELSPSHQAKREIRFLELQKVASSSSG NNFLSGSPASPMGDILQTPQFQMRRLKK QLADERSNRDELELELAENRKLTEKDA |
| 7068 | 15119 | A | 7752 | 775 | 1128 | REGLYLSRFFPHSKLPRTQPDGTSVPGEP ASPISQLPPKVESLESLEYFTPIPARSQAP LESSLDSLGDVFLDSGRKTRSAARRTTQI INITMTKVRLGQGLQGSNSHFLSRASLQ |
| 7069 | 15120 | A | 7753 | 331 | 530 | LKIFFFFPSGGDMSKNVQSQMAKLNQQ MAKMMMDPRVLHHMGMAGLQSMMR QFQQGAAGNMKGMM |
| 7070 | 15121 | A | 7754 | 1 | 1517 | MVLADLGRKITSALRSLSNATIINEEVLN AMLKEVCTALLEADVNIKLVKQLRENV KSAIDLEEMASGLNKRKMIQHAFKELV KLVDPGVKA WTPTKGKQNVIMFVGLQG SGKTTTCSKLAYYYQRKGWKTCLICAD TFRAGAFDQLKQNA TKARIPFYGYTEM DPVIIASEGVEKFKNENFEIIVDTSGRHK QEDSLFEEMLQVANAIQPDNIVYVMDAS IGQACEAQAKAFKDKVDVASVIVTKLD GHAKGGGALSAVAATKSPIIFIGTGEHID DFEPFKTQPFISKLLGMGDIEGLIDKVN LKLDDNEALIEKLKHGQFTLRDMYEQFQ NIMKMGPFSQLGMIPGFGTDFMSKGNE QESMARLKKLMTIMDSMNDQELDSTDG AKVFSNNSGRIQLARPSCVSTSDVQELL TQYTKFAQMVK*MGGIKGLFKGGDMS KNGARSQIAKLNQQMAKMMMDPRVLH HMGGMARLQSMMRQFKQGAAGNMKG MMGFNNM |
| 7071 | 15122 | A | 7755 | 42 | 449 | FGLFNRLPYPPQHPKPHYSRIPGA/HAPP GPQNPSTFLSPLYCWGPSSKSPGAPKRC PSSISTPPSATPPRTL TGSWPGQRCQKD GEAQSYQVRQDPTASQPAGQSRLPSWS GNQTYLQGLHGRGPRARTLQLPG |
| 7072 | 15123 | A | 7756 | 3 | 358 | LLIHSTHPPTYPIHPPGHFFLPLFFPFF FSFSPSFHPSTHPLIHLSTYPIHPSVYPPV PLSLSVYSSIHLPTPEYFLFQPVAH/RRSH GRISSMPGEQSPIRLWKSPPSKPPFPW |

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| 7073 | 15124 | A | 7757 | 1 | 1668 | MLVHTOPPEVHQYNHSSAATRSRFQRL QLQLIWGWSQVLPMSAFYQIIQASGLRL HACVTPGAGTHSLPFLPSVGNLPSNKG SRVYCFFAADLFDILLPLMNIYQEFVRNH QYSLQVLANCKQNRDFDKLLKQYEANP ACEGRMLETFLTYPMFQIPRYIITLHELL AHTPHEHVERKSLEFAKSKLEELSRMIV EGCDILLDTSQTFIRQGTMKNSNTIIVKH EWGRQLHSDWTLTLLSGPDILCSSKEDRS AWPTAVAVPSADDTQAKAQEKLALASKP FHIRLGTMSQS*SLHQRTQE\GKLP GHHRTFTLQIPLNSSAPPLSTAWRTDGG QCPLLCFTGFCFCNSHSCSRTWEAPPEEE DDICLPTSQARCNEYVGLRKSIMLVQKK DKKNITCRSLTPSEEGLTIVKLVFSEI MFNLDFKIVVEPPDAAFTVLLAPSRQ EKAAWMSDISQCVDNIRCNGLMTIVFEE NSKVTVPHMIKAKVNGCTMSHLDNSLT LPFTDTEQGRSSSWTAGHVKAPCPLHAQ LPLLASLFLQELQAFARMSFPYP |
| 7074 | 15125 | A | 7758 | 1 | 2247 | |
| 7075 | 15126 | A | 7759 | 1 | 3711 | |
| 7076 | 15127 | A | 776 | 3 | 383 | QGFRKLPLKTTTGKEKTHSCIVGLGHVN SGKTTTTGHLIYKCGGFDKRTIDKFTEA ADKAKGSFKNAWDLDKLKAERERGITID ISLWKYETSRYYVTIIVAP*LIDFIINMSTG TSQADCAGLIV |
| 7077 | 15128 | A | 7760 | 1 | 226 | SLEFSQSKLQYLSRVKHDEVS D TENIRIN LAIERMIVEGCDILLDTSQTFIRQWDHEN QQHNHSHKARVGQAVTF |
| 7078 | 15129 | A | 7761 | 41 | 1065 | GRLGPHWSPQREGAQA WQAAGPEPCP AGRQLRPGEKSSTAAPGP GAKLPPTARG QGRPAALSAGPTEPAEPTPTRNSGWPA SAPPV/PRWGQPLLGVPGPEAGRYSAVAP SLSALRFPWWPQDVPVAVQSATDDAY EALSPSSCAFAMPSSVPA YPSITVTPDEE QNLNHYIQVLENLVRSVPSGEPGREKKS NSPKHVYSIASKGSKFELVTHGDASTE NDVLTNPISEETTTFTPGGFTPEIGKKKHT ESTPFWSIKPNNVSIVLHAE EPIYENEEPE PEPEPAAKQTEAPRMLPVVTESTSTSPYVT SYKSPVTTLDKSTGIGDLYRIRRCSSALR |
| 7079 | 15130 | A | 7762 | 3 | 342 | KERSREKTGGGGDLQREVAREDRRWRR S\QREDAREDRRWRRSSERGLRRQAVA EIFRERDAREDRRWRRSSERGRPRRQ/RG GGDLQREDAREDRRWRRSSEREMPEKT GGGG |
| 7080 | 15131 | A | 7763 | 205 | 338 | NPYIYSQLFFDKGTKNH WGRDSL FNKC CSEN LISHARKIKLDP |
| 7081 | 15132 | A | 7764 | 1 | 666 | GDPGAGPGDHNRFDCGPQPPPPKCELL HVAIVCAGHNSSRDVITLVKSM LFYRKN PLHLHMVTGAVARNIMETL FHTWMVPA VRVSFYHADQLKPQVSWIPNKHYSGLY GLMKLVLPALPAELARVIVLDTDVTF SDISELWALFAHFGVILLRLDRLRQAG WEQMWRLTARRELL/GLPATSLADQDIF NAVIKEHSGLVQRLPCVWNVQLSNHTL AE |

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| 7082 | 15133 | A | 7765 | 3 | 1289 | INFPTTSGLDGDPGAGPGDHNRSDCCPQ PPPPRCELLHVAIVCAGHNSSRDVITLV KSMFLFYRKNP LHLHLVTD A VARNILETL FHTWMVPAVRVSFYHADQLKPQVSWIP NKHYSGLYGLMKLVLP SALPAELARVIV LDTDVTFASDISELWALFAHFSDTQAIGL VENQSDWYLG NLWKNHMPWPALGRG FNTGVILLRLDRFRKAGWEQMWRLTAR RELALSLPATSLADQDIFNAVIKEHPGLVQ RLPCVWNVQLSDHTLAERCYSEASDLK VIHWNSPKKVLVKNNHVEFFRKIYLILL ENQGNLLLEEVFLCPSQPPTGADQLQR PLPQLDEEDPCFEFRQQQLTVHRGHLLF LPHEPPPPRPHDVT LVAQLSMDRLQMLE ALCRHCPGPVSLALYLTDAEAQQFLHFV EANGVGIDRV |
| 7083 | 15134 | A | 7766 | 530 | 820 | |
| 7084 | 15135 | B | 7767 | 1 | 954 | MATAATIPSVATATAAALGEVEDEGLLA SLFRDRFPEAQWRERPDVGRYLRELSGS GLERLRREPERLAEEAQLLQOTRDLAF ANYKTFIRGAECTERIHRLFGDVEASLGR LLDRLPSFQQSCRSPRAARNAVSIMAAG AGTAGPASGPGVVRDPAASQPRKRPGRE GGEGARRSDTMAGGGGSSDGSGRAAGR RASRSSGRARRGRHEPGLGGPAERGAGE ARLEEAVNRWVLKFFHEALRAFRGSR YGDFRQIRDIMQALTFFRGTLDQSSKQE LSLDLSSESIKNIQVNITYSLRSRDCANFD ILYDIKPF* |
| 7085 | 15136 | C | 7768 | 97 | 408 | MKTKVQPRLTVRVARNCSPKNKAHDNK QNWSWEEDSQITEPSAGLNSSQEAVSAP PSKPTVFNOPLPGKPNKYEDLLCRNFG AGWWSWGLGLVLLPGIKETFS* |
| 7086 | 15137 | A | 7769 | 1694 | 1866 | PLIACSFFLFLFFFLLRQSLGSVHPGLGV QWRDLGSLRPPFPGLTQFSLSLPRSWN |
| 7087 | 15138 | A | 7770 | 106 | 317 | CSAETEREIGRRK*CIQESSPSPLSIKKCP ICKAD*YL*SHLGATADAAPLFQLSSL*Q DLPSYREADL |
| 7088 | 15139 | A | 7771 | 321 | 449 | |
| 7089 | 15140 | A | 7772 | 2516 | 2717 | FVKSKALAFFLSFFFFFLKQSLSVTQAG VQWPVDSLQPLPPRFKRFSCLSLPSSWD YRCVPQCPAN |
| 7090 | 15141 | A | 7773 | 3 | 282 | |
| 7091 | 15142 | A | 7774 | 1 | 1126 | MRPGSLTDVLEPRSEGGKEKSIPERRNG PCKDPGAAACKLCLTSVLFATNRHMYL HNLLLRQGVSRASRQSALTQSSGTPAMY QCSKTYIYFQGIQVDYQEVTHTGPLSIEG SMLDIKIYVNRGEHKNGVLEEAIATIL KEVLEGLDYLHRNGQIHRNSRKELNDR FEFTPGRGPKGNDGECDEKHTTVLMRV EQQWDHTERKTQTQMSTEAKVNDTAD GVSQELFSAGLVDGHDVVIACPSRNLRL FIGIISTFPGAQAKTLGIVLDFSFSHTSHPT HLNVPRILPLL TISHPITFQAPLNSQLSSCI HPFAAIPASVLASLPVLISTARDPGTSH YSSALGFIGQIPAYMELSPVIGELCLSK VTE |
| 7092 | 15143 | A | 7775 | 2 | 1622 | |
| 7093 | 15144 | A | 7776 | 1 | 698 | MAAKLVGIEFDPCWVKMLMEKGHQKT REHNPYSMEQSEKAGVTDNIQGTKAL AGSRQSVANGKNSHCKENVTWLLIHYV QPMKPYEVFWIEFVTHQKATKYLCQLPT TSPDAVFPFGELLAELLKIPFVYSLRSPG YAJEKHSGGLFPSPYVPVVMSELSDQM TFIE/RGRPTTLSETMAKADIWLIRNYWD FQFPHPLLPNVEFVGGLHCKPAKPLPKTL GHGWDRAP |
| 7094 | 15145 | A | 7777 | 1 | 1584 | |

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| 7095 | 15146 | A | 7778 | 2 | 1627 | AATGKQALHCIRMSMKWTSALLLIQLSC YFSSGSCGKVLVWPTEFSHWMNIKTLTD ELVQRGHEVTVLASSASISFDPNSTLTK FEVYPVSLTKTEFEDIKQLVKRWAEPLK DTFWSYFSQVQEIMWTFNDILRKFKCKDI VSNKKLMKKLQESRFDVVLADAVFPFG ELLAELLKIPFVYRPRFSPGYAIEKHSGG LLFPPSYVPVVMSELSQMTFIERVKNMI YVLYFEFWQIFDMKKWDQFYSEVLGR PTTLASETMAKADIWLIRNYWDFQPPHPL LPNVEFVGGLHCKPAKPLPKEMEVEFVQ SSGENGVVVFSLGSMVSNITSEERANVIA SALAKIPQKVLWRFDGNKPDITLGLNTRL YKWIPQNDLLGHPKTRAFITHGGANGIY EAIYHGIPMVGVPLLADQPDNIAHMKAK GAAVSLDFHTMSSTDLLNALKTVINDPL YKENAMKLSRIHHDQPVKPLDRAVFWIE FVMRHKGAKHLRVAAHDLTWFYHSL DVTGFLACVATVIFITKCLFCVWKFVR TGKKGKRD |
| 7096 | 15147 | A | 7779 | 1 | 187 | SGRPFFFFFGLPFLFFFFF*DRVSLLLPRL QCNGTISAHCNLCLPGSSDSPASASRAE LP |
| 7097 | 15148 | A | 778 | 213 | 500 | SKRCLSLGRGASSLEAAEHLSCCPQADG LSRSPQWASAPPRQLLSCPSAGPRGPLQL ARSPGSRGPWVPPQGPPHQHSALT*AP AQRKRRKNG |
| 7098 | 15149 | B | 7780 | 436 | 711 | DVYKIGGIGTVPVGRVETGVLKPGMVVT FAPVNVTTTEVKSVMHHEALSEALPGD NVGFNVKNVSVKDVRRGNVAGDSKND PPMEAAGFTAQ* |
| 7099 | 15150 | B | 7781 | 26 | 384 | MHHEALSEALPGDNVGFNVKNVSVKDV RRGNVAGDSKNDPPMEAAGFTAQVIILN HPGQISAGYALYWIAIVDMVPGKPMCV ESFSDYPPLGRFAVRDMRQTVAVGVKA VDKKAAGLAS* |
| 7100 | 15151 | A | 7782 | 3 | 523 | FAPVNVTTTEVKSVMHHEALSEALPGD NVGFNVKNVSVKDVRRGNVAGD/SKND PPMEAAGFTAQVIILNHPGQISAGYAPVL DCHTAHIACKFAELKEKIDRRSGKKLED GPKFMVPGKPMCVESFSDYPPLGRFAV RDMRQTVAVGVKAVDKKAAGAGKVT KSARKLQKAK |
| 7101 | 15152 | B | 7783 | 32 | 188 | MVVTFAFVNVTTTEVKSVMHHEALSEA LPGDNVGFNVKNVSVKCVIWFASPX* |
| 7102 | 15153 | B | 7784 | 60 | 209 | MHHEALSEALPGDNVGFNVKNVSVKDV RRGNVAGDSKNDPPMEAAGFTAQ* |
| 7103 | 15154 | A | 7785 | 3 | 313 | |
| 7104 | 15155 | A | 7786 | 13 | 555 | |
| 7105 | 15156 | A | 7787 | 3 | 366 | IGY/NPDTVACV/PILGWNGDNMLEQSAN MPWFKGWKVTRKDGNASGTTLLEALD CILPPTRPTDKPLRLPLQDVYKIGGIGTVP VGRVETGVLKPGMVVTFAFVNVTTTEVK SVMHHEAQKAK |
| 7106 | 15157 | A | 7788 | 1 | 513 | EAGISKNGQTREHALLAYTLGVKQLIVG VNKMDSTEPYPYSQKRYEEIVKEVSTYIK KIGYNPDTVAFVPISGWNIAKFAELKEK IDRRSGKKLEDGPKFLKSGDAIIVDMV PGKPMCVESFSDYPPLGRFAVRDMRQ TVAVGVKAVDKKAAGAGKVTKSAQK AQKAK |
| 7107 | 15158 | A | 7789 | 1 | 1099 | |
| 7108 | 15159 | A | 779 | 1 | 615 | |

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| 7109 | 15160 | A | 7790 | 1253 | 2560 | SLVMLPLFDMVPGQAHVLLRASQDYPPF GSLCWFVIMRTDSCGWVSIKSSGQKRLL ELIDAPGHRDFIKNMITGTSQADCAVLIV AAGVGEFEAGISKNGQTRHALLAYTLG VKQLIVGVNKMDSSTEPYSQKRYEEIVK EVSTYIKKIGYNPDVAFVPISGWNGDN MLEPSANMPWFKGWKVTBKDGNASGT TLEAVDCILPPTRPDKPLRLPLQDVYK IGGIGTVPVGRVETGVLKPGMVVTFAPV NVTTEVKSVMHHEALSEALPGDNVGF NVKNVSVKDVRRGNVAGDSKNDPPME AAGFTAQVIILNHPGGQISA\GYAPVLD HTAHACKFAELKEKIDRRSGKKLEDGP KFLKSGDA\APLVDMVP\GKPHVCLRSFS DYPPPLGRFAVRDMRQTVAVGVIKSS\VD KKAAGAGKVTSAQKAQKAK |
| 7110 | 15161 | A | 7791 | 39 | 362 | AEKWARNMPFFPDLMQTDQVSLRLTLW SELFGLNAAQCSMPLNEAPLLAAAGLQ AYPMSADRRVAFMDHIRIFQEQAEKFRA LHVGSPEKQCLKAIVLFTSNTWGRG |
| 7111 | 15162 | A | 7792 | 19 | 384 | FISSIKFIMSFNFTSLFFHFIISLQGFIS SSK\SHFISFHVISSVHLIFSSHFMGSSQ LFSSDHFIISCHRFMSYLLRSVQFHFNISF HYFRSSHLITSCHHISCNQNSSSSQHFIS |
| 7112 | 15163 | A | 7793 | 16 | 450 | TQGS HQSPPPGS\PHAAHTCCPRGGEA GGTGSLLGQGHTRPAALKDWPGR PEGHKVRSDDPPGRPASSTVQLKGLSGER DGCPLLRGPGPHRAEGSPSRALRPPGTR GNTATRTPVSSGMRAASCQAWRNEVRS LMVQAP |
| 7113 | 15164 | A | 7794 | 1 | 427 | |
| 7114 | 15165 | A | 7795 | 1 | 330 | |
| 7115 | 15166 | A | 7796 | 3 | 1229 | SPPSPLPGLASQDSRPVFPSPTPAMAAVP TQPSKEGPWSPESPMRLITAPLPPGP SMAVPTLGPGEIASTTPPSRAWPTQEGP GDMGRPWWAEVVSQAGIGIQGTITSST ASGDDEETTTTTITTTITTVQTPGCSW NFSGPEGLSDSPTDLSSPTDVGLDCFFYIS VYPGYGVEIKVQNISLREGETVTEGLG GPDPLPLANQSFLLRGQVIRSPHQALR FQSLPPPAGPTFHFYQAYLLSCHFPRR PAYGDVTVSLHPGGSARFHCATGYQL KGARHLTCLNATQPFLLWDLKEPVCIAA CGGVIRNATTGARIVSPGFPGNYNNLTC HWLLEAPEGQRLHLHFKEVSLAEDDDR LIIRNGDNVEAPPVYDSYEVEYPPPPPL QPHYHRVSV |
| 7116 | 15167 | A | 7797 | 110 | 342 | FVLFTKVYEGERAMTKDNNLLGKFELT GIPPAP*GVPQIEVTFDIDANGILNVSAVD KSTGKENKITITNDKGKEA |
| 7117 | 15168 | A | 7798 | 1 | 335 | NFCTREDHQYAPLDPKHGHLPPRMPPSE RLMAAEAAFYSPPYHDPPTNSEGWEHT GLYESFRALKRSPRRKGPEKRNSGSPRSR NRKSRGRSSSRNSRSS*SSGSYSRS |
| 7118 | 15169 | A | 7799 | 110 | 409 | |
| 7119 | 15170 | A | 78 | 226 | 481 | CLAHSRHSINISTCTGAEGHESESFSYWG TRGPSATMACDGLTRTGHSPPSRARSP LLCARSLTKAACQ*AVPVTWCHCWRPQ G |
| 7120 | 15171 | A | 780 | 140 | 459 | RSSLLPCLGLWTHLIPVKVRDSLGPFAFR GEKADMPVLYDRLLKLMEMLYFKSGTI PMFYG*APRRVYIIGERIHYCGYSVLPMA VEQDVLIAVEPVKTYALQLAN |
| 7121 | 15172 | A | 7800 | 40 | 621 | |

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| 7122 | 15173 | A | 7801 | 1 | 338 | GTSFYLYRKGYLSLSKGVPM SHYAGTLL LLLAGVACLGRGIVRWTPHYRKTMTIP* ASHRNQSSKYPRHVANYNCDFRSWPDD FHCDEPITRNESQGGPIRRSVHTASPKPM |
| 7123 | 15174 | A | 7802 | 1 | 390 | ILDCHTDDSGTYRAVCTNYKGEASDYAT LDVTGGDYTTYASQRIDEVPRSDPELT RTEAYAVSSFKKTSEMEASSSVREVKSQ MTETRESLSSYEHSASA*MKSAAL*EKSL EEKSTTRKIKTTLAAR |
| 7124 | 15175 | A | 7803 | 3 | 235 | VNSAEAEAEQANTNLSKFRKVQHELDE/ AVALPHFDLLIQLVLHLADEAEERADIAE SQVNKLRAKSRDIGTGGLNEE |
| 7125 | 15176 | A | 7804 | 2 | 561 | MRPHRLDEAEQIALKGFFKQLQKLEARG RELENELEAEQKRNAESVKGMRSERTP SKELTYQTEEDRKNLAAACRTLVDKLQL KAKAYKRQAEAEAEQSPTPNL*SKFRKV QARAGLRABERADIAESQVNKLRAKISR DIGTKGLEMKELAFATSLNLAPPLGRCP ANAPCWSLCNSFLGREAE |
| 7126 | 15177 | A | 7805 | 3 | 303 | GRRPPALIDSRSPSPASPPTQ*CRPPSPFPGP APPPRLWLAPPPCPPPPPHGYGPPFARKR RGAALGLTRVLPSPGSAVRRSPGPGPGS ACDKVFRITTSR |
| 7127 | 15178 | A | 7806 | 190 | 389 | RRTYTSHLLACLRLQGLAFSPRLECGGKIR AHCSLQLYGSSDPPT*APQTAGTKQHNQ RIAQCNAADN |
| 7128 | 15179 | A | 7807 | 3 | 271 | FFLRQSHSVTRLECTGAI*AHCNLCPLPGS SDSPASAS*VAGITGMCHHARLIFVFLVE TGFHHVQAVLELL/NLMICPPQPPKVLG LQA |
| 7129 | 15180 | A | 7808 | 610 | 923 | FYLSEAEFFFFFETES/HLLSPRLECSG MMSAHCNLRPLPGSSDSPASAS*VAGITG GHHPAQLIFVAF/MYQPGFCHVGQAGQQ LLA*VICLPQPPKVLGITGA |
| 7130 | 15181 | A | 7809 | 487 | 796 | LSIFFFFEGRGAIVANVSLNFPGSKKPP PSLSKEPGTTGAAPPREIFFPPKTRLGFA LHPGSPPPGPWAPLWSKGEKVILKKH KVGRGRGFSPVSPFF*KPPPSLSKEPGTT GAAPPREIFFPPKTRLGFALHPGSPPPPG PWAPLWSKGEKVILKKHKVGRGRGFS PVSPFF |
| 7131 | 15182 | A | 781 | 595 | 1060 | ARFLPKYQSPTGPHPSFNAFLSLGAMCV LPRPNFHS�AVRSPVPGGPAPLVPGKE* EGLGVTSQSRPDCSPMSGTPRCRS*LRP AAGRGCSPLLGGCPWTVTHPLRTKAGC TLSWAQPPVLPVGGEGPRCASPVAVL GFSPCALCHLDPPVK |
| 7132 | 15183 | A | 7810 | 1 | 340 | GTSQVLTLTIAEV**NLG*VGCK*CKHTE AKRMPCAEDYLSVVHEQICVAHENTPVS DRVPIRCPESLAIRLPCFSALEVDETYGD* EYNAEAFTLHADICTLSEKERPIKKQ |
| 7133 | 15184 | A | 7811 | 3 | 337 | IESSLHQVESMHGAGNAKKNWQ/RIQEH FFFATFHPLKDYCL/EGTNLVEADNQAE WTDVQKKIIPWNSRVSDLDLAELLFQDR AARLGKISIRLIRCGPSLHSDKPTNFRE G |
| 7134 | 15185 | A | 7812 | 3 | 926 | YGEENLKTSICTFLAVLSHLDIITQNIPEK KLILKQALIVVLQWCFNHNFSVRLYALV ALKKLWTVCKVLSVEEFDALTPVIESSL HQVESMHGAGNAKKNWQRIQEHFFAT FHPLKDYCLETFYILPRLSGLIEDEWITID KFTRFTDVPLAAGFQWYLSQTLKLP GDWSQQDIGTNLVEADNQAEWTDVQK KIIPWNSRVSDLDLELLFQDRAARL/GKSI SRLIVVASLIDKPTNLGGLCRTCEVFGAS VLVVGSLQCISDKQFQHLVSVAEQWLPL VEVKPPQLIDYLQKKKTEGYTII |

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| 7135 | 15186 | A | 7813 | 3 | 360 | ATCSSDQSVKVWDKSESGDWHCTASW KTHSGSVWRVTWAHPFQVLAFCFTD RSSAVWDEILSESRDNL*GHTHWVKRTT LEDSIVSATCV*SFLSHVGIMLLSCGTFFP ACICGVFP |
| 7136 | 15187 | A | 7814 | 9 | 305 | SHLLRSLRQENRLNPRGGGCNQPRSGHC TPAWATRAKLHLKKQTNKMLANLIQQH IKKVIHHYQVGFTPGMQG*FNICKSVSVI YHINRTTHKNVAAAA |
| 7137 | 15188 | A | 7815 | 3 | 217 | AASTMPMSFEWQRO*RFPPFYTLQPNVN TRQKQLTA*CSLVLSLCRLHKQSSMTLIK TRLTSDSITVMLDC |
| 7138 | 15189 | A | 7816 | 15 | 335 | QHFWERFHVTKDRINTVERQETDWKIFA TYLMKKV*ISRKCYNYSKLVRRKKQLNR KWAKEKNKQSQKKKQSGQ*TKTVQPQ* NKRAN*RYLSPISLAKSNKLN |
| 7139 | 15190 | A | 7817 | 1 | 331 | GLIEILVIYVSDTPVK*DV*SDIFEQ*AYG KIDGGNDVCDLQSSEGTNTKMKNNNEEM MIGEAMDETGHGETENEGISTKTSKPD EAETNMLIAEMDTFVCDTVMESTEG |
| 7140 | 15191 | C | 7818 | 51 | 200 | MSTPXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXS* |
| 7141 | 15192 | A | 7819 | 3 | 219 | MLAGCSRTPELR*STHCSLPKCWDYRRA HNAQPFLTLN*RSETRRSL*F*IMWLPLE FLGFPLESQQGCTA |
| 7142 | 15193 | A | 782 | 71 | 237 | EQPGMVHTHCNPSTLGGRGGWIT*DQEF KTSANMVKPCLCWRYKKLAGHGGAC L |
| 7143 | 15194 | A | 7820 | 1 | 358 | VHCLVPDLLQSNNPCYWGVMCKYAA EALLEGKPEGTFLLRDSAQEDYLFVSFR RYSRSLHARIEQRNHNFSFDAHDP*VFHS PDITGLEHYKDPSA*MIFEPLLSTPLIRT FPFCL |
| 7144 | 15195 | A | 7821 | 260 | 481 | LILKFV*NHKIPQIAKTILSKENKAGGITL PDAKISCKAVVTKTALYWHNHRHIEQW NRIANTEINPNICNQLI |
| 7145 | 15196 | A | 7822 | 1 | 306 | VKAKAKKLQIQIQLLELYCSYDMQEED FAHRAMDYFPKIENNLSTRMDHVMVSSF CIENWHQLESLSLLILHNMPHYEEDFEFE GLRLDMVQ*RLTSCSDAG |
| 7146 | 15197 | A | 7823 | 3 | 396 | SSLSSLSSSVSVTFGFGTFPSAVSSSIPDG GLALAFSSSGLSTSFSSP*SHSSSSPPVPP LSSDTRRSTSPADMAAPSAT*TRRSTAPS NPFPSLAAPREKGGNPPTNERRKLETPI PGRRRQRROR |
| 7147 | 15198 | A | 7824 | 3 | 344 | HEHECYAKVLYELKPVGEEPQNVSKQN CDLFEQLGQYEF*NALLVRYTKNVPQGT TPALGQVLRNLRKVSSKCKKHPEAKTM PCAEDYLSVILNQLCALHDSAVSDRVS RCWT |
| 7148 | 15199 | A | 7825 | 1 | 413 | RAGYRQKWGSLATVIGQLGLPSGEGLV WPQRRREGHRNAHCSELVDDLHVITQ NRANHRPRCGSLLSELKFAPLALQPGR QSKTLSQKKNKQTTTKNTKKQPGSVA HACNPSTLGG*GRQITLPSGVRDQPGQH |
| 7149 | 15200 | A | 7826 | 37 | 363 | ASDWNQDRARGRGQGGCETRDSSESQS GTNGQPPAEASKDSWSSGGMAR*APSP QRQKAGYPGSPSPQAPASMRSLGPPQF QEPPQALFPLEVPIPSPHTRNKMAR |
| 7150 | 15201 | A | 7827 | 3 | 354 | HERAFLNNSCFL*AFDPYQCDRYLFKIV TDVYYTPYVLIYYI*APLPLLQLTHHF LSLFFL*VLNIYALVYLSTALPLSLFISIS PRYSLCLFFHFLSLMLFLSSLSMYCSHY |
| 7151 | 15202 | A | 7828 | 2 | 269 | ARVAPLKGVQEQEVREHEVTKPEKEK GEETRIENGKLIVSDSCGRVYVSGKIYY PM*AYNDGLILERYQIMPDIIVSYVFIMI |

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| 7152 | 15203 | A | 7829 | 2 | 350 | KDIRVGHRQNRALPPQASPTVAPGQPT ALPPTGHSGPTMGWPSRLSQLSLITAPTS ASPTVVKLPSGACWPLSSTFASSPLSLVQ *P*NSDSHDATSAMAPSESRECLSPWPA R |
| 7153 | 15204 | A | 783 | 236 | 404 | EDGHHSGLHSKQKQPAWPSMVTHTCN PNTLGGRGGWIT*GQEFETSLTNMEKPC L |
| 7154 | 15205 | A | 7830 | 2 | 376 | SHCLEPKDIRVGHRQNRALPPQASPTV APGQPTALPPTGHSGPTMGWPSRLYQLS LITAPTSASPTVVKLPSGACWPLSSTFAS SPLSLVQ*P*NSDSHDATSAMAPSESRE CLSPWPAPRA |
| 7155 | 15206 | A | 7831 | 176 | 379 | SVTDHPIYNCNLSPSPNPGSPDPSDVLFF VVMTDYLLP*CVICCCFLSDPPHCSHPV GGSFFGIN |
| 7156 | 15207 | A | 7832 | 1 | 344 | NSGRVSGNLSPLPPGPPRPLEEATP VLLSQGIPEREDSFRNLRTDLYIHQLKS* DSPEISSLCQGEETPRHSDKHNS*NAAS EGKCGFPSPPTMEVEIASHDEEDVIHS |
| 7157 | 15208 | A | 7833 | 355 | 535 | PNRPITGEVTTKNLTKKSLRDPGFTDEF *TFKEGFIPTLTKTVKEGLHPTFLYEASIT L |
| 7158 | 15209 | A | 7834 | 61 | 250 | RSRLCAPVRESHTYLIMPGLCC*FFLYYI FFGFFFSVVFCLLSFYSPFFSFVSSVSFV*F WVF |
| 7159 | 15210 | A | 7835 | 3 | 66 | DAWEKKICETEDWLFJHQRISSSRMKR NKEQLQDV*NTIKRTNIRIIGVIEKREKG RKLI*EIMAENSPNLGKDMSIQVYEAQRS PYRIHKKTSPPKHMIKLSKAKSRR*IRG |
| 7160 | 15211 | A | 7836 | 3 | 146 | HMVAGAVAGILEHCVMYPIDCVKTRMQ SLQPDPAARYRNVLEALWRIIRTEGLWR PMRGLNVSASCAGSAYALYFACSD*LTQ LPAIAMCWRRPSGGL |
| 7161 | 15212 | A | 7837 | 2 | 329 | VASGRRKNNLSKVTGLEVPSTPDRPC SGRQSLNPPVTSFPNPSQRNRTPPPTTRQ MATL*EALHGSHLPPPGRACERTSSPGPR TTRPQVSDRRASQSTSYYVGPGRP |
| 7162 | 15213 | A | 7838 | 2 | 356 | EAGAHT*ITMKNQRLKETVDDTVEVSD FTVSRNAHEAFNTAFTTLAACAASIG*V LLYLTLTTCPC*CKTKRQNNMLHQSNA NSSILRGPASDASADERNACARKRAVL LEPLKD |
| 7163 | 15214 | A | 7839 | 3 | 264 | |
| 7164 | 15215 | A | 784 | 2737 | 2915 | KNVVHTHQGILYSHKKEQD*LGVVAHT CNPSTLGGRGGWIT*GQEFETSLTNMVK PCLY |
| 7165 | 15216 | A | 7840 | 42 | 226 | |
| 7166 | 15217 | A | 7841 | 1 | 507 | LQLEAEEQRKQKKRQSVSGLHRYLHLL DGNENYPCLVDADGDVISFPITNSEKTK VKKTTSDFLEVTSATSLQICKDVMDALI LKMAEMKKYTLENKEEGLSDTEADAV SGQLPDPTTNPSAGKDGPSSLVVEQVRV VDLEGLKVVYPSKADLATAAPPHVTV VR |
| 7167 | 15218 | A | 7842 | 51 | 340 | PILVYRPDVPD*VAKDYASFRNYT*GPLL DRVFTTY*LMHTHTQTVDFIRSRAHQFGG FSYGKMTVMEVEDLLDGLMDESDPDLN FLKSFHA*KJAY |

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| 7168 | 15219 | A | 7843 | 44 | 1352 | KMLYKNFIMQSQELTALWEAKVHPAML GLDELGRSGCGHCTQADLRFGDAAGRD PGQDNDRNTAEPAPPPPRVMAAAAAL RAPAQSSVTFEDVAVNFSLEEWSSLLNEA QGCLYHDVMLETLTLISSLGKRQTLHTR ERPYESIECGKAFAEKSSLINHRKVHSGA KRYECNECGKSFAYTSSLIKHRRIHTGER PYECSECGRSFAENSSLIKHLRVHTGERP YECVECGKSFRSSSSLLQHQRVHTRERP YECSECGKSFSLRSNLIHHQRVHTGERH ECGQCGKSFSRKSSLIHLRVHTGERPYE CSDCGKSFAENSSLIKHLRVHTGERPYEC IDCGKSFRHSSSFRRHQRVHTGMRPYK* SKFWKFCSPGFLLLQGQRVHTGSRCEC DKWGIFFS*NASFFT*KSAPTEEVPECN ECEKAFSPLSLVT |
| 7169 | 15220 | A | 7844 | 2 | 353 | NLLYQFWIHTEVINNLGPLELILNTRSHH RVHDGRNRYCIDKNYAGVLIWDKSFSGT FEAENEKVYVGLTHPINTFEPIKVQFHHL FSIWTTFWATPGFFNKFSVIFKGP*WGP KP |
| 7170 | 15221 | A | 7845 | 3 | 386 | TVRVCACDHHGNMQSCHAEALHPAGL STGALVAILLCIVILLETVVLFAALRRQR KKEPLIISKEDIIDNIVRYNDEGGGEEDTQ AIDIRTLMNVPPI*DTHLRRCFAP*TSLYY HRATPTRSCYHP |
| 7171 | 15222 | A | 7846 | 151 | 352 | YCCTYYIFVLFIP*SSCGLTLIFITCILFGSI SFFLFFITIVFSIIVTTFKFRLLYSIHL SYLLC |
| 7172 | 15223 | A | 7847 | 2 | 265 | VKPSP*PLTGALSALLMTSGLAM*FHFHS ITLLILGLLTNTPPVQKGLRYGILFITSE/V FFFAGFF*AFYTPA*AYPQLGGTAQQDT |
| 7173 | 15224 | A | 7848 | 1 | 156 | GIRHEAYHIVKPS*PLTGALSALLMTSG LAM*FHFHLKKKKKIGSSFIAVG |
| 7174 | 15225 | C | 7849 | 512 | 778 | MTSGLSHVDFTSNSITLPHTRAYXTNLT NHIPMMARMLTRRKAHTKGHHTRTCSK KAFRYGDKSYLFTSGSFSSQGFILPFLP LQA* |
| 7175 | 15226 | A | 785 | 361 | 710 | DLFWLF*MDKFLDTYTLPRLNQKEVK |
| 7176 | 15227 | A | 7850 | 15 | 613 | LKTTHLLFQVSVGQESRCGLAKSSGSKS LTRVKVRGQPRWLCHLKAQLGKDLLLS SLTWLLAACGSSPVVGLWASAPGLLLAS HHPRFSATWVFHKVAHNTAAGFMSTGK QEG*RDKITAKQKFASYNLISEVTTHHFL PYSIYEKQVTRSSPHTKERDSPRG*LSEG KDHWEFPQKLPATDVIALFYENKHQTH YIHL |
| 7177 | 15228 | A | 7851 | 66 | 355 | KSMTDGHQITVTNIRQLPARTLYTHWPR EFSP*SPPLERMHTRGARREARQKAPRIR DKRRGKSRVHCLGEELANGGWDRIRW GKGERQGDSEGRV |
| 7178 | 15229 | A | 7852 | 3 | 358 | HASAHASQGDDQLERDHEN*DRFVRQ VVGINNYRISEESGHPYNIFGKIFHDCAD LDTSEH*LCKCDSFDKTLKPTINLVSYNR NFA*TNIDENFRCGKSPSYSSCYSKHEEL HNGM |
| 7179 | 15230 | A | 7853 | 79 | 413 | LSKGTGRKRDGLTLPAHPKAKTDPAAAP QGQPGVGVRSPPCPG/QREQQGSAGSP GWMGGGCPVPS*PLKGONQPPSSLGG SKGSFFSPDPAPAVARGRRVRGEERGQVR E |
| 7180 | 15231 | A | 7854 | 171 | 173 | LTAEACLSFSPSLPSSLGVSQCPHHGGLG PAHPSALPQPPGCIFEAAWPPRALT*PLSS PLTPPAPGHCRIRRGEEGASAAFPGLGT GLVLSFEDDHRLQD*QAHTQSQPGASP QTLCCFRGLGHAGELLTPPTVQPLFPE SASKWPQLFGPRILPGPPKGSPTTKAWPP GVCGQQLPLVKGHPG*PSPASGRSRCEV SVPSQBVVILGIGWGLAPAGCSQHWB |

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| | | | | | | SVPSCPVVPLPLGWGCLAPAGCRSQHW D |
| 7181 | 15232 | A | 7855 | 27 | 263 | FHCFISNF*VANRSSLLIDFSVGLLKCKS FIFFNAILHYCLMMVCEYDSLFLSYMF LLIFFYFYIYIFIYLLFIHPY |
| 7182 | 15233 | A | 7856 | 92 | 354 | VLNSI*SGNQGKSYANVYRLLYLDPIPKI YAEAYTP*NVNSTNLETKSPKTIQKFPED REFKNDFFEKTNGDRETGAHPFLLFL V |
| 7183 | 15234 | A | 7857 | 464 | 2848 | GETGMSTALHTTTVAMRCPMLGGGGGP TYGPPQPWGHPDVHIMQHHLVPIQARLG SIAEIDLGVPVPMKTFKEFLSLDDSDV ETEAVKRYNDYKLDFFRRQMQDFFLAH KDEEWFRSKYHPDEVGKRRQEARGALQ NRLRVFLSLMETGWFDNLLDIDKADAI VKMLDAAVIKMEGGTENDLRILEQEEEE EQAGKPGEPSKKEEGRAGAGLGDGERK TNDKDEKKEDGKQAENDSSNDDKTKKS EGDGDKEKKEDSEKEAKKSSKKRNRK HSGDDSFDEGSVSESESESESGAEEEEKE EAEALKEKEKPKEEWEKPKDAAGLEC KPRPLHKTCSLFMRNIAPNISRAEHSCK RYPGFMRVALSEPQERRFFRRGWVTFD RSVNIKEICWNLQNIRL/RECELSPGVNW DLTRVRNINGITQHKQIVRNDIKLAACL IHTLDDRTQLWASEPGTPPLTPSLPQNPI LKNITDYLIEEVSAEEEELLGSSGGAPPEE PPKEGNPAEINVERDEKLIKVLDKLLLYL RIVHSLDYNTCEYPNEDEMPNRCGHH VRGPMPPNRISHGEVLEWQKTFEEKLTP LLSVRESLSEEEAQKMGRKDPEQEVEKF VTSNTQELGKDKWLCPLSGKKFKGPEFA RKHIFNKHAEKIEEVRKEVAFFNNFLTD AKRPALPEIKPAQPPGPAQILPPGLTPGLP YPHQTPQGLMPYGPQPRPPILGYGAGAVR PAVPTGGPPYPHAPYGAGRGNYDAFRG QGGYPGKPRNRMVRGDPRAIVEYRDL APDDVDFF |

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| 7184 | 15235 | A | 7858 | 1073 | 3541 | GETGMSTALHTTVAMRCPMLGGGGGP TYGPPQPWGHPDVHIMQHVLPIQARLG SIAEIDLGVPPVMKTFKEFLLSLDDSV ETEAVKRYNDYKLDFFRQQMQDFFLAH KDEEWFRSKYHPDEVGKRRQEARGAL QNRLRVFLSLMETGWFDNLLLDIDKAD AIVKMLDAAVIKMEGGTENDLRILEQEE EEEQAGKPGEPSKKEEGRAGAGLG DGE RKTNDKDEKKEDGKQAENDSSNDDKTK KSEGDGDKEEKEDSEKEAKKSSKKRN RKHSGDDSFDEGSVSESESESGQAE KEEAEALKEKEKPKEEWEKPKDAAG LECKPRPLHKTCSLFMRNIAPNISRAE LCKRYPGFMRVALSEPQPERFFRRGWV TFDRSVNIKEICWNLQNIARGARSLNR WC SRGKGLRAAVSLASGLRECELS PGVNRDLTRRVNRNGITQHKQIVRNDI KLAAKLIHTLDDRTQLWASEGTPPLPT SLPSQNPI LKNITDYLIEVSAEEEE LLGSSGGAPPEE PPKEGNPAEINVER DEKLIKVLDKLLLYL RIVHSLDYNT CEYPNEDEMPNRCGIIH VRGPMPPN RISHGEVLEWQKTFEELTP LLSVRES LSEEEAQKMGRKDPEQEVEKF VTSNT QELGKDKWLCPLSGKKFKGPEFV RKHIFNKHAEKIEVKKEVAFFNNFLTD AKRPALPEIKPAQPPGPAQIIHVPRVVL PPGLTPGLPYPHQTPQGLMPYGP PRPIL GYGVTGGPPYPHAPYGAGR GNYDAFR GQGGYPGKPRNRMVRGDP RAIVEYRDL DAPDDVDFF |
| 7185 | 15236 | B | 7859 | 145 | 226 | MAVNCSEMRLKSSWNGCAIANEGDCHL EATSICSSTSFMDMLGEFRHCESSILL AST AX* |
| 7186 | 15237 | A | 786 | 2 | 424 | |
| 7187 | 15238 | A | 7860 | 136 | 1559 | ILTMREIVHIQAGQCGNQIGAKFWE VISD EHGIDPTGTYHGSDQLDRISV YYNEA TGGKYVPRAILVDLEPGTMD SVRSGPFG QIFRPDNFVFGQSGAGN NWAKGHYTEG AELVDSVLDVVRKEA ESCDCLQGQLTH SLGGGTG/SPGMGT LALISKIREEYPDRIM NTFSVVP/SPK VSDTVVEPYNATLSVIH QLVENTADE TYCIDNEALYDIFRTLKLT TPTYGDL NLHLVSATMSGVTTCLRFPG QLNADL RKLVSVNMVFPRLHFFMPG FAPLHQP VESQQYRGSHKCRELTQQ/VSF DAK EH*WAACGPPATGRYLTVAAAFR GR MSMKEVDEQMLNVQKN*QLTLWE W FPQQCSRTACLFTSQPRGPSRWAVHLS LGNRHSHSRELFQSGIFGSSFTWPC FRRK AF/LFWH/YTQGEHGHTMGVST EG*EA TLNDLRL*SIKQLPRMPTQEE EDFGEEA EEEA |
| 7188 | 15239 | A | 7861 | 2 | 304 | ARGLCPLGYTGLKCETDIDECSP LCLNN GVCKDLVGEFICECPSGYTG QRCENINE CSSSPWLNGICVDGVV CYCCTFV*GFCI FKFS CSSCPLYTI |
| 7189 | 15240 | A | 7862 | 1 | 345 | GTSGETSRFL*DVLQMNDFGTRWR FYAT VIYQKPQLKSLILE*RETWV LGTDTLQ TKEEKDPRLRKTLVYVAP LLVLGSDVL EALSGAAPLRLFLKDA IRDQARIGRAERT VL |
| 7190 | 15241 | A | 7863 | 2 | 343 | VRSAYPRLLENSLAGQRRHHLCH PLLP AGGARAPQPQPQLLGARPG GRCRM RRRPQAPRAGRGAALARAL* PLSSTASR RGACPGAAPSDSPEDP ASDHGHSPLGG RC |

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| 7191 | 15242 | A | 7864 | 1 | 338 | QIDEIVTETLLTEAERGAKVYLTTGYFNL TQAYMDLVLGTRAHEYQILLASPEVNGFF GAKGVAGAJPAAYVHIERQFFNDECSL* QSRVQLSEYWRCSGRSLSEFVRHDI |
| 7192 | 15243 | A | 7865 | 174 | 361 | |
| 7193 | 15244 | A | 7866 | 1 | 1259 | VRCRPVRNSRVDPRVRMAAVFLVTLYE YSPLFYIAVVFTCFIVTTGLVLGWFGWD VPVILRNSEETQFSTRVFKKQMRQVKNP FGLEITNPSSASITTGITLTTDCLEDSLLTC YWGCSVQKLYEALQKHVYCFRISTPQA LEDALYSEYLYQEYFILSSDIPISTEN*T SYG*SVANLLIILGILEACLLQNKHSPCI RTCSVYRISVSGTGFAFRLIYPLALIIRL LMDKVPLTY*SFLGY*KHVYCFRISTPQA LEDALWSEYLYQEYHFIKKDSKEEYICQ LPRDTNIDDFGTVPRSRYPLVALLTSLDE DDREIYDIISMVSVIHIPDRTYKLSRILY QYLLLAQQGFHDLKQLFMSANNFTPS NNSSEEKNTDRSLLEKVGLSESEVEPSE ENSKDCVVCQNGTVNW |
| 7194 | 15245 | A | 7867 | 106 | 387 | |
| 7195 | 15246 | A | 7868 | 2 | 766 | |
| 7196 | 15247 | A | 7869 | 149 | 420 | CGTDKTFFWSCTVRENLSYSEELLSRR QICKNKNDPPGDRD*FDYSRSDYEHSRR GRSYDSSMESRNRDREKRERERDTR KRSRKSP |
| 7197 | 15248 | A | 787 | 1 | 462 | |
| 7198 | 15249 | A | 7870 | 1 | 443 | GQDSRSRDNGPDGMEPEGVIESNWNEIV DSFDDMNLSSELLRGIYAYGFEKPSAIQQ RAILPCIKGY/DCDLYETLTITQAVIFINTR RKVDWLTEKMHARDFTVSAMHGDMDQ KERDVIMREFRSGSSRVLITDLLARGID VQQVSL |
| 7199 | 15250 | A | 7871 | 2 | 363 | ELDTLCDLYEP*PSPSIIFINTRRK/VDWLT EKM HARDFTVSAMHGDMDQKERDVIM REFRSGSSRVLITDLLRIGRGGFRGRKG VAINMVTEEDKRTLRIETFYNTSIEEMP LNVADLI |
| 7200 | 15251 | A | 7872 | 3 | 449 | NLQEWKLDTLCDLYETLTITQAVIFINTR RKVDWLTEKMHARDFTVSAMVCLPAA SLLWVCPSEVSYLKPGFLEPRCLPGLLHI CFLFQHGMDQKERDVIMREFRSGSSRV LITDLLVSRGN**QRQKGSKVIPSPRG HQCLSGK |
| 7201 | 15252 | A | 7873 | 236 | 533 | |
| 7202 | 15253 | A | 7874 | 1 | 366 | AEIRDRSPCGELHVEREEWKLDTLCDLY ETLTITQAVIFINTRRKVDWLTEKHAR DFTVSAMHGDMDQKERDVIMREFRSGS SRVLITDLLVSRGN**QRQKGSKVIPS PRGHQCLSGK |
| 7203 | 15254 | A | 7875 | 5 | 1285 | FLRIMSASQDSRSRDNGPDGMEPEGVIES NWNEIVDSFDDMNLSSELLRGIYAYGFE KPSAIQQRAILPCIKGYDVIAQAQSGTGK TATFAISILQIELDLKATQALVLAPTREL AQIQKVVMA LGDYMGASCHACIGGTN VRAEVQKLQMEAPHIIVGTPGRVFDMLY RRYLAPKSIIRMLVNEADEMLSRGFKD QIYDIFQKLNSTQ/VVLLSATMPFDVL EVTKKFMRGPVIRILVKKELTLEGVIRQF LHQPNWEEEWKLD*CDLYETLTITQ AVIFINTRRK/VWDWPHPRKMHARDFT VSRHAMGDMGPKGNETVIMEGSRSGS *QSF*LPT*PCWARGIDVPAFSLVINYD LPTNRNENYIHRUGSTVDRFGRKGVAINM VTEEDKRALRTLGA SYNTSIEEMPLNV ADLI |

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| 7204 | 15255 | A | 7876 | 3 | 378 | MDTTPLSYES*SDEYLVTNM*LQDAFC RGLVKPGLNVLLKGPINAVIDVNGLKQC LA*FKRYLECL*RLDVTLCVPV*IGGSDA PLPHNKDHKAADP*DYFQR*MSFYRQA HAAMLAVLPRLHH |
| 7205 | 15256 | A | 7877 | 2 | 397 | RESESCAAADTPALETLSFHGDWEIIEVF NRDLGSTYPDDLAL*MEDVDFEEYEE* GYD*GWVLYPQEGVIGNMEGPDYS*VTF ALHSSSVYRVSLDPKTYTLAVTGGYDD GAFVWLLTYG*LLFE*ASHE |
| 7206 | 15257 | A | 7878 | 3 | 399 | NSQVLLDSPIQLSKITENYECITELSGLLK REQSSTVNASNLENDEARLKAYLENRSE IDSLKTSNPIDL*EASISQAGSIN*SRF*SS GMNKSVDVRIDNFNGSIGDRJLLTAANVI LAWCRLYGLMRQNV |
| 7207 | 15258 | A | 7879 | 1 | 424 | PVLRVARERSLPGPQEGPHGRASESASPL APSIAPSPPGPPALSASHIMGSQALRSPET PW*SPWDPPAPLDLVSPWQFPFGPHASA TP*RSPLGLQTPQAPGSWAPHVPATPQA SGLPAPHVTETP*ASS*LAMPVPETP |
| 7208 | 15259 | A | 788 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGTG AQLSELHCDKLHVDPENFKLLGNVLTV LAIHFGKEFTPEVQASWQKMVTGVASA LSSRYH |
| 7209 | 15260 | A | 7880 | 156 | 312 | LFSLACRYHVYPTCRNTSGILGFTVSVVT NAIPFIS*LSSFYIYFLYNFG |
| 7210 | 15261 | A | 7881 | 15 | 394 | FGCLLQGRRPLKSHSPWQPGASGRPAQ GKHKNR*RGQNPSNLSHPAPTTPWPGIK CPLPRAGPSLSSLLPGRVLCARPEFPLHG RGLEPSASLLPSALAPSLRGLKGTERR LKADQAWGGWKE |
| 7211 | 15262 | A | 7882 | 2 | 102 | NKILIIKTNSRKK*KIE**RDNNQSNNNKN HNK |
| 7212 | 15263 | A | 7883 | 3 | 397 | NFLYTFLYFPNFV*SAHCF*NQKKKNKY FLLREKCLLNCFPHLYVAFYVYIPSFNLS GC*YLPSCSIFYVFIPLSHPLLFFLCFSLS FSLPFFLSLFCFFLAFLFHPSFILLDSSA CLLCISCFHL |
| 7213 | 15264 | A | 7884 | 190 | 339 | DGKGLLQVCLPLQDVYKIGGIGTVPVGR VETGVLLKPGMVVNFA/PVNVTT |
| 7214 | 15265 | A | 7885 | 377 | 1073 | LQGHRLRTGAVLIVAAGVGEFESWYSPR MGRPESMPFLAYTLGVKRLVVGVNKM DSS*PPYSQKRYEEIVKEGSTYIKKIGYN PDTVAFVPISGWNGDNMLEPSANMPWF KGWKVTRKDGWASGTTLEALADCILPP TRPT*QSPCGLPSSRDVYKIGG/LGTVP VGPSGRLGVLLKPGMGGSPLAPVNVTE VKICSEMHGGRF*VEALSWGDNVGLSM FQGLLFCSK |
| 7215 | 15266 | A | 7886 | 2 | 415 | SVGDPCPSTASVDQCTIVP*PMEGPLLLY RRCIEGVGGIFLWDPQPSSPQHGPATPST GEPGFVVHQDLSHIQQPAAVVAALNN HKPPVRS*PPSATPEAFT*FSKCDDLDEE LSLLRYCHAFSEC*HDIRPSHIHP |
| 7216 | 15267 | A | 7887 | 1 | 360 | TERFGM*GGEAVCLYEPPVSELLRRCGN CTRESWVVSFYLSADHELLSPTNYHFLS SPKEAGGLCKAQITAIIFQQGDIFVDLET SAVRPFVWWQVEAIPVDYLPSCSFVMIPT LYCSP |
| 7217 | 15268 | A | 7888 | 152 | 378 | WEGGSGTILARRFWDLQAYRPHAQVP GFLR*SHLMAVGHAETDLTALTMLILT PEAWQLHTILYLSGLLAMLP |
| 7218 | 15269 | A | 7889 | 302 | 564 | YWLFYDFMIAEKILNGYFCCCC*DRSCP VAQAGELWHERGSLQPRPPGVKQCSYF SLLSSWDRRHVPPHLANF*TFCCRDRVSP VLP |

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| 7219 | 15270 | A | 789 | 38 | 485 | APSPDAMGHFTEEDKATITSLWGKVNVE DAGGETLGRLLVVYPWTQRFFD/SFGN LSSASAIMGNPKVKAHGKKVLTSLGRC HKSTWDDLKGTFAQPDVNCTCDKLHV DPÆENFKLLGKCCW*PVFGNPIFGKEFTP EGAELPGQKDG |
| 7220 | 15271 | A | 7890 | 1282 | 4603 | GSLPCLEHVSLNNPLSIIPDYRTKVLAQ FGERASEVCLDDTVTTEKELDTVEVLKA IQKAKEVKSKLSNPEKKGEDSRLSAAP CIRPSSSPPTVAPASASLAPQPLSNQGIMF VQEEALASSLSSTDSTPEHQPIAQQGCS SLESIPAGQAASDDL RDVPGAVGGASPE HAEPEVQVVPGSGQIIFLPFTCIGYTATN QDFIQLRSLIRQAIERQLPAWIEAANQR EEGQGEQGEEDDEEEEEEDVAE |
| 7221 | 15272 | A | 7891 | 1 | 286 | SPPTVVPASASLPQPLSNQGILGDE*VIL VS*ACLLARPARKRGCCAVPSGAEARDT QERTPPARAPGDAELGVRSWENSSTRCF KSQKNIPTP |
| 7222 | 15273 | A | 7892 | 3 | 417 | PPPLWFNQDPHVESKGLAAGRVPVSTSQ GRTQFRGSAPPKDPLPRTGPSANRRVP HTFQPDISFPGSPKPPS*DRHPNPSLRSP LVSHSVHNQAGRWAKVQATARERKSDT KSIWLWRWRRILKRTRSNSLYTLHG |
| 7223 | 15274 | A | 7893 | 2 | 236 | KKSNLRMLAEHGGSHL*SOLCRRRLRQEN HLISGGGGCSESTSHHCTPAWGTE*DFVS EKKKKKLTGWDPDSGRKWWC |
| 7224 | 15275 | A | 7894 | 3 | 254 | LECNGTISAHCNLRMLMSG*FSRLSLPSS *DYRRPRLRPANFCLVEMGFHHVQGAG LKLQTSGLPLSLPKCWDYRAHPLA |
| 7225 | 15276 | A | 7895 | 1 | 185 | RQSLALSPRLCSGAIIAHCSEPLGLRQL CCLSLPKC*DYRHEPLSLACFLFYYPEH LT |
| 7226 | 15277 | A | 7896 | 1 | 182 | KLVGLEPVSTYSIRVSAFTIVGNGNQFSN VVKFTTQESG*IQFLSLKCFLLYLPFFSF S |
| 7227 | 15278 | A | 7897 | 4 | 329 | AGEGGLQALILRDGAWPQPPSGD*QVKG LEPLTPAPAGSSQGP GPPIASSPVGQS KTD TATTKVGPVGGGQ PAMHQQLPP SPGDPA AEDAHTWGERSLSGMKGK |
| 7228 | 15279 | A | 7898 | 115 | 408 | HWKERGSLYPA*TOGSACVLPGQGHLP RPQATPPTTAHLVPPQHCRPGPAAPAP* QGMSTPTTATLFSRLQGRQLP MGAPSG QGPWLYCRGEGPRA |
| 7229 | 15280 | C | 7899 | 128 | 253 | MNSPDWELWQDNSPQDSCVLIPRTCDH AASRRDRSSGVIE* |
| 7230 | 15281 | A | 79 | 421 | 899 | IASLFLIVKVEEVSQTAIWKKKKCDEYIP GTTSLGMSVFNLSNAIMGSGILGLAFAL ANTGILLFLVLLTSVTLISYINLLLICSK ETGCMVYEKLGEQVFGPQGFVIFGAT SLQNTGGKKNMLFFT*LEYTHHTSFFSK WLFVRLLLLSRSEINLLFI |
| 7231 | 15282 | C | 790 | 128 | 274 | |
| 7232 | 15283 | A | 7900 | 856 | 1071 | SFALVAQAGVQWHDLGSLQLPPRFK*F SHLSLPSSWDFRCPEPYWLIFVFLVETGF HHVDQAGLELLTSGD |
| 7233 | 15284 | A | 7901 | 87 | 395 | RSGGGVPPRNPPLGGRGGGFQGP GFQI TLSPKGKPLFFLKSNFPG*WAPPLKPPF KGG*TKKIFLTLEGGVPINGNFP PPPPGG KNFFSKKKKKKKKK |
| 7234 | 15285 | A | 7902 | 28 | 403 | GGTIYGNCVVPATVPAGSPGVPVAVGGQP GPLPVL*RTSPETCPPLGVTTGSLCLAPY HLSFSGGHGLPGTPREAG*REGGNSLQL QLPNPKPFLPSRPEDPTWSPSSQGEELRR RKVRCDLKS LT |

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| 7235 | 15286 | A | 7904 | 1 | 609 | SHKTNVQQCYCYCGPGDWYLMQLQC CKCKQWFHEACVQCLQKPMFGRFYT FICSVCSGPDYLRPLQWVDIAHLCL YNLSVIHKKKYFDSELELMTYINENWD RLHPGELADTPKSERYEHVLEALNDYK TMFMSGKEIKKKKHLFGLRNRVPPVPPN VAFKAEKEPEGTSHEFKLKGRKASKPIS DSREVSNGI |
| 7236 | 15287 | A | 7905 | 440 | 608 | CVKFLDTSQADTPKSERYEHVLEALN DYKTM*VDLFYVSL*GRHLVSIRNNGIV |
| 7237 | 15288 | A | 7906 | 49 | 796 | SHFIYFLTIVISSLVNEVC*SSIFLMNLQ VVLVYIFWLLLLYELCCRIFSHFVVCFTM FINIVTF*F*YLQIVFLYG*LGFFYGYVK NIVNILLHAL*FCLSHFGFIPLGTIFNI*Y EVIFLLL*G*SVVPALFIEKKQKQKTFLL LL*SAFSVVYWQYMQRSFMGSLLYWFF SCANVHSLHYFMIFKKIFDI*YQSPFTSLL FINSLWFLVLCSSLYILEIAYHVSLKKA HIENLIGVAMNL |
| 7238 | 15289 | A | 7907 | 178 | 565 | KGGATCPESPQDRKRRGNLDMEKLYSE NEGMASNHGKMENE*QPQDQRKPQVTL YSGRQEVKRKRGKDRKQGNRR*GNV*R IKGKPESEGEAKEGKSERESESEMEGGS EREGKPEIEGKPESEGEPE |
| 7239 | 15290 | A | 7908 | 3 | 413 | VTGVLVYLAVERLISGDYEIDGGTMLST SGCAEAENIMG*TLHQSGHGHSHGTTN Q*EENPSVRAVFIHVIGDFMQSMGVLVA AYILYFKPEYKYVDPICTFVFSILRLGTTL TILRDVILVLMEGTPQGVYFTAV |
| 7240 | 15291 | A | 7909 | 119 | 427 | LESLSHKRSSPRHIVIRLSKAKTKKSVLR AVRQKYQITYKRTPISLSDCSAQTLQA RRDLGPTFCLLKNNNQIILYPVK*SFIN EGKIVFFREISPERIC |
| 7241 | 15292 | B | 791 | 72 | 524 | LPAPPGRIKRADLATRPSKVIRVRRGGRK RPVPGATLRKPVHGHVNLKQFARSLQS VAERAGRHCALRVLNSYVWGEDSTY QWITKPVHKhREMRGLTSAGRKSRLG KGHKFHHTIGCLAGQLGEGAILSSSTVTA NISKVCKIHT* |
| 7242 | 15293 | A | 7910 | 13 | 235 | DLINKISKAAGYKINTEKSVAFLYTNSNQ TEKEIKKAIPFTITTKNKTLYGINLTKEV *ELYQENFETLMKGI |
| 7243 | 15294 | A | 7911 | 39 | 141 | LSIRGLNIIKRQRL*DWIKQDSTLCCP* EIH |
| 7244 | 15295 | A | 7912 | 1 | 285 | QQRPPGLRPPHPRGQDQLWLKGKGGW AAQL*EGPSGGSRRGRVERERGRRRKGR KGRA*RGTRKAGGEGRRRETALASPLRG HRSPQERPRPTL |
| 7245 | 15296 | A | 7913 | 1 | 452 | TAKTTFRNAHSHKLS*NVCKPVEETQR PPTLQEIQQKIDSYNTREKNCLGMKLRE DGTYTGFIVHLKLRRPGTVPAIRPQSI YDAIKEANLAVTTDKRTSFYPLDAIKQ LHISSTTTVSEGIQGLVKKFNGVDNPQKV ALFKRIHK |
| 7246 | 15297 | A | 7914 | 1 | 484 | NVLCGNNQISDLGILLPEVCMAPEEKGD KDDQLNKETEDYLSLFEGLKVTEDSL SYEDNQDDSDLLQDLSPEEASYSLQEN LPSEDESLSLDDLAKRIEIAEVVPTGLV SILKKRNDTVGDHPAQMQHKPSKRRVR FQEIDDSLDQESLGFGDGAL |

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| 7247 | 15298 | A | 7915 | 2 | 1121 | HYATDRFPFERVRILLYTYSYVPSFPS YTKCCFEFLTTFSSSLESKTCLGTESSKE SQHTVEPLGSSPCCHQMDVQTDSPSLSV TAGKDHMEELLCSAEATLALHTQSSSETA GSPSGPDSSDACCDDSRQLAQTEACQ DVARIEGIAEDPKVFLSSKSKTEPLISPGC DRIPPALISEGKYSQAQRKELRLPLRDAS EALPTDQLENNELNELQQPDLTDSGKS PQAQADSNSENVLCGNQISDLGILLPE VCMAPEEKGDKDDQLNKETEDYLNSSL KGCLKDTEDSLSYEDNQDDSDLLQDLS PEEASYSLENLPSDESCLSLDDLAKRIEI AEVNQR*STIKSKMAFKKHIVLNLIALFL |
| 7248 | 15299 | A | 7916 | 2 | 390 | SDSRETRVVNLKDSVFLYCKLFGGK NQVKNENGCKDWQHLSHLSKHEESEM HINNSVKYSLKSDLKKNKAIDAAERRL YENEEK*WCAVVVHVLYLSCFLGMMIR NLTLRLKTSVLAIVSTIVL |
| 7249 | 15300 | A | 7917 | 1 | 240 | KRGEKAPETSKTTSTWRIPCRKRRLSNR DFPDLSTGEELPETCGSCLRRSGREN*D AETWPAQCPECESKAAVSTRFLF |
| 7250 | 15301 | A | 7918 | 3 | 420 | EPLSSPLFCP*NQSKIHPPIFLAPTWPHP HHFPPGPGQPPFLSTGSHLVL*QKPKGA HEHLSGIPPSLAQNPTWVPPHPGKRSSPH SATRPCKICPRLLAPSTLLTPSNLTGP*PL LPGALPGLLGPENFCTGCFL |
| 7251 | 15302 | A | 7919 | 2 | 127 | RFWDYGRIALVS*ADSESRFQRLSSTSSS GQQDFENELVGI |
| 7252 | 15303 | C | 792 | 56 | 289 | MNFTNFTYISGSGGAGEYCAFSKLPGES HRIVWWNLWPFPRPRLSACRCQPQRH LPCALWELVLVNPTGCSRISSE* |
| 7253 | 15304 | A | 7920 | 1 | 346 | DSRSPSPASPPTQ*CRPSSFPGPAPPRLW LAPPFPPPPPHGYGPPFARKRRGAALGL TRVLPPPGSAVRRSPGPGGSAWDKTLK MKQKKFGRSVGLWRELIRDCSLAELLSA |
| 7254 | 15305 | A | 7921 | 184 | 291 | |
| 7255 | 15306 | A | 7922 | 481 | 716 | VFFFFFFETECRSIAQAGV*CSLRLPPPGSS DSRASVSRVAGIVGACHHAQLIFVFFVA MGFHHVGEAGLEHLTSSDLP |
| 7256 | 15307 | A | 7923 | 4 | 423 | VARERRLPGPQEGPHGRAAGSASPLAPSI APSPPGPPALPASHILGSQALPSPETPW*S PWDPPAPLALVSPWQFPFGPPAPATP*RS PLGLQTPQAPGSWAPPVPATPQASGLPA PHVPETPWASS*LALPVPETPWDL |
| 7257 | 15308 | A | 7924 | 3 | 436 | GYLSEVVEENTPPKMEKEGLEIMIGKKK GIQGHYNscyLDSTLFLCLFAFSSVLDTVL LRPKEKNDVEYYSETQELLRTEIVNPLRI YGYVCATKIMKLRLKILEKVEAASGFTSE EKD/PAGQKVQDCYFYQIFMEKNEKVG VPTIQ |
| 7258 | 15309 | A | 7925 | 3 | 187 | VLAGLELEDECAGCTDGTFRGTRYFTCA LKKALFVKLKSCRPSRPFALLOPVSNQIE RCNSLAFGGYLSEVVEENTPPKMEKEGL EIMIGKKKGIQGHYNscyLDSTLFLCLFAF SSVLDTVLLRPKEKNDVEYYSETQELLR TEIVNPLRIN*YCSRFPRLSAVTL |
| 7259 | 15310 | A | 7926 | 4 | 343 | KLEN*KMVLKEIKEDLNKQTDILFS*LQR LITVRMSILPKLIYKFSAPAIQIPA*FL*IKIII KCMRKKG*TRIAETASSSSSPSQSFILSPK LDHRGGITANCTPPWAIK GKLL |
| 7260 | 15311 | A | 7927 | 1 | 531 | FYHADHAALKDEMTEY*VFLQIKRYLY HGRLLCKHPDAALLAAYIIQAEIGNHDS G*HPEGYSSKFQFFPKHSEKLERKIAEIH KTELSGQTPATSELNFLRKAQTLETYGV DPHPCKDVSGNAFLAFTPFQFVVLQGN KRVFHFIKWNEVTKLFEGKTFYLYVSQK KKGIGSCP |

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| 7261 | 15312 | A | 7928 | 115 | 348 | KSCLNIFGLKQTTSSLRWNRVKK*AHTY G*QLIFNKGAKIIHWIKYNPANGICYWISI CKKVNLDPYLIPYTHIQNGS |
| 7262 | 15313 | A | 7929 | 4 | 430 | AWLSALNSSLPATWSCCPSLGASHKLQ WEATSPTVPPRAPSQVKCAACEPTPTLP CLPFQPPPSLSSQAQVLLTGHGP*GPLR RQGEGLLRSGCQARLTQPNSEGGAV S*TGRPGDGAUGEAPETTRDCTAPP AS |
| 7263 | 15314 | A | 793 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFGNLSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGT AQLSELHCDKLHVDPENFKLLGNVLT LAHFGKEFTPEVQASWQKMTGVASA LSSRYH |
| 7264 | 15315 | A | 7930 | 1 | 380 | GTRLLVRYTPKEPVWPTFVEVFGDLG QVGPE*C*HPEAKRMPCAQDYLSVVLN QLCVLYEKTPLSDRDTKCTESLVNRRP CFSALEGDEAYDPQELNAETLTFHADICT LSEKERQIYKQTVL |
| 7265 | 15316 | A | 7931 | 2 | 388 | NVQKSLAFLYTNNQSVESQIRNAIPFPA TKRIKYLGIPTREVKGLYNENYKTLLE FREDPNKWKNFPCSWVGRINIIMAMLS KAM*RFPRVHIKIPGTFTLGKPIKFIW NQKRAQIPRATRA |
| 7266 | 15317 | A | 7932 | 72 | 373 | TSTLKKLEEKQTQSRKEIKIPAEINAIEN KQIEKISKTKSCSF*KIKITNP*LKQ*TKE KI*INNIKNRGQVTMAFVAIKRISREYC Q*LYTNKFNI |
| 7267 | 15318 | A | 7933 | 2 | 259 | KQWKPAAPGPANPLPRGTSGPE*KGPHS DKAKPFPSPFFKKRQWGGAPSRSKARG KGQPPKGGHLKGPLRVVNGV*RAPLNR TAA |
| 7268 | 15319 | A | 7934 | 3 | 335 | QIKPPRLRDTPHSFTPYHPVRRGLVYFPS APSPAKGEQLHTRTRHNVLGSHPRRLP RSS*SSHRVTRGSLGSVPPARSTSYGPSR QWDLACPLTPEGVWRTKNKPEAL |
| 7269 | 15320 | A | 7935 | 37 | 281 | GPSPYTDPTPTYP*LTLLTNPRTNSTLPP TLHLPSRPTSPSPSTSLPSSLVLRFFLKIQ SGKRRAYPEHFWGQNGERKV |
| 7270 | 15321 | A | 7936 | 13 | 234 | DLINKISKAAGYKINTEKSVAFLYTNSNQ TEKEIKKAIPFTITTKNKTLYGINLTKEV *ELYQENFETLMKGI |
| 7271 | 15322 | A | 7937 | 3 | 426 | VLEELPISVLFNSSVPAWQWLAHVYHS HGMMAAQMCYIKTLQLASQRRSWSWA KLSSLWRLALLALKGCMANISNDYWPS LVQEATTEALKLCFCPLAVLLALLQFK RKMVST*TLCLLERVVYHPGPSKFIGSN WPAV |
| 7272 | 15323 | A | 7938 | 132 | 393 | ETNSLFGPVKQKQNDLG*LNPPPRGFK KFSGTLRLRRSGNYRPSPPRVFGF*GKRGL NWWAKGGLDLS*NNPPWPSSQGARIM GES |
| 7273 | 15324 | C | 7939 | 170 | 394 | |
| 7274 | 15325 | A | 794 | 38 | 604 | APSPDAMGHFTEEDKATITSLWCKVNV EDAGGETLGRLLVVYPWTQRFFDSFGN LSSASAIMGNPKVKAHGKKVLTSLGD AIKHLDDLKGTFAQA*SELHCDKAAM WIPENFKLLGNVLTFRFGQSHFRQKNF TPEGCKASWAERWVTCSWPVALFLQDT TEAQLPMNAELFKDKAFILASNYK |
| 7275 | 15326 | A | 7940 | 107 | 379 | PPFVAQLGGKGGNLG*LNPPPRG*ROFSS LGPPISGNYGPPPSRVIFGLRKKGVSPS GPGGFGIPDLKIGPFNPPKGLG*RGGPWG PNQ |

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| 7276 | 15327 | A | 7941 | 83 | 409 | PEISGFFFDHHGKLETPKRNFGNYPNT WKLNTLLNDQGVIEGSSSSLKWLKTN EKGNPYQSL*DTAKAVLKGNLTAISAYI KNREKLQNKQCIFNYPEKQEQM |
| 7277 | 15328 | A | 7942 | 15 | 334 | QHFWENFHVTKDRINTGERQETDWKIFA TYLMKKV*ISRKCYNYSYKLVKKQLNR KWAKEKNKQSQKKKQSQ*TKTVQPQ* NKRNAD*RYLSPISLAKSNKLN |
| 7278 | 15329 | A | 7943 | 1 | 400 | ESRLICQQMYMGEKPFPGSCCEKAFSNK SYLLVHQQTAAEEKPYGCNECGKDFSSK SYLVHQRHITGEKLHECSECRKTFSFHS QLVIHQRIHTGENPYECCECGKVFSRIDQ LVSHQKTHS*QKPYVCNEW |
| 7279 | 15330 | A | 7944 | 46 | 364 | SHLPNSSFEQKYAYEFVPGYQKHYSLSK FPWFFFAEMEKLILKFKWKS*SHITEAIL RRKNKVGDLTSDVKSSL*RYDNQLLSV *Y*YKHRRIGPWDHGRPDHIL |
| 7280 | 15331 | A | 7945 | 3 | 312 | VPCSQLNKAITSTTRCLRGFVCSSSCYR RRARERGMEKQTRERERQR*RRERQR GEERQGGKREPHSRARGGGGSRERER VREL*SDSDRSLEREALLR |
| 7281 | 15332 | A | 7946 | 225 | 720 | GLAHSVVRHSSFWGHLQDSGPLVPPGA GQGSGLLLAAEWVGKASPWGPAPACPT PHSEALVCSFRTSPPTPHAHGPGVSGPA SVLAALRLGLHLLRGCGGTPTSPQTLQ DEEAN*GHRGHGDRLLRLTQAPTAQPL WHRPWQKDWPNNLLPRLSFWCRPPRP |
| 7282 | 15333 | A | 7947 | 43 | 418 | AYWGRKTPWLTISFVWPTPGSPYDNGR PLCYSDSDAVLLCFDISRPETGDSALKKV RLDQLSNL*LSMRKKESGPCHECLLLTS RNGSQGRKRFAQGHTISYSSGTGTWVSL PHCLPPFLLSH |
| 7283 | 15334 | A | 7948 | 2 | 221 | AGPGGSPHGYVGSPLRISTRHLCAATR SLLHIDPLIVLPLVDLKDRIII*NLWGLQP LPPASLLQPTALYS |
| 7284 | 15335 | A | 7949 | 1 | 409 | SPGTCGRRPQTM/PPGAPDFPAVEGRSLG LSPSQGGPAGAGGDAGPQEDVRQPPGEL AHGPLLPAQTG/SPGPQGLWLHRNPTS/G PPSQIGEGAEQGDGADAPQIQCKNVL KIRRRKMNNHHKYRKLVKKTRFLRRKV |
| 7285 | 15336 | A | 795 | 23 | 153 | |
| 7286 | 15337 | A | 7950 | 2 | 361 | YSTSPAGQVGRGPSQGGPAGAGGDAGP QEDVRQPPG/EAGSRPAASCPDWIPG/AA GHVAPPQSYQCPSQIGEGPGGTPEQA DQVRERPEAHLAEGGAKGSPRRAGRPPR STCGANESG |
| 7287 | 15338 | A | 7951 | 337 | 1067 | NLKAHPRRPFNPPLASGPFPLILAGADTW *GIGGWKPTSSLRVPGIQSGAGSERGREP SSPGG*RTSSWGPASPAPAGPPCEGERP RLPGPAGDVL*RETADPAAQHSMRQAK AGGRLPKERPSTAGKSGAPGAWSVGGG HRSQGSSTRLLKTLVLRPPSGTSGPSRP RSAAATRRFLRTAPAGVLAAPDSALAQA PPGPKGDGFRGCGPWYYPQVQNRFTTQ GPDSQRADGSAGSRLRK |
| 7288 | 15339 | A | 7952 | 127 | 440 | SLRYTFLYTFPILEHIIVLMQQTCLHGF SIYLLIHTFILQIHPFHTLFQQTCSIIQLY FLV*YFAYVYTFILYLSYFPLYYY*AC FETFDSFNEIGRV |
| 7289 | 15340 | A | 7953 | 2 | 341 | |
| 7290 | 15341 | A | 7954 | 288 | 802 | GVIMATSELSCEVSEENCERREAFWAEW KDLTLSTR/AEREGCSLHEEDTQRHETYH HQGGQGVLAQRSPWLMRMGILGRGL QEYQLPYQRVLPPIFTPAKMGATNEER EDTPIQLQELLALETALGGQVRDRQEVA EITKQLPPVVPVSKPGALRRSLSRMSQE AQRG |

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| 7291 | 15342 | A | 7955 | 72 | 488 | HEAGSRMNGDHNSDVFSQD*QDFVQHF CQIGRVLTEDEMGHPEIGDAIARLKEVLE YNAIGGKYNRGLTVVVAFRELVPRKQ DADSLQRAWTVGWCVE/ADDIMDSLT RRGQICWYQKPGVGLDAINDANLEACI YR |
| 7292 | 15343 | A | 7956 | 1 | 236 | GTRVVAFRELVPRKQDADSLQRAWTV GWCVELVRGVGQRRSFLQWW*LGWE GEGWA*NFLGCVCVSLSLVCYQGI |
| 7293 | 15344 | A | 7957 | 317 | 1395 | TGDQNSDVYAQEKQDFVQHFQSVIRVL TEDEMGHPEIGDAIARLKEVLEYNALIG KYNRGLTVVVAFRELVPRKQDADSL PAGPWTVGWCVELLQAFVLVADDIMD SSLTPGNRSCWYQKPGVGLDAINDGN LLAEACIYRLKLKLCREQPYLNLIELFL QSSVYQTEIGQTLDLLTAPP/QGNVDLSEF TEKRYKSIVKYKTAFYSFYLPAAAMYM AGIDGEKEHANAKKILLEMGEFFQIQDD YLDLFGDPSVTGKIGTDIQDNKCSWL VQCLQRATPEQYQILKENYQKEAEKVA RVKALYEELDPAVFLQYEEDSYSHIMA LIEQYAAPLPPAVFLGLARKIYKRRK |
| 7294 | 15345 | A | 7958 | 3 | 484 | ETPVPATSAAIRILVLLPSLRVTSPGRQGP SVDRVVFPPFKFRPERSRHAAAGPNVVR PQPKPHEVGGERGRPNAPANSFRSCSN LSPQYSLPKQNKSSNP*IPNKPTPPASPS GRTDGLSLLQPLPGSDGQASPTMRSSPAI SSALEIEFGKTNPFH |
| 7295 | 15346 | A | 7959 | 3 | 432 | SGSSRPRGSAQPRPGPGACGMAAPTSE*S SPPAWQPRPPCGGLHHCPACVHPRDSDG GSPAPAAACCHTPHGRPWPEFEGQRPQT QPQPQGPWVRPVLTLFAGRVASVPLVS LCAWASGSQPGPPSGSGRALCTGLGAP PA |
| 7296 | 15347 | A | 796 | 84 | 358 | APRADAMGHFTEEDKATITSLWGKANV EDAGGEALGRLLVVPWTQRFDSF/GQ LSELHCDKLHVDPENFKLLGNVLVTRFA IHRKEFTPE |
| 7297 | 15348 | A | 7960 | 2 | 331 | VCKLQQLPAHSGSPNIHISQLCPSHAW GLLVSSGCVTLRESFFLCFALVLQRKS SSLGILSCPGSIFTALNSTNLYLGLGGF CLVFF*DRVSLCHPGWSEVVQS |
| 7298 | 15349 | A | 7961 | 25 | 364 | LFYLYHLLFFGFLFLFLIKLGSSLFINFS KKSVL*FTNWIYFSVLVYTFDFCFIHSFFG FSLIYFIIHVGFLKFIGFILSFI*ITVFIGQA QWLTPIVILWVAEVRGSL |
| 7299 | 15350 | A | 7962 | 174 | 469 | NGPP*RKKFSLIPRKIWAPPGFF*/EGPPL FFFFFFLTESCSVA*PGMRWHNPGLLQPL PSGFKQFCSLSLSSWDYRCPLPHPANFF VVVFLVETFC |
| 7300 | 15351 | A | 7963 | 65 | 2774 | |
| 7301 | 15352 | A | 7964 | 243 | 687 | PHPIPHSEENFEFLIVSSTGQTWHEAASF EERDAWVQAIESQILASLQCESSKVKV RV*GGVEDWPQELTLVLTAGNDTAEVV *EESRGV*EGGAWRQSQCPQPSLQLR TDSQSEAVAIQAIRNAKGNISCAHASAD AWVEA |
| 7302 | 15353 | A | 7965 | 3 | 368 | PSDPEVAGDPIFPFGPPSCPEVKDKTKSSI SLGWKPPAKDGGSPIKGYIV*MQEEGTT DWKRVNOPYKLITTWECGPNLKLRLK YRFRVKA VNEAGESEPRDTTGEIPATDIQ EEPEVFID |
| 7303 | 15354 | A | 7966 | 3 | 78 | FKIQNLIASVTRVMVADCSRFDSPDLLL EAGDPATSPCRIFDLGSDNEEVVAIPDPS HPKEGLSYSLSCVLLGRSLPRCLISCIYPL CLSVASGPHKFY*PHCQHRPHGDGGRLO PLRQP |

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| 7304 | 15355 | A | 7967 | 195 | 345 | NDISANPAIKKFWKLPKCPTTEGWLNT* LYIHLVEYYATLKVCGDLYVR |
| 7305 | 15356 | A | 7968 | 2 | 801 | WRNSADVWYCGGPLLDTLPSNWSGT CTLVQFAIPFALAFLQPEKEKPOHRKIRE APYGSFDSQVYLDATGVPQGVPHKFA QDQIAAGFESIFWWVTISKIDWINIYY NQORFINYTRDAVKGIAEQLGPTSQMA WENRMALDMILAKKGGVCVMIKTQCCT FIPNNTAPSGSITRALQGLTALSNELAKN SGVNDPFSGWLERWFGKWKGHASILTSL AARIGVVILFGC*VTPCIRGLVQRLIETVL TKTSLSSPPPYSD |
| 7306 | 15357 | A | 7969 | 113 | 362 | WLHAPECFSQCPSQSPS*LCQCPESDP DPRSVVGPPLSQAGSPGRPGGTVITLCLL WPHLAPLFLHWSPGKCTSLLVVQHS |
| 7307 | 15358 | A | 797 | 1 | 428 | |
| 7308 | 15359 | A | 7970 | 1 | 955 | MTQPFNYSAFERIIFAGSPGHTVFSSERSL LVRPRSHPEPKGEHYVTGSPTPENQRTS AAMSKPHSEAGTAFIQTQQLHAAMADT FLEHMCRLDIDSP/RRPLPATPQKPPW VPWRPPSSAAVGP*SSSPSLADVKSQVL VTCCLACHCHWQREEWVLVTLGQGCLS VSEFRV |
| 7309 | 15360 | A | 7971 | 113 | 716 | RSLGQCQHSWQSSPGGPRPQPRPPGLGP CTAQGRCHGTGGPDE/TVWGFRVTAMM GARGRYL/AHLVSRLEMWGSYIRVHFT RPQEVPSGRSNSSPSHPAQ*GLWPLQHLL RRTPPEARAAHPISPISAC*VTICPLPPFH RPRDQDHLAPARSASPTVP/QPMVGRTP PTP*TLTQRGSPGPMSPAPIPLAANDSDK PSST |
| 7310 | 15361 | A | 7972 | 244 | 1510 | KFPKKTPPHLGMESAITLWQFLQLLL DQKHEHLICWTSNDGEFKLLKAEVAKL WGLRKNKTNMNYDKLSRALRYYYDKN IHKKVIGQKFVYKFVSFEILKMDPHAVEI SRESLLLQSDCKVSPEGREAHKHGLAV LRSTSRNEYIHSGLYSSFTINSLENPPDAF KAIKREKLEPPEDSPPVEEVRTVIRFVT NKTDKHVTRPVVSLPSTSEAAAASFLA SSVSAKISSMLPNAASISSASPFSSRSPSL SPKSPLPSEHRSLEAACHDSDSLPLELN LSSGSKTKSPSLPPKAKKPKGLEISAPPL VLSGTDIGSIALNSPALPSGSLTPAFFTAQ TPNGLLLTPSPLASSIHFWGSL*SKFVP LSPARLQGPSTLFQFPTLLNGHMPVPIPS LDRAASPVLLSSNSQKS |
| 7311 | 15362 | A | 7973 | 1 | 1230 | |
| 7312 | 15363 | A | 7974 | 3 | 358 | LPAPGARPEWLLFPAPVVGVLWCWTPQS IISLHFFLNVPVQTLSSSSSSSSP*RT*LP MTLS*VGAVSGFKPISRPPPEPHSGHNSPS LSQPSLTILVSSNSPGSGKARGPQCQAW L |
| 7313 | 15364 | A | 7975 | 194 | 372 | LFG*LKAPPPGLKQFSGLSLRRSGNYGPP PPPPVYFFVFLKKNGFPLVTQGLNLRT WG |
| 7314 | 15365 | C | 7976 | 238 | 459 | |
| 7315 | 15366 | A | 7977 | 1 | 505 | AGGAGEETPHQESQRQGCALPQEPPLYP PCPAIHPPPLPLGGLLLFPSLPSLALSCMV PPPWAAQEGI*MENHQPPPEKKRLWGPPP ANSPPPARPLNPHLFQAGTGCPCPREV TPSPWAEPPPLPGPPSEIAHLTTVRRGA ALANVNHENISDTEENKLNAFVTA |
| 7316 | 15367 | A | 7978 | 39 | 141 | LSIRGLNIIKRQRL*DWKQQDSTLCCP* EIH |

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| 7317 | 15368 | A | 7979 | 8 | 532 | FNYLLKFKIRPPHAFQMFPMSSQGKEG PETAESLSHHGCLSL*R*EISWAPPTCG AFPSSAATLGASPVLGASVPLGAAGMQR GRRGHRIPGDTWGLLLPGAGGTDAESPA HNWEP*TSVPPSRPGHSPGPSAGLQSGRP PL*GDCEWGRKAGKGHAY*VGPPELHT LPLSDP |
| 7318 | 15369 | A | 798 | 2 | 476 | VNVEDAGGETLGRLLVVPWTQRFDFS FGNLSSASAIMGNPKVKAHGKKVLTSLG D/ASSASAIMGNPKVKAHGKKVLTSLGD AIKHLDDLKGTFAQLSELHCDKLHVDPE NFKLLGNVLVTVLAHFGEFTPEVQAS WQKMAEDVTGVASALSSRYH |
| 7319 | 15370 | A | 7980 | 1 | 9786 | |
| 7320 | 15371 | A | 7981 | 27 | 13822 | VPFSVAAAEEPAQPARAARPRGRSPGA APPQLAMDPPRPALLALLPALLLLLL AGARAEEMLENSLVCPKDATTRFKHL RKYTYNYEAESSGVPGTADSRSATRIN CKVELEVQLCFSILKTSQCILKEVYGFN PEGKALLKKTKNSEEFAAAMSRYELKLA IPEGKQVFLYPEKDEPTYILNKRGIISALL VPPETEEAKQVLFDDTVYGNCSHTFTVK TRKGNVATEISTERDLGQCDRFPKIRTG |
| 7321 | 15372 | A | 7982 | 40 | 400 | ELFGHIALQTIAYSILWDLKFLMRNLALG GGLLLLLAESRSEKSMFAGLMMFTLL HFDASFFSIVQNIIVGTALMILVAIGFKTK LAALTLVVWLFAINVYFNAFWTIPVYKP MHDFLKY |
| 7322 | 15373 | A | 7983 | 1 | 900 | FRAAGAGADGREPASERASRAEPPAVA MGQNDLMGMAEDFADQFLRVTKQYLP HVARLCLISTFLEDGIRMWFWQWSEQRDY IDTTWNCGYLLASSFVFLNLLGQLTGCV LVLSRNFVQYACFGLFGIIFYTIAYSIL WDLKFLMRNLALGGGLLLLLAESRSEG KSMFAGVPTMRESSPKQYMQLGGRVLL VLMFMTLLHFDASFLFLVQNIIVGTAL MILVAIGFKTKLAALTLVVWLFAINVY FNAFWTIPVYKPMHDFLKYDFVQTMVS IGGLLLVVALGPGGVSMDEKKKEW |
| 7323 | 15374 | A | 7984 | 2 | 397 | GRVGRPTRPPTRPPTRPTRSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS PFFGVSPCVPEILKSSSPRIGCPRN*AFPFK RGNL |
| 7324 | 15375 | A | 7985 | 5 | 230 | IGNFKNVFSIVNITTRQNTSTDIENLKNN HV*NTVSNS*YTVFSSACGFTTKISHLLR H*TSLDKF*KLDVLWS |
| 7325 | 15376 | A | 7986 | 1 | 366 | NPSIVGGQDLCKGNYKTQIKDLLADGSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS KTPTSFLIELGKTIVQFL*NQKRV*ITKVIL SKKPQKTENKTKLEAFHSTLCYLP SNYA TRL |
| 7326 | 15377 | A | 7987 | 3 | 361 | ISKKKFFLKGFFFLGFF*KKPPFFFPFPPPP G*RGKKKIFFFFWVKKNPLEKNFFSLFLK KGGPPTPPGGFFFKKKRAPQGGGPPKI FFFFFFFFFFFFFFFFFGDGVLLCCPGWSAV |
| 7327 | 15378 | A | 7988 | 2 | 359 | GLPS*HYSPPQLPH*SHSHTIAPKAEEKA NRKETHFSRSPQQISGRCPQDKSLAKV DFLDQLRPMVGHSLGRGPHLPKHMPT PEQIQEEPEAHHLPLVCEQLPLLPWEDF VYGSSR |
| 7328 | 15379 | A | 7989 | 490 | 583 | NH*SPMFGYCICVCFETESCSVAQAGVQ WYNRGSLLQPPPLPGPKGFVCLSLPSSWDY RRRPP |
| 7329 | 15380 | A | 799 | 23 | 349 | |
| 7330 | 15381 | A | 7990 | 1 | 129 | QPGPEGKIRFFLKIPNLTPSGGKSLKFPLF KRVKPENCLSLRG*GCN*PGPEGKIRFFL KIPNLTPSGGKSLKFPLFKRVKPENCLSL |

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| 7331 | 15382 | C | 7991 | 96 | 380 | |
| 7332 | 15383 | A | 7992 | 202 | 499 | ILGFVQWHDHSSPQPKTPGLKQSSCLNF LSS*DNRHMPPLANFFIFVEMGSCYVA QACLELLGSSNPLASVSQNAIGTSMSC TQLFLLLLNRFPAL |
| 7333 | 15384 | A | 7993 | 1 | 206 | NSSVFLHLQALGIPLHLAYVSVFPPTPG* GSGHGRSLLSISVGQGLPPQRPSPAPFH LDIIHQGPAPW |
| 7334 | 15385 | A | 7994 | 2 | 349 | TCHRRKRRNPRHGEVGLGYPTDESAPF SAPALGPGEPRVPGSSSGRASGH*WYPN AVESP*EEGEL*GRRGETLVAEKKKKPR HGEVGPSPMEKKCLPISP*AGPRGPRRP WF |
| 7335 | 15386 | A | 7995 | 269 | 364 | GHLAIGHPPF*MSFNHGRKTRTWNYLG SEEQ |
| 7336 | 15387 | A | 7996 | 1 | 314 | PSRSFISNH*PHQDV*PRFFNGIHL*YSHT PGINHVEPEPNSTRSKACWEGFGSSNSG NGSFLGAR*VDVQEVLTITWRVIRVWN* CFGRNSAPMAQSKSSSES |
| 7337 | 15388 | A | 7997 | 65 | 354 | YFYIYFSIYHFIAPPYFSLVFLHLCVPL SSFLSR*KIHVCLKDFKNFS*TIPKLSKL LELLESISLFFL*NVDFIILEIPLYSAILK RVYF |
| 7338 | 15389 | A | 7998 | 1 | 957 | |
| 7339 | 15390 | A | 7999 | 97 | 4146 | |
| 7340 | 15391 | A | 8 | 190 | 383 | TRMIHITSVYSHPHQAQLRGCEVLRHKA HLVLP/AWSTSCSGIPRGQQTAAQQGYR CFLAWSLEA |
| 7341 | 15392 | A | 80 | 44 | 377 | TFFLYLENLNTAVRFWKLPYIHCCKNPG GAGLICIAFWLTKAFVFGSDYSLVTVR VK*VFKPFLKDVEIRR/FTWTIRQPDVA FLRVPDYHALIKQPMLETD*MRLANS |
| 7342 | 15393 | A | 800 | 17 | 535 | APSPDAMGHFTEEDKATITSLWGKVNVE DAGGETLGRLLVVPWTQRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDATK HLDDLKGTFAQLSELHCUKHLDDLKGT AQLSELHCDKLHVDPENFKLLGNVLTV LAHFHGKEFTPEVQASWQKMTGVAS LSSRYH |
| 7343 | 15394 | A | 8000 | 97 | 2728 | |
| 7344 | 15395 | A | 8001 | 1 | 2295 | |
| 7345 | 15396 | A | 8002 | 97 | 4027 | EKEPYEEISAEADREPQQLQNYWSEVRY TVRCIYRQAGTPLADDQDQSLVPDKEGV KELVDRLCERDPYQLYQRLEQQAREYV LEMKVRLRLQLSAAAKVKAPSGLQGGP QAHQFISLLLEEYGALCQAARSISTFLGT LENEHLKKFQVTWELHNKHLFENLVFSE PLLQSNLPALVSQIRLGTTHDTCSEDY STLLQRYQRSEELRRVAEEWLECKRI DAYVDEQMTMKTQKQMLTEDWELFKQ RRFIE |
| 7346 | 15397 | A | 8003 | 1 | 450 | GVPYKRHIEGF*PGLNGPLKFNGPSSSS SDGLRLRFSGSGGQSPNWVPLGSYQGR SRPVPPGGSSAEPFPPSPASGGTHVPQLR ALPPLHGHSAAPHLSLALTVPVPPVVRT L*GHWGPGPPTLDAPPSPSHLQVPLSSQG GIPPHWT |
| 7347 | 15398 | A | 8004 | 16 | 303 | GENPLMRWPEALPGVFKTCFSPPT*GYG GGLMFLCHHADSINFSAFQPINNADFV IEIEGTTQVSCQPDHTQPRGWGVCLLP HLYWGPPPIG |

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| 7348 | 15399 | A | 8005 | 146 | 808 | RIFSLCSAALSCKHGNPQDCSRRAPGNV PAAISRAPSLVLGLRARTVTRKGGLRPR KGEQGPSPSPDPAVKGPGAEPGQARFAP VYQILIGAPRWEPLLSTGGYTVSGSSPVV EVGTRANQPRQ*ALPASHLPPLASRSSSS SHLYTAAPPLVSRGSGGSAGRALDSSFP QHSLAKPRPSAGLEAPGHWGRTGGDRR RKGTGGEPTFAEVEALPASARP |
| 7349 | 15400 | A | 8006 | 111 | 369 | FGPGPPL*SPLF*GSSSSHSGVGK*NPSFL PGGTPVFFKNPKFPPPWGPPVSPPLFWG GETGNWGNPGGOTLEGPGYPLALPGG K |
| 7350 | 15401 | A | 8007 | 85 | 394 | DWRRRRRDRSS*REDCQSTIYVRKRAK SNCWCWSKEKSKSHERDSIPRIEKEKMR SRSKGRDHENVKEKEKQSDSIGNDQEGS RSREKSNQFDSKSNERDH |
| 7351 | 15402 | A | 8008 | 2 | 2255 | |
| 7352 | 15403 | A | 8009 | 1 | 1845 | |
| 7353 | 15404 | A | 801 | 17 | 533 | |
| 7354 | 15405 | A | 8010 | 12 | 450 | SEPP*ITSVDPRVRGNASTGYGKIWLDDV SCDGDSEDLWSCRNSGWGNNDCSHSED VGVICSDASDMELRLVGGSSRCAGKVE VNVQGA VGILCANGWGMNIAEVVCRQL ECGSAIRVSREPHFTERTLHILMSNSGCT GGEASLW |
| 7355 | 15406 | A | 8011 | 121 | 342 | QNESVVHMKTF LAVFKLPLKIRQIKCIYI FYN*ELKLYSVILKYFFLYDFRPVCLVLS EIPFMSTWFLLVSTFR |
| 7356 | 15407 | A | 8012 | 3 | 383 | EKGPLSPKVLFNHLCQKAPRFKDFQQD SQELLHYLLDAGRTE*TKRIQASILKAFN NPTTKTADDETRKKVKTYGKEGVKMNF IDRIFIGELTSTVMCEEANISTVKDPFIDI SLPIIEERVSKP |
| 7357 | 15408 | A | 8013 | 18 | 280 | KCRSRN*TA*FHRLNAKALSLTLLNVY QKKHLVEILSYHNCDSQTRNAPELDCLIR LQAQNIQQRHIVFLTGKESTPKLSTMNIG M |
| 7358 | 15409 | A | 8014 | 3 | 271 | FFLRQSHSVTRLECTGAI*AHCNLCPLGS SDSPASAS*VAGITGMCHHARLIFVFLVE TGFHHVQGAVLELL/NLMICPPQPPKVLG LQA |
| 7359 | 15410 | A | 8015 | 609 | 921 | FYLSEEAEEEEFFETES/HLLSPRLECSG MMSAHCNLRPLPGSSDSPASAS*VAGITG GHHPAQLIFVAF/MYQPGFCHVGQAGQQ LLA*VICLPQPPKVLGITGA |
| 7360 | 15411 | A | 8016 | 140 | 346 | FPPICYLLEIGSHSVVQAGVQWHRHSAQ YP*IHEHKQSSCVSLMSS*HYSHVPPSPG NILL*RRGSCV |
| 7361 | 15412 | A | 8017 | 2 | 348 | AGVPPGNPPLWGEGGGSPRGGLKPG FPQRGNPFFFKKSQTPPGGGPPLIPPPW GGGAGGSPLPQGQRFQ*TKIGPFPSPRGK KKKPPFPKKKKKKKKRKEKSEMPGFMV LNA |
| 7362 | 15413 | C | 8018 | 282 | 497 | |
| 7363 | 15414 | C | 8019 | 267 | 473 | |
| 7364 | 15415 | A | 802 | 160 | 434 | LISVIPALWEAKAEDHMRSGVQDQPGQR GKTPSLRKIHRLARHGGMHL*SQLLGRL KHKNRLNPGGKSCSEPRSHHCSSAWAT DQDSVSKK |
| 7365 | 15416 | C | 8020 | 435 | 821 | MKSRVIGWASGLKNEIFFFFWDRDR YRAMLPRLVLNLLFLIEPPVSILVKHWD YRHEPPPRXRLPFCMMRLEGPHCFRDF ATYKKQSVRTVAGLFSCLIKFSAHTNLD QRIWDLNPISGYFPN* |

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| 7366 | 15417 | A | 8021 | 121 | 818 | HSKGSQVQSPGPEPSSAGPKPGAQPQPT WGLAAPEEGREGGKCGRHCRNSKPLSQ PCAGVWSGRGAEEGGAGPDHPARTGP PSSPSCSAGLPDL**GLKPPLEASSMDPGF VLEGGPRVREGVCQDGI*A*ELEEVPSPG GSATSGAATLSDRRGNGASQARLP*PS HWLPRAK*APQG*ASPGSPTACPAHPHS WKGSAGPGMGRGRVVGDRGGAWGT GSHCNTPSS |
| 7367 | 15418 | A | 8022 | 11 | 368 | SFTCCFQMHTKLLCLNLTCLNTFLSTGAFF LIVLTWLSPIAVRLSLNVISERPFLFILSVV DPCAHLIYLSLLFVS*VLPQYVIALFVPH KRM*ETMYACLPVCP*LLTACLEHNCSEF I |
| 7368 | 15419 | A | 8023 | 3247 | 5031 | EGLRGTALLLTGGGRGP*GQPQQ/PGGP ASSPSAAPGPAAAEACSTALWPTVSL RAPSPCPPQAGQGYGSWG/GEPG/NSM ASGGDG/EPLSQGLAPAGTGLARLQGP GHWAVSLWPSLRGFGGPGQTGQSPLSQP HSALTGRGRSPGALGPPPPQRPQRPAP DPARPQR*TPLTAGATTTPQHLPQGNCR CSLLLLFLLLLFLLLLFLLFFLLFLLF LIFLLLLLFLPISLRNRSQWDLGGGEQ HVREAHPPDPVEQPRFVSIVGEVSEVLV GQTQRHSSWEAHLKWGRHGEHLGLEVI GPLPNPRKAWMPHLLQLGPRDAEHRGH ESVVASSEGRVAPVGRPHRAALSRAAAL NEGTTGGARGAAAAGVRVMLRLQRGGG EHGGRQSSQGAVPREGVPRESVLLQLSL WACGVRLSPSRAGSRVQG |
| 7369 | 15420 | A | 8024 | 87 | 567 | KQPPPHGESAAWAATSRPGWWLLCRPA EGRTPGWTAFDVHPTLMQKLEHSGNFS GQSPQCQLEALPRPSTCPLGSSRSGREG PLPPT*ELFPNGQSVRCQVGGPGYDSWC PGPGPAPCPPT*P*GPQALTSAPGPNK HPGLELGRRGPERAPGPF |
| 7370 | 15421 | A | 8025 | 2 | 347 | KALACPPTCCVLGVHHAWSAGGFGPHR PLVRRHIAPAGHQVLSFLHPTLCCHPKS NCTPCGSRRAVPTPTPLPAPGPQAFCPVP GSHWLAWSPRGRSPPTSVAPTQPY*QPP SC |
| 7371 | 15422 | A | 8026 | 3 | 359 | HEGTVQQPQARGLYEDLLMSEGENDED DAGSDDNGDNIFSAIHLSESGRSDA*FG GIRPKQSRMLKENTRMVMDNEERLLFY EGDCGEASHGLEDSCLSYGSYEDDPDK WNTQNTSFC |
| 7372 | 15423 | A | 8027 | 2 | 424 | |
| 7373 | 15424 | A | 8028 | 3 | 456 | PQTQREPTMVLSPADKTNVKAAWGKVG AHAGEYGAEALERMFLSFPTTKNYFFPHF DLSHGSAQVKGHGKKVADALTNAVAH VDDMPNALSALSDLHAHKLRVDVFNFK LLSHCLLVTLAAHLPAEFTPAVHA\SLDK ILASVSTVLTSKYR |
| 7374 | 15425 | A | 8029 | 3 | 198 | RQGSCSVTQPGVQWNNLGLL*P*PPGLK QSSYLSSPSSWDYRCVPTRLANSYFKFI* YVFFCLF |
| 7375 | 15426 | A | 803 | 1223 | 1338 | RWPLWSFIIETKRRTL*SQLLRRLRQENL LNLGGGGCS |
| 7376 | 15427 | A | 8030 | 1 | 346 | LFAQPNPVTFKIRIYCMSKDIDKVRARP PEWEKICANHVNKGLGSRIYKVLLLE* KNIVRLNQKANAQFYAGYKLRCYRKFS NKSIVNE*KVLLFMR*EYIPVSTHFICCVI L |
| 7377 | 15428 | A | 8031 | 60 | 523 | |

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| 7378 | 15429 | B | 8032 | 68 | 679 | MGKEKXHNIVVIGHVDSGKSTTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFKYA WVLDKKAERERGITIDISLWKFETSKY YVTIIDAPGHRDFIKNMITGTSQADCAVL IVAAGVGEFEAGISKNGQTREHALLAYT LGVKQLIVGVNKMDSGTGIAILTGD FPSLE PRHVSTWLQHVVTIPTRNWHKCYCVGV VANFLN* |
| 7379 | 15430 | A | 8033 | 53 | 1497 | KLPLKAKMGKEKTYINLAVIGHVDSGK STTTGHLIYKCGGIDKRTIEKFEKEAAEM GKGSFKYAWVLDKKAERERGITIDISL WKFETSKYYVTIIGAPGHRDFIKNMITG TSQADWCCPELLLLGVGEFEAGISKNGQ TREHALLAYTLGVKQLNAGANKMDSTE PPYSQKRYEEIVKEVSTYIKKIGYNPAT VAFVPISGWNGDNMLEPSANMPWFKG WKVSRKDWQCQLGTTLEALDCILPPT RPTDKLLRLAFQDA*QNGGIGTVPVGR VETGVLPKPGMGVTFAPVNVYNGK*KS VEMHHEAFECKLFPDGKCGAFNVKNV SVKDVRRGNVAGDSKNDPPMEAVAGFT AQVILNHSQQISAGYAPVLDCHTAHIAC KFAELKEKIDRRSGKKLEDGPKFLKSGD AAIVDMVPGKPMCVESFSDYPPLGCFAY RDMRQTVAVGVKAVDKKAAGAGKVT KSAQKAQKAK |
| 7380 | 15431 | A | 8034 | 3 | 309 | RFTGHYRMLSGEPYEWIEWGKRLSSN TALTQHQRHTGENPFECCKEKGAFNQK ITLIQHQRVHTGEKPYEC*ACGKTRFWG GRFILHQNLPTQKTPVQA |
| 7381 | 15432 | A | 8035 | 3 | 366 | RDSVVEILFEQDNKEQSVATLILDSLIQCP IDTRKQLAENLEMMFDVGKTQPPLLKRA FSTEK*KFD*/ITNLASYQIFNQL*ANCTK YVGC FVIEDYSGSESILCLLALIYNSFDF VSLV |
| 7382 | 15433 | C | 8036 | 310 | 546 | MGIMSVPPHPQNVDPYPLDGEKILHILGF NPEIQLWEILFEQDNGRAISWPLLILGFPL YSVPIGHQGRQLGRRNLGRS* |
| 7383 | 15434 | A | 8037 | 97 | 333 | HRIRPICSPOYMEKVYVTKNNNYRILEID MNFFFPPETEGVGGQVLEVMPHEELKPS IFFFF*DRVSLCHPGWSAVVQS |
| 7384 | 15435 | A | 8038 | 250 | 378 | TESLYLNTIKATYEFKTANITLNNEMLKA FSLRLDTR*EHSLS |
| 7385 | 15436 | A | 8039 | 280 | 759 | GYINNGGRKRRTELKPTERSCRAEGGG VEGGPPACPPPTNCLQRLQPHLGSCTEIS GQERE*GYINNGGRKRRTELKPTERSC RAEGGGVEGGPPACPPPTNCLQRLQPHL GSCTEISGQERESGGGEGNSGSPNNRVH GFSKAGHGLGVGEEEEERQLWL*TGRK QRPNIPIRRLPQASLHLPASPCQPAVPG ALSSPRRWQPASHSCSPSPRHKTS |
| 7386 | 15437 | A | 804 | 1057 | 1354 | SQHFGRLWQVNHLSGAPAQPGQQGKT PYLLKIQKLAGRDGARL*SLLRRLRQE NRLNLGGGGCSEPRSCHCTPAWVTKRD SFSKTNKQTENNKKRIL |
| 7387 | 15438 | A | 8040 | 1 | 401 | ILVLDPPPQPKLLSVKGNPEDFIFRQFFF SPYPLFPFPFSSYAKPPVSNETFPFPHRF SKLLSQGPADMPPLPGSLP*LLHYSACM LHHLLFCSLAHCAFRLSCQGCQYLHGL MHMFRSGHMHYAAGR |
| 7388 | 15439 | A | 8041 | 32 | 378 | CVYTFIC*EISGLFPVWG*YRK*GSSSSSS SSSSSSSSSHFNKYSSCMFNFF*NC*TVL QSGCTILLHHWCMRVLSP*COHLAV FFSHAILLSV*LHLTVIFICIPQITS |
| 7389 | 15440 | A | 8042 | 30 | 434 | DGSSLCRPGWSAEQDCVSSGGEKKKKG RDNIEDEACSSRPSR*LFEENIHLVHALIE EDQLANIIDISAGSAYTILDEKLTLSKRFT RWVPKPLPSDQLQTRAFLMEILNGWD |

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| | | | | | | QDPEAFLQRIVTGDET*FYQR |
| 7390 | 15441 | A | 8043 | 3 | 340 | IPKPMAKLPFMKYRDLHTNLLYSRMETG PKHIPMKTLLKIMEDIALGMDNLSLMNY LYLELTARNCMERDDMTDCEADFGLSR KRYSGENYLHCRIANRPV*GSAIESLAHR |
| 7391 | 15442 | A | 8044 | 3 | 378 | LIKKHVDFDLATNVQEEKIAALEDFAHQ LITAGHYAKGDIFSRREVLDRWRRVKT QMIEKRA*V*KSQTLQQFNRDVDENEA WISEKLHTASDDSYKDPNTIQLCKLLSK HOKHQAF*TELPAT |
| 7392 | 15443 | A | 8045 | 169 | 375 | SSSSLPLHITNPNLHQQLPPQLPAYTGA EGDPCALLS*YCLIHLLNTEAVNNITFLG KQPCCKRYDKV |
| 7393 | 15444 | A | 8046 | 27 | 289 | RSPKTHGGRRWGMVRPGTAPT/PCCPH RPQLP/CQPLLPPE*SLLEGRSSSLDSGM EESQTHAAPACRTWCSDGPR*PWMGPA ARCSG |
| 7394 | 15445 | A | 8047 | 3 | 284 | LFLWRRQLTLTENPRWWPTLGDGQARD CSDACCPHRPQLPSSHCSQTKSSPIEVPR PPKHR*GGVCAGPSHLPGGPGSSPSPCP WPGSGLF |
| 7395 | 15446 | A | 8048 | 459 | 1020 | EPPRGAEGQGVPGGKGPETSAAPAPTPA REPERVPGGA/PPAPECACAEVAAPAPA GGSLPAGPRPWERPWAAGAP/QGDKG PGEAATSPA/RGDSGVEPRGGGVPLPRH AGPQARRCEPTLPHDLYSGQVQPEHRAA G/LHPRSSGTI*APCTTCRVA*V*DSSIPE SREELRPSKKRSFRSEKEK |
| 7396 | 15447 | A | 8049 | 3 | 417 | VTCGKAFAQAQLIVHQIHTGKKPYDC GACGKDFREKVHLVRHQRTHTGEKPYD RSERGKAFSHKSDLIHHRVHTGEKPYEC CECGIAFSQKSPLIHCRIHTGERPYECIK CGKAFYHK*QLSIAHRAHTGDIAG |
| 7397 | 15448 | A | 805 | 831 | 1082 | SQHFGRRPRADHLRSGDRDHPAQHGETP SLLKROKLASHGGRHL*S*LLWRLRQEN HLNPGWGGCSELRWHRCTPAWATSKNS F |
| 7398 | 15449 | A | 8050 | 29 | 223 | LIKKLASCGEHLYS*LLKRLRWEN*SSL GV*GCGEL*SQHCTPTWVME*GPAQKH KNKTKKLL |
| 7399 | 15450 | A | 8051 | 194 | 372 | ICQPLSLSTANHPVLCLCFTHKNLHIFIA ALFIIAKSWKQP*CTSVDIEWLGLAPLY |
| 7400 | 15451 | A | 8052 | 1 | 325 | FFFFF*DRVSLLLPKLECNGTISAHCNRL PGSSDSPASASSFFTHVAPLPQLRHY*I FYDGTSLYAG*YSQNLLIYSAPRQPQY HFKDMNKILDSIQRSYTKI |
| 7401 | 15452 | A | 8053 | 228 | 481 | QFFRNTIFF*DRVSLLLPKLECNLSAISAH NLCLPGSSDSPASASRVAGITGTCHHTRL LAFVFLVETGFYHVSQSGLELLTSGD |
| 7402 | 15453 | A | 8054 | 175 | 431 | LIVKMPFLK*SWKIF*MSK**VMLIH*GF VFLFVCAFF*DRVSLLLPRLCNGPISAH NLHLPDSSDSPASAYIKGFVRQLSHEE |
| 7403 | 15454 | A | 8055 | 257 | 453 | TKGGGYTQRTAIQFILFIYLFY*DGVSLL LPRL*NGAISAHCNLHLPSSSDSQKTK KNFCTQ |

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| 7404 | 15455 | A | 8056 | 277 | 1230 | ISFHLSTFGAPSF FFF FEMEF SLL LPRLEC NGAISAHNRNLRLPGSSDSPASASPVGWD YRHVHPRSANFVFFFSRDGVSPCWSGLV SNSRPQMIPPSRPPKVLDTGLATMPGLCL ANFCGRNRVSLMCPSPWSPELKQSTCLSL PKCWDYRRAAVPGLFILFFLRHRCPTLT QDEVQWCDHSSLQPSTPEIKHPPASASQS SWDQRHAPLHLANFYFYF*FFETESHVS TRLECSGAILAHCNLCPLGSSYSAPAS* VAGTTGAH/RRLANFFVFLVEMGFHHVR QVDARSLDLVICLPRPPKVLGLQDVSHH RPAYF |
| 7405 | 15456 | A | 8057 | 1 | 467 | FFFLF*EGV SLL LPRLECSGAISA/HCNLH LPGSSDSPASASQEDGITGVRYHAWLIL/ VFLVEIGFHHVGQADLKP*PQVIHPPLFF FFLRQSFALVAQAGVQWCDLSSLQTPPP RVQGILLAQPEYLVAGFTGMRHHTRLF FFFAFLVETGFHPC |
| 7406 | 15457 | A | 8058 | 274 | 321 | |
| 7407 | 15458 | C | 8059 | 69 | 254 | MDHLYNXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXIEQFXXXXXERERNKNPFPAGD DIISRGVGQ* |
| 7408 | 15459 | A | 806 | 144 | 441 | GYQLPLQDELVLGQFLFQVSKIRFFSARK ITCNSHFLLLKFF*FPHIICK*VSFSSEAAA AADRAGASHPRJHNLQRLQENSIRGPK YSSHTVSADAW |
| 7409 | 15460 | A | 8060 | 32 | 169 | NPVPPYPLCPALVFFLLIYLLIY*PSPLLR MSAPAGKGFLFLSL |
| 7410 | 15461 | A | 8061 | 417 | 490 | |
| 7411 | 15462 | A | 8062 | 424 | 579 | |
| 7412 | 15463 | A | 8063 | 1 | 2157 | GFQKRCRHRIAQLFAVGALVCLVLLHL SAMISASRAAAARLVGAAASRGPTAAR HQDSWNGLSHEAFRLVSRDYASEAIG AVVGIDLGTNSCVAVMEGKQAKVLEN AEGARTTPSVVAFADGERLVGMPAKR QAVTNPNNTFYATKRLIGRRYDDPEVQK DIKNVPFKIVRASNGDAWVEAHGKLYSP SQIGAFVLMKMKETAENYLGHAKNAV ITVPAYFNDSQRQATKDAGQISGLNVLR VINEPTAAALAYGLDKSEDKVIAVYDLG GGTFDISILEIQKGVFEVKSTNGDTFLGG EDFDQALLRHIVKEFKRETGVDLTKDNM ALQRVREAAEKAKCELSVVQTDINLPY LTMDSSGPKHLNMKLTRAQFEGIVTDLI RRTIAPCQKAMQDAEVSKSDIGEVILVG GMTRMPKVQQTVDLFGRAPSKAVNPD EAVAIGAAIQGGVLAGDVTDLVLLDVTP LSLGIELGGVFTKLNRRNTTIPTKKSQVF STAADGQTQVEIKVCQGEREMAGDNKL LGQFTLIGIPPAPRGVPQIEVTFDIDANGI VHVSADKDKGTGREQQIVIQSSGGLSKD DIENMVKNAEKYAEEDRRKKERVEAVN MAEGIIHDTETKMEEFKDQLPC/ADECN KLKEEISKMRELLARKDSETGENIRQAA SSLAQQASVKKLFRNGLTKKMGS*AEEGS GSSGHWGNKREDSKGREKPVN |
| 7413 | 15464 | A | 8064 | 500 | 752 | |

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| 7414 | 15465 | B | 8065 | 1 | 1713 | MALWRGSAYAGFLALALTWRDRKKKF PGDDEAPGVKRTWAAGAGMRGRQWLR KRVEVVCTGRSANTVCAGVRAAGLVEK SPPPSLSRVGRRFRFCGDLDCPDRVLA EI STLAKMVECTGSTLGGGGYKKILKL TAD AKFVEEHEGKKDIDSPTFLSSASSWWSSS SAYGSRPPGGFELKLIGQQGESGDVKAT VAVLSFILSGAAKHSVDGKSLASELQQL GLPKEHAASPCCCYEKQSPLOKHLRVC SLRTWSLAARVAEGTAETVDPSPAAPKTS VWSSRVCWGRLLATISPSVNETDTCGME DRRLVVC RPWRAQCHMKAWGWRHP EE GGTHSGAPSAVLQALAVAIQLGGHLADP LLQVDPLSSCGAVSLDILIYLVFYYRTAS VPETYIVKTLFKKLESQS LIQSNVLTRSN SMKAERGEEAAKEKSEASRGWFMRFKE RSCLHNIKMQGEAASADVEAAASYPKD LAKITDEHGYTKQVRCIQNSLLLEGNA EEVRKIIVCSMSPLKPGGPVTLVEEFLC ASKASVS AVSGWISKWRNWQEIRQEE REDRASLPDLQASES* |
| 7415 | 15466 | A | 8066 | 1 | 3053 | MRPGFVVSVGMVEGVPGEPDPYPVL CY TPWPGHDL PASRAALAQGRSWSLHRMI GQDSGRRRSRRQH FAPGTSSGLRSAPGL TRAGPAPPEAVSPSHVIVDSADLAGPEKE IPGPWLPRAMYEA PGVKRAWAAGAGM RGRQWLRKRVEVVCTGRSANTVCAGV RAAGLVEKSPPPSLSRMGRRFRFCGDL D CPDRVLA EI STLAKMVECTGSTLGGGGY KKILKL TADAKFVEEHEGKKDIDSPTFLS SASSWWS |
| 7416 | 15467 | A | 8067 | 330 | 452 | |
| 7417 | 15468 | A | 8068 | 3 | 347 | |
| 7418 | 15469 | A | 8069 | 3 | 1279 | |
| 7419 | 15470 | A | 807 | 165 | 1222 | QSKRLNAKRYLLTDNVVKLKEFQKKV AVACNLSGTKETYFRNLKKKLTQNK LIL KGELITLLHLCESRDHVELAKNVIYRYH AENKNFTLGEY*FGPLFVRLCYQLDLEE SAGELMKDQHLRGFFSDSTLFNILMDML FIKGKYKSALQVLIEMKNQDVKFTKDTY VLAFAICYKLNSPESFKICTTLREEALLK GEILSRRASCFAVALALNQNEMAKAVSI FSQIMNPESIA CINLNIIHIQSNMLENLIK TLKNAAEGNLSKFVKRHVFSEEV LAKV REKVKDVPALVAKFDEIYGTLHITGQVT TDSLDAVLCHTPRDRKSH TLLNKR MVS RRTFQPLSQSL LAE |
| 7420 | 15471 | A | 8070 | 1 | 496 | LLGVAPSRAFQEEILR/DRASFHE/RPNLF ALKHPTSKAECTAEKCYRVTKGRGIFPS GSPFKSVTLEDGKTFIPGQGNNA YVFPG VALGVIAGGIRHIPDEIFLLTAEQIAQEVF EQHLSQGRLYPPLSTIRDVSLRIA KVL D YAYKHNLDSYTPWKEAMNVQTV |
| 7421 | 15472 | A | 8071 | 228 | 448 | |

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| 7422 | 15473 | A | 8072 | 3 | 1877 | EGEDRGLPRTMGAALGTGTRLAPWPGR ACGALPRWTPTAPAQGCCHSKPGPARPVP LKKRGYDVTRNPHLNKGMAFTLEERLQ LGIHGLIPPCFLSQDVQLLRIMRYRQQ SDLDKYIILMTLQDRNEKLFYRVLTSDV EKFMPIVYTPTVGLACQHYGLTFRPRG LFITIHDKGHLATMLNSWPEDNIKAVVV TDGERILGLGDLGCGYGMGIPVGLALYT ACGGVNPQQCLPVLLDVGTNNEELLRDP LYIGLKHQRVHGKAYDDLDEFMQAVT DKFGINCLIQFEDFANANAFRLNLYRN KYCMFNDDIQGTASVAVAGILAALRITN NKLSNHVVFVQAGEAAMGIAHLLVMA LEKEGVPKAEATRJIWMVDSKGLIVKG RSHLNHEKEMFAQDHPESNSLDEVVRL VKPTAIGVAAIAEA\FTEQILRNMAFPR RAPIIFALSNPPRKAECTAEKCYRVTEGP RGFFASGSPF*GVLIWEMGKTFIPGGRG NNAIYVFGVATGVIA\GGIRHIPDEIFL LDSRAKLQEVSEQHLSQGRLYPPLSTIR DVSLRIKVLDYAYKHNLVASYYPEPKD KEAFCKIPGSYTPDYDSFYT/VDSYIWAQ GKAMNVQTV |
| 7423 | 15474 | A | 8073 | 325 | 587 | |
| 7424 | 15475 | A | 8074 | 124 | 343 | |
| 7425 | 15476 | A | 8075 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGRLLV VYPWTQRFDFSFGNLSSASAIMGNPKVK AHGKKVLTSLGDAIKHLDDLKGTFAQLS ELHCDKLHVDPENFKLLGNVLVTVAIH FGKEFTPEVQASW/QEDGDWSGQCPVLQ IPLSSLPMQSFQ |
| 7426 | 15477 | A | 8076 | 3 | 573 | FCPRGQEFGEKNLLVPDAHGVISQRR KATITSLWGKVNVEDAGGETLGRLLV VYPWTQRFDFSFGNLSSASAIMGNPK KVKAHGKKVLTSLGRCQSTLDDLKGT FAQLSELHCDKLHVDPENFKLLGNVL VTVLAIHFGKDFTEGCRASWQKMGD FSGQCPVLQIPLKPLGP*IQSFQ |
| 7427 | 15478 | A | 8077 | 2 | 347 | |
| 7428 | 15479 | C | 8078 | 213 | 263 | MGFHHVSQDCLDLLTS* |
| 7429 | 15480 | C | 8079 | 637 | 1452 | MGIAAASVLGDLAVVFGMHVPAQADG QDHPQELDHGTHAHAEDDAQVLLQPR LHLLHAALLVHRPVLRVATLGPVAGG LAEALPHRKAVVLFPLDFAGTGVDLR AIHEL SVVCPVVEADPAAALHLSLHVVP GILQAVLATAVVVSNELSHDATHLLLQL AHVEVEEGPRHLGNEDQEQESKVQPQ QAADLVGDADAAQEAHEHSDCPHADED IGPHPKRAGGGLQDRDETALVGQDPHPE AQDHCAQDKEDQVEEEKVFGDFDTG* |
| 7430 | 15481 | C | 808 | 324 | 500 | MGNWGRSSFLKLQNLVFLKMRSDQA QWLTPKIPALWEAEAGSSEVRSLRSW STW* |
| 7431 | 15482 | A | 8080 | 226 | 314 | |
| 7432 | 15483 | A | 8081 | 2 | 350 | KTLLFFFFRFEPHNLLTSMICGLVYNQ PPQHLVHILLKRRIWPQGNILGINKRPG TVAHTCNPSTLGGRRGRITRSGVRD*PG QHSESPSLTIQKNYPGVMAGACNPSYS GG |
| 7433 | 15484 | A | 8082 | 172 | 287 | IVYASEEKI*TFQEQGWPGAVAHTCNPST LGGRGGRITRSGDRDHPG*HRPP |
| 7434 | 15485 | A | 8083 | 14731 | 15030 | IAGCRPGAVAHSCNPSTLGGRRGQI/TLR SGV*DQPGQYGETPSLLKIQLGRRGGR RLKSQLLREAEAGESLEPGRQFAVSRHR ATALQPGNRARLHLKK |
| 7435 | 15486 | A | 8084 | 1 | 193 | |
| 7436 | 15487 | A | 8085 | 1 | 346 | |
| 7437 | 15488 | A | 8086 | 3 | 522 | |

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|------|-------|---|------|------|------|---|
| 7438 | 15489 | A | 8087 | 1 | 840 | HMELPYGTLTDDMRRNLNIPVLQDDGFL FLWVTGRAMELGRECLNLWGYERVDEII WVKTNQLQRIJRTGRTGHWLNHGKEHC LVSSSGAQFNRWSTKKNHLISY*EKVQR CGFIR*SVILW*AGGVKENPQGFNQGLD L*CDRS*GMCFSGLQSFHIFVGYQLFMV GCILIPRFFLI*INIIGKGLGAILCNLKKQ LVFIS*VRSTSHKPDDEIYGMIERLSPGVR KIELFGRPHNVQPNWITLGNQLDGIHLLD PDVVARFKQRYPDGHSKPKNL |
| 7439 | 15490 | A | 8088 | 13 | 323 | |
| 7440 | 15491 | A | 8089 | 3 | 218 | |
| 7441 | 15492 | A | 809 | 1734 | 1910 | NWVGGQQEGREFFQV*WATDLKSA*GE EIEPDIPKLKPGGQKWETGLRFLHFDK WFF |
| 7442 | 15493 | A | 8091 | 3 | 332 | |
| 7443 | 15494 | A | 8092 | 1 | 1431 | MHKAGLLGLCARAWNSVRMASSGMTR RDPLANKVALVTASTDGIGFAIARRLAQ DGAHVVVSSRKQQNVDQAVATLQGEGL SVTGTVCHVGKAEDRERLVATAVKLHG GIDILVSNAAVNPFFGSIMDVTEEVWDK TLDINVKAPALMTKAVVPEMEKRGGGS VVIVSSIAAFSPSPGFSPYNVSKTALLGLN NTLAIELAPRNIRVNC/LAPGLIKTSFSRM VLGEPEDCAGIVSFLCSEDASYITGETVVN LSVMFTGGGVCRAASWKEGGTGTPTPT RESRQREPGETSSTDITQENKVNGLPA NPQRPAEGRPVRKTNKQKGIASSTAKD SINIRTKDIHTKTPSIGHQHQRPKVDKT TKMERNQSKKAETSRNQNVSSLPKEYKS SPAREQNWENKFDDLTDVSFRRSVITN YTQLKEHVLTHCKEAKNLDKMLNEWLT RMKNLEKSLNDLMELITTVQELHEGYTS FNS |
| 7444 | 15495 | A | 8093 | 195 | 434 | |
| 7445 | 15496 | A | 8094 | 43 | 1601 | SMHKAGLLGLCARAWNSVRMASSGMT RRDPLANKVALVTASTDGIGFAIARRLA QDGAHVVVSSRKQQNVDQAVATLQGE GLSVTGTVCHVGKAEDRERLVATAVKL HGGIDILVSNAAVNPFFGSIMDVTEEVW DKTLDINVKAPALMTKAVVPEMEKRGG GSVVIVSSIAAFSPSPGFSPYNVSKTVLLG LTKTLAIELAPRNIRVNCLAPGLIKTSFS RMLWMDKEKEESMKETLRVIRLGEPE DCAGIVSFLCSEDASYITGETVVNLSVMF TGGGVCRAASWKEGGTGTPTPTPRESR QREGENQARSSPRMALRPEFPPEASTS WMGPEPVGNRERPCPKARKVGASPRAL RRLGSATRMLSRRAALRAGVGARAPRPG GGRGAHATATVWSGLASAAALTARALL KRSLACAAAPQRCGWRRLLCSSLGSRG QGGQAHRGAHLRVVRYGTASVFGTPRL VASQIQHVPSGPAPRPGASHPATPSIQL RQPLHLSPIAVPGASSAGAGA |
| 7446 | 15497 | A | 8095 | 2 | 172 | |
| 7447 | 15498 | A | 8096 | 3 | 823 | |
| 7448 | 15499 | A | 8099 | 346 | 461 | |
| 7449 | 15500 | A | 81 | 457 | 489 | PP*ITLG*KTCSQARWLMPIPTLWKA EVGRSLELRSLRPAWATRRNPSTKN/LKIS WGRQGSSELRSRHCTPAWQHSETPI |
| 7450 | 15501 | C | 810 | 226 | 306 | MTTSPPPSALQKKEMEILPVILRVPS* |

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| 7451 | 15502 | A | 8100 | 3 | 1560 | SSLWRRQPELKAYRTMEYMAESTDRSP GHILCCECGVPISNPANICVACLRSKVDI SQGIPKQVSISFCKQCQRYFQPPGTWQC ALESRELLALCLKKIKAPLSKVRVLDAG FVWTEPHSKRLKVKLTIQKEVMNGAILQ QVFFVDYVVQSOMCGDGHESEKLDKF WKAVIQVRQKTLHKKTFYYLEQLILKY GMHQNTLRIKEIHDGLDFYSSKQHAQK MVEFLQCTVPCRYKASQRLISQDIHSNT YNYKSTFSVEIVPICKDNVCLSPKLAQS LGNMNQICVCIRVTSIAHLIDPNTLQVAD IDGSTFWSHPFNSLCHPKQLEEFIVIECSI VQDIKRAAGAGMISKKHTLGEVWVQKT SEMNTDKQYFCRTHLGHLLNPGDLVLG FDLANCNLNDHEVNMNSDRVPDVLI KKSYPDRTKRQRRRNWKLKELAREREN MDTDDERQYQDFLEDLEDEAIRKNVNI YRDSAIPVESDITDDEGAPRISLAEMLEDL HISQDATGEEGASMLT |
| 7452 | 15503 | A | 8101 | 1 | 171 | |
| 7453 | 15504 | A | 8102 | 3 | 231 | RRQAQIAAGRVLVVALFGCGGLHSRL DGAAILCLPGHCHGSRVEVYETHQCGL VGLKLLRGGREQSDRGSLGLT |
| 7454 | 15505 | A | 8103 | 48 | 532 | NLMNICRGPCLLPGAPFMRDLAAVA/SV GLP/LVRRQAQVAAGRVLVVALFEGCG GLHSRLDGAAILCLPGHCHGSRVEVY APQCGLVGLKLLRGGREQSDEGSLGLT *DAQLGPGAHEPEIRAWE*TAVIISLV SLEPRDGGGRVARLGAREAIGNP |
| 7455 | 15506 | A | 8104 | 3 | 421 | AAEASVGL/PLLRQAQIAAGRVLVVAL FGCGGLHSRLDGAAILCLPGHCHGSRVE VTYETHQCGLVGLKLLRGGREQSDRG SLGLT*DGQLGSAEDYTISSCPHLTGIV GLIPGLDSADGQGGRVPRLGARESVRDT |
| 7456 | 15507 | A | 8105 | 94 | 582 | LSHPLPL/LGRQAQIAAGRVLVVALG CGGLHSRLDGAAILCLPGHCHGSRVEVY ETHQCGLVGLKLLRGGREQSDRGSLGL T*DGQLGSAEHQSVSVPSLTVIISLRL EVGDGEVAVSPRAGAREAIRNSAPLVVA STTFKPHQVPRGLSCLLLMPRDVVPTVS TAQSAGEPDRGSQSGRGRG |
| 7457 | 15508 | A | 8106 | 2 | 332 | GSLQGLPGQSFSGGLPLLRQVRVAAG RVLVVALFGGFGGLHSRLDGAAILCPG HCHSSRVEVTDQTH*CGLVGLELLRGG EQSDSGVGLGLTQDGLRSTSEDKVC |
| 7458 | 15509 | C | 8107 | 30 | 653 | MTCSPLLLTLIHCTGSWAHSVLTQPPSV SAAPGQQITISCSGRLNVGNVFSWYQ QLPGTAPKILIYDNDKRPSGVPARFSGSK SGTSATLAIQTGLTGDEANYCYGAWDTS LDNWVFGGTEVTVLGQPKAAPSVTLF PPSSEELQANKATLVCLISDFYPGAVTVA WKADSSPVKAGVETTTPSKQSNKYAA SSYLSLTPEQ* |
| 7459 | 15510 | A | 8108 | 484 | 632 | PWSHFRRF*LTMRIEGLLSAGRRA/WM PWGGRDPSPGILQL*SPVGGVRDENL* TFCRGHCLLHGAPFMRDLAAVAVFGLP LLRRQAQVAAGRVLVVALFGGFGGLHS RLDGAAILCLPGHCHSSRVEVTDQTH*CG LVGLELLRGGREQSDSGVGLGLT*DGDL GPTSEDSKGATTSKRAAVIISLVVSLEPR DCQGGRVGRHGAREAIINP |

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| 7460 | 15511 | B | 8109 | 27 | 1337 | MAWTPLLLLFPLLLHCTGSLSQPVLTOSS SASASLGSSVTLTCTLSSGHSYIIAWHQ QLPGKAPRSLMKVEGDGSYKTGRGVPD RFGSSSSGANRYSISNFQSEDEADYYCQ AWDSSTAHS DTGRGIVGRPPVRQCWP LLLLGLAMVAHGLLRPMVAPQSGDDPD GASVGSSRSLRSLWGRLLLQSPQRAD PRCWPRGFWSEPSQLCYVFGTGKVTVL GQPKANPTVTLFPPSSEELQANKATLVC LISDFYPGAVTVAWKADGSPVKAGVETT KPSKQSNNKYAASSYLSLTPEQWKSHRS YSCQLQWGLGLGASQGGFLYEPVSQCV VFGGGTKLTVLGQPKAAPSVTLFPPSSEE LQANKATLVCLISDFYPGAVTVAWKAD SSPVKAGVETTTPSKQSNNKYAASSYLS LTPEQWKQAQKLQLPET* |
| 7461 | 15512 | A | 811 | 168 | 258 | GHLGPRQKQARGL*GHRVQVLHNYVI PM |
| 7462 | 15513 | C | 8110 | 54 | 410 | |
| 7463 | 15514 | A | 8111 | 1 | 175 | |
| 7464 | 15515 | A | 8112 | 1815 | 2017 | GQGA VAHTCNPSTLGGQGGRITLRSGV QNQPDQHGETLSLLNISGVWWRAPVIAA FQEAETGESLEP |
| 7465 | 15516 | A | 8113 | 1109 | 1482 | |
| 7466 | 15517 | A | 8114 | 266 | 399 | |
| 7467 | 15518 | A | 8115 | 6 | 361 | |
| 7468 | 15519 | A | 8116 | 688 | 1127 | |
| 7469 | 15520 | A | 8117 | 2 | 311 | |
| 7470 | 15521 | A | 8118 | 2 | 51 | |
| 7471 | 15522 | A | 8119 | 203 | 365 | |
| 7472 | 15523 | A | 812 | 229 | 434 | TEELKRCRQTLPSGCGVLPWRARLAVG VS/GRRGRSSSPMLTPSAAPCGNPGSLTS NLPAAGCKPSCQAW |
| 7473 | 15524 | A | 8120 | 152 | 314 | |
| 7474 | 15525 | A | 8121 | 11 | 380 | RLHRFFLGESEQSPASSSSSSSSSLTPSQ TROHGLRSIMKDLHSDDYEEESYEVDD NDNDSKMERPANR*RTRSRTVSLSDGSD SESRTSS*PLHYEPPLLYTNNNQILEVE SPITHSL |
| 7475 | 15526 | A | 8122 | 124 | 1924 | ITAEGRRRGGYHTTPQQTSGPPGMASS CSVQVKLELGHRAQVRKKPTVEGFTHD WMVFVRGPEHSNIQHFVEKVVFHLHESF PRPKRVCKDPYKVEESGYAGFILPIEVY FKNKEEPRKVRFDYDLFLHLEGHPVNH LRCEKLTFFNPTEDFRRKLLKAGGDPNR SIHTSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSTSFSPKPHKLMKEHKEKP SKDSREHKSAFKEPSRDHNKSSKESKK PKENKPLKEEKIVPKMAFKEPKPMSKEP KPDNLLTITSGQDKKAPSKRPPISDSEEL SAKKRKKSSSEALFKSFSSAPPLILTC SAD KKQIKDKSHVKMGVKIESETSEKKKST LPPFDDIVDPNDS DVEENISSKSDSEQSP AS\SSSSSSSFHTIPGPGQQGLARSIMKD LHSDD\NEEEADEAEDSDNDSEMERPVN RGGSRRRVSLSDGSDSESSASSPLHHE PPPPLLKTNNNQDSWKWKSPIKQSK\SD* GKLKNGEC*QGLT*MELVGAFTGRFIDF EEERHILQQIVNLIETGHFHTNTTFDFD LCSLDKTTVRKLQSYLETSGTS |
| 7476 | 15527 | A | 8123 | 2 | 319 | |
| 7477 | 15528 | A | 8124 | 1 | 323 | |
| 7478 | 15529 | A | 8125 | 31 | 118 | |
| 7479 | 15530 | A | 8126 | 1 | 4938 | |
| 7480 | 15531 | A | 8127 | 472 | 4356 | |
| 7481 | 15532 | A | 8128 | 2 | 236 | |
| 7482 | 15533 | A | 8129 | 503 | 638 | |

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| 7483 | 15534 | A | 813 | 1060 | 1542 | GRDMVAPDASWKEASGCNAPARICPGQ AFRANGCSDPTLGIQHQLFRSRLSPKVL GPVGPWELGGE*DEAPSASFFSHWEVL GRLLVGASGSPSVKQEPAAALERARVPGD AARRQPRDRKGPPGPPCCSEHPAPVRAP LVAGLG DAGSGAPRAKLGVM |
| 7484 | 15535 | A | 8130 | 464 | 2848 | GETGMSTALHTTVAMRCPMLGGGGGP TYGPPQWGHDPDVHIMQHHLPIQARLG SIAEIDLGVPPVMKTFKEFLSLDDSDV ETEAVKRYNDYKLDFFRQQMQDFFLAH KDEEWFRSKYHPDEVGKRRQEARQALQ NRLRVFLSLMETGWFDNLLLDIDKADAI VKMLDAAVIKMEGGTENDLRILEQEEEE EQAGKPGEP SKKEEGRAGAGLGDGERK TNDKDEKKEDGKQAENDSSNDDKTKKS EGDGDKEKKEDSEKEAKKSSKKRNRK HSGD DSFDEGSVSESESESGQAEEEEKE EAEALKEKEKPKEEWEKPKDAAGLEC KPRPLHKTCSLFMRNIAPNISRAEISLCK RYPGFMRVALSEPQERRFFRRGWVTFD RSVNIKEICWNLQNI RL/RECELSPGVNW DLTRVRNNGITQHKQIVRNDIKLAACL IHTLDDRTQLWASEPGTPPLTSLPSQNPI LKNITDYLIEEVSAAAAEELGSSGGAPPEE PPKEGNPAEINVERDEKLIKVLDKLLLYL RIVHSLDYNTCEYPNEDEMPNRCGIIH VRGPMPPNRISHGEVLEWQKTFEELTP LLSVRESLSEEEAQKMGRKDPEQEVEKF VTSNTQELGKDKWLCPLSGKKFKGPEFA RKHIFNKHAEKIEEVKKEVAFFNNFLTD AKRPALPEIKPAQPPGPAQILPPGLTPGLP YPHQTPQGLMPYGPQPRPILGYGAGAVR PAVPTGGPPYPHAPYGAGRGNYDAFRG QGGYPGKPRNRMVRGDPRAIVEYRDL APDDVDFF |
| 7485 | 15536 | A | 8131 | 2 | 433 | |
| 7486 | 15537 | A | 8132 | 1073 | 3545 | GETGMSTALHTTVAMRCPMLGGGGGP TYGPPQWGHDPDVHIMQHHLPIQARLG SIAEIDLGVPPVMKTFKEFLSLDDSDV ETEAVKRYNDYKLDFFRQQMQDFFLAH KDEEWFRSKYHPDEVGKRRQEARQALQ NRLRVFLSLMETGWFDNLLLGH*TKLI AIVKMLDAAVIKMEGGTENDLRILEQEE EEEQAGKPGEP SKKEEGRAGAGLGDGE RKTNDKDEKKEDGKQAENDSSNDDKTK KSEGDGDKEKKEDSEKEAKKSSKKRN RKHSGD DSFDEGSVSESESESGQAEEE KEEAEEALKEKEKPKEEWEKPKDAAG LECKPRPLHKTCSLFMRNIAPNISRAEIS LCKRYPGFMRVALSEPQERRFFRRGWV TFDRSVNIKEICWNLQNI RGARSLNRWC SRGKGLRAAVSLASGLRECELSPGVNRD LTRVRNNGITQHKQIVRNDIKLAAKLI HTLDDRTQLWASEPGTPPLTSLPSQNPI LKNITDYLIEEVSAAAAEELGSSGGAPPEE PPKEGNPAEINVERDEKLIKVLDKLLLYL RIVHSLDYNTCEYPNEDEMPNRCGIIH VRGPMPPNRISHGEVLEWQKTFEELTP LLSVRESLSEEEAQKMGRKDPEQEVEKF VTSNTQELGKDKWLCPLSGKKFKGPEFV RKHIFNKHAEKIEEVKKEVAFFNNFLTD AKRPALPEIKPAQPPGPAQIIHVPVRVVL PPGLTPGLPYPHQTPQGLMPYGPQPRPIL GYGVPTGGPPYPHAPYGAGRGNYDAFR GQGGYPGKPRNRMVRGDPRAIVEYRDL DAPDDVDFF |
| 7487 | 15538 | A | 8133 | 188 | 391 | |

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| 7488 | 15539 | A | 8134 | 1 | 998 | MAVMLHSAKWPLPVLLQGLTMQPPLPS KHISERSEEDSRQPLYSVILIFYEAGFAIL VFDKTDFOQPKVKRDKKEGHYIMVKGSM QQEELTILNIYAPNTGASSFIKQVLGDPQ RDLDSTIIVGDFNTPLSILDRLMRQKIN KDIQDLNSALDQVDLIDIYRTLHPKSTEY TFFSAPHHTYSKIDHIIGSKTLLSKCKRTE IITNSLSDHSAIKLELRIEKFTQNHHTTWK LNNLPLNDYVWNNEIKAEINKFFETNEN RDTMYQNLWDTAKAVFRGKFIALNGH RRK*ERSKINTLTLQLKELEKQEQTTHSKA SRRQEITKIRAELEIDS |
| 7489 | 15540 | A | 8135 | 1 | 1674 | |
| 7490 | 15541 | A | 8136 | 3 | 361 | |
| 7491 | 15542 | A | 8137 | 3 | 174 | |
| 7492 | 15543 | A | 8138 | 3 | 326 | |
| 7493 | 15544 | A | 8139 | 1 | 82 | |
| 7494 | 15545 | A | 814 | 166 | 437 | ADHLKSGV*DQPGQHGEILSLKLQ*FPG RGG AHL*SQLLGRLKQENHLNPGGGGC SEPRLCHWTPVRATVGDSVQKK*KSQD GPRAKLG |
| 7495 | 15546 | A | 8140 | 2 | 372 | |
| 7496 | 15547 | A | 8141 | 1 | 352 | |
| 7497 | 15548 | A | 8142 | 2 | 395 | |
| 7498 | 15549 | A | 8143 | 4274 | 5256 | HTLFGDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPNLRLVRPEVD VMCTAFHDNGETFLKK*VIRCL*FKIKK HGVTP*ANTL*KLP*QKYFQH*DLEVLL* *FFKEVVDFTTKFYTAKNMIKDILKFIET GYNLSQKFIDKFFNVFRRYVYVYVVID FVLVSNIILPKFNHLCCTHTHTHTLTLFST YLKNDKDKTIMCKLSLIG*LAESLEFGGS GENVDYNYFCNIVCYRK/ADCFSLKFR YLVEIARRHPYFYAPELLFAKRYKAAP TECCQAADKAACLLPKVLCRIEKKSL SNLILSILWDLGLSV |
| 7499 | 15550 | A | 8144 | 23 | 136 | |
| 7500 | 15551 | A | 8145 | 1 | 248 | |
| 7501 | 15552 | A | 8147 | 3 | 231 | |
| 7502 | 15553 | A | 8148 | 30 | 217 | |
| 7503 | 15554 | B | 8149 | 49 | 754 | MAGAAPRLPWSRPHGSCGWWMQPLQ GPGRRAVAAAWEVATPVFMPVGTQAT MKASRPNSWTLWVAASAWELPSGSK AGGTAAFPDGVAGVSVRGDGGGLRFRS PYDGNETLLSPENPCSRMRWAPGVVT GALLQVNPLAGPVHAAHQRPDKQNLFA IIQVGWGTQISGPPALKRFGSAWHSRAFLT HCCTVTTRPCTTSRPHRLPAELMSAV RTSIVEKRFPDSCGTSWAPX* |
| 7504 | 15555 | A | 815 | 3 | 238 | SGDRDHPG*HSETLSLLKIQQUAGRGGG RL*SRLRLRLQENGVSPPGGACSEPRS HHCTPAWETERDSVSKKKKKKL |
| 7505 | 15556 | A | 8150 | 1 | 593 | RQSRWREQLPRLSWRLVPRIMRLVAEC GRSRARAGELWLPHTVATPVFMPVGT QATMKGITFAEFLDALGCRICLGNTYHL GLRPGPELIQKANGLPRLS*IWPSLILLN GTAAVFQMVSLVSLSEVTEEGVFRSPY DGNETLLSPEKSVQIQNALGSDIIMQLDD VVSSTVTGPRVEEAMYSIRWLDRCICS H |
| 7506 | 15557 | B | 8151 | 374 | 613 | MTALDLFLTNOFSEALSULKPRTKESMY HSLTYATILEMQAMMTFDPQDILLAGN MMKEAQMLCQRHRRKSSVTDSFSSL* |

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| 7507 | 15558 | A | 8152 | 2 | 1922 | VETPPQGSVHSGHLGSVVGDPHTGTGN AGERGPRGKGARVLALDSSGMDSSPSLP LIRTPESLHEALDQCMTALDLFTNQFS EALS YLKPRTKESMYHSLTYATILEMQA MMTFDPQDILLAGNMMKEAQMCLQRH RRKSSVTDSSSLVNRPTLGQFTEEEIHA EVCYAECLLQRAALTFLQGSSHGGAVRP RALHDPSHACSCPPGPGROHLFLQDEN MVSFIKGGIKVRNSYQTYKELDSLQSS QYCKGENHPHFEGGVKLGVGAFNLTL MLPTRILRLLEFVGFSGNKDYGLLQLEE GASGHSFRSVLCVMMLLCYHTFLTFVLG TGNVNIEEAELLLKPYLNRYPKGAIFLFF AGRIEVIKGNIDAVSDGGPGRGWGSLGV SQTSRKSGETCDILRDRIDWGRGGGPREN QPESRRRGPSPGRAAWEDKGGGGICGA WDFDWEI*DCSIAVEGGGGRCLEAEVR KAHLFRA*RLGWSLVPLPHYSSLLFHF VTKNQSPRRGLYLSPTSCKT*EVKPGLE ARSPGSWGPT*A*HRAGPLCPGGVPVCC GVGRFGGCRGVGAGWAPVRLTRRCLQ AIRFECECEAQHKKQFHHMCYWEL MWCFTYKGQWKMSYFYADLLSKENCW SKVG |
| 7508 | 15559 | A | 8153 | 1 | 285 | |
| 7509 | 15560 | A | 8154 | 3 | 409 | |
| 7510 | 15561 | A | 8155 | 1 | 390 | |
| 7511 | 15562 | A | 8156 | 17 | 221 | |
| 7512 | 15563 | A | 8157 | 2 | 366 | |
| 7513 | 15564 | A | 8158 | 1270 | 1692 | |
| 7514 | 15565 | A | 8159 | 2 | 261 | RPRRSSSTS*SPH*PPAVAAAPSGAPPWG LSCPRRPRAPAAAPPEALGQPGSTRG AAEVAGAAGSRPPQPFYSDQSRFCCIKS |
| 7515 | 15566 | A | 816 | 4005 | 4345 | SQHFRPRRADHLRSGVQDQPDQHGET PSLLGGRGGRITKSGDRDHPG*HGETPSL LKMQ/EKLAGRGGGRLWSQLLRLRQE NGVSPGGRACSEPRSCHCTPAWLTEQDS VSKK |
| 7516 | 15567 | A | 8160 | 44 | 463 | |
| 7517 | 15568 | A | 8161 | 2 | 318 | |
| 7518 | 15569 | A | 8162 | 1 | 349 | |
| 7519 | 15570 | A | 8163 | 38 | 368 | |
| 7520 | 15571 | A | 8164 | 43 | 376 | LSMANGPPHCTECTAFPRESGKNCKVCI FNTDGTLVAVRTGQKADIISVSSKGLLH SFYLLKAVCLEFSPKNTAL*TGLPYSTSK DATAGIPNLQLYDVKTGTCLKSFLQK |
| 7521 | 15572 | A | 8165 | 22 | 192 | |
| 7522 | 15573 | B | 8166 | 852 | 931 | MYSPPDPRTVKSGVDGAMLSRKEKPLG* |
| 7523 | 15574 | A | 8167 | 1 | 202 | |
| 7524 | 15575 | A | 8168 | 2 | 330 | |
| 7525 | 15576 | A | 8169 | 1 | 281 | AAWILKARALTEMVYIDEIDVDQEGIAE MMLDENAIA/PSSTPITQAGRPTGLRPS TQSGRPGTMEQAJRTPRTAYTARPTSSS GRFVRLGT |
| 7526 | 15577 | B | 817 | 1 | 9234 | MGAPTLPPAWQPFLKDHRISTFKNWPFL EGCACTPERMAEAGFIHCPTENEPDLAQ CFFCFKELEGWEPDDDDPIEHHKKHSSGC AFLSVKKQFEELTLGEFLKLDREKAKNI AKETNNKKKEFEETAKKVRRAIEQLAA MD* |

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| 7527 | 15578 | A | 8170 | 1 | 769 | QAAWILKARALTEMVYIDEIDVDQEGIA EMMLDENAIQVPRPGTSLKLPGTNQTG GPSQAVRPITSHSEKPITGFLRPSTQSGRP GTMEQAIPTPTAYTARPTSSSGRFVRL GTASMLTSPDGPFIN*SRLNLTKYSQPK MAKALPEYIFHHENDVKTALELAALSTE HSQYKDWWWKVQIEKRYRGLMYREA EKQIKSSLKQEMVDITFLYLAKVYVSLD QPV TALNLFKQGLHKFPGEVTLCCGIARI YE |
| 7528 | 15579 | A | 8171 | 2441 | 2706 | FCFGLSCLLPFFFFFFFEMESRSVAQAG VQWCDLSSLHPLPPGSSNAPASASRVAG TTGAYHQCLANFGFVFLVETGVSLCWL GWS |
| 7529 | 15580 | A | 8172 | 1258 | 1733 | ILFWIIQLNLECSEFSWRLRQGRGIMLFFF PFLFFFETESHVAQTGVQWCDLGSLOP PPPGLSDSPALASSVSWITDVRHHLWLIF VFLVETGFRHVGQASLKLPTSGDLPTLA SQSAGITGVSHYAWLIFVFLVETEFHHV GQAGLELLAPSDPPA |
| 7530 | 15581 | A | 8174 | 196 | 390 | |
| 7531 | 15582 | A | 8176 | 84 | 307 | |
| 7532 | 15583 | A | 8177 | 3 | 383 | DIKILIASPSATHIHKETTRATSSPYRDTQ SRTASPNRAGKGVIEQTEKSHPRSPNVLS AALSQRTTVPEEELNPKILALQNAQRKR KMEHDGSLFQAVGI/DLACRL/LGQSM ESGLPQLTSYDCEV |
| 7533 | 15584 | A | 8178 | 2 | 691 | |
| 7534 | 15585 | A | 8179 | 2 | 202 | |
| 7535 | 15586 | A | 818 | 1577 | 2233 | SGCLLSPPSVGRQNSPVELGGAGLSRAG WAPQERGRAALLLISPGPNVRGGPDWLP SVLQMRGLPLWDLGGRPDVGRMSPGGR PGSCWATQLRFHISLAPLFSWAGRSGS RLNPSTLGGRGGPITRSGDRDHPG*HGET LSLLKIQKISQACWR/CACSPSYGRLRQE NGVNPGGGACREQRSGHCTPAWATEQD SVSKKKKKKSGSTIRLKHILHKII |
| 7536 | 15587 | A | 8180 | 1 | 62 | |
| 7537 | 15588 | A | 8181 | 116 | 333 | |
| 7538 | 15589 | A | 8182 | 55 | 351 | QWSYLPQVMFTGENIPVHPHVYSNGHI CLSILTEDWSPALSVQSVCLSIISMLSSCK EKRRPPDNSFYVRTCNKNPKKTKWWYH GKFEHRDIHKGKKM |
| 7539 | 15590 | A | 8183 | 3 | 474 | DGSIMASMQRLQKELLALQNDPPPGM TLNEKSVQNSITQWIVYMEGAPCTLYEG EKFQLLFKCRRRYPFDSQGMFTGENIT DHPHVYSNGHMCLSILTKNWFALSVQS VCLSIISMLSSCKEKTDDHPDNSFYVRT CNKNPKKTKWWYHDDTC |
| 7540 | 15591 | A | 8184 | 1 | 232 | |
| 7541 | 15592 | A | 8185 | 3 | 367 | |
| 7542 | 15593 | A | 8186 | 1 | 203 | |
| 7543 | 15594 | A | 8187 | 2 | 333 | ARVKRLGMFNIQHCKKLSSWVLLMKYL GNATAIFFLPDEGKLQHLENELTHDIITK FLAETFLHFPKLSITGTDLKSVLGQLGI TKVFSNGADLSGVTEEAPLKLKAD |
| 7544 | 15595 | A | 8188 | 1 | 853 | EYRRFLVDRHLQLTTGNGLFLSEGLYLV DKFLEDVGRLYHSEALTVNFGDTEEAKK QINDYVEKGTQGKIVDLVKELDRDVTFA LVNYIFFKGKWERPFEVKDTEEDFHVD QVTTVKVPMMKRLGMFNIQHCKKLSSW VLLMKYLGNATAIFFLPDEGKLQHLENE LTHDIITKFLNEDRRSASLHLPKLSITGT YDLKSVLGQLGNTKVFGRGSQHEKRRRT EATKECRKTQNNRGTERVATAT*THNQ KRKRAQQGNTREKENGKQREQPFVFL MIEQN |

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|------|-------|---|------|------|------|--|
| 7545 | 15596 | A | 8189 | 3 | 157 | |
| 7546 | 15597 | A | 819 | 151 | 454 | FQKIGPGAVAHACNPSTLGGRRRITRSG GRDHPG*HSETPSLLKIQKLAGRGGGCL *SOLLWRLRQENGVPNGGGACSEPRSRH CTPAWVTERDSVSKKK |
| 7547 | 15598 | A | 8190 | 3 | 362 | |
| 7548 | 15599 | A | 8191 | 3 | 333 | |
| 7549 | 15600 | A | 8192 | 174 | 361 | |
| 7550 | 15601 | A | 8193 | 1 | 1143 | VRCPVRNSRVDPRVRMAAVFLVTLYE YSPLFYIAVVFTCFIVTTGLVLGWFGWD VPVILRNSEETQFSTRVFKKQMRQVKNP FGLEITNPSSASITTGITLTDLEDLLTC YWGCSVQKLYEALQKHVYCFRISTPQA LEDALYSELYQEYAFILSSDIPISTEN*T SYG*SVANLLIILGILEACLLQNKHSPCI RTCSVYRISVSGTGFAFRLIYPLALHRL LMDKVPLTY*SFLGY*KHVYCFRISTPQA LEDALWSELYQEYHFIKKDSKEEYICQ LPRDTNIDDFGTVPRSRYPLVALLTSD DDREIYDIISMVSVIHIPDRTYKLSRILY QYLLAQGGFHDCLKLFMSANNFTPS NNSSE |
| 7551 | 15602 | A | 8194 | 2 | 499 | |
| 7552 | 15603 | A | 8195 | 3 | 486 | |
| 7553 | 15604 | A | 8196 | 80 | 1281 | LPAQKLDTMCEDETTALVCDNGSGLV KAGFAGDDAPRAVFPISVGRPRHQGV VGMGQKDSYVGDEAQSKRGILTKYPIE HGIITNWDDMEKIWHHTFYNELRVAPEE HPTLLTEAPLNPKANREKMTQIMFETN VPAMYVAIQAVLSLYASGRITGIVLDSG DGVTHNVPIYEGYALPHAIMRLDLGRD LTDYLMKILTERGYSFVTTAEREIVRDIK EKLCYVALDFENEMATG/PSIHPPMEKS YELPDGQVITIGNERFRCPHTLAFQPSFIG MESAGNHETTYSNMKCDIDIRKDLAYA NNVMFGGHPRLYPWEFADRMQERDSP ALAPQAPMEDQGFIRPRSAKYSVWIG RLPSWPSLSHLPSKMWITEAGSTDEAGP FPSSNRKCF |
| 7554 | 15605 | A | 8197 | 2 | 228 | |
| 7555 | 15606 | A | 8198 | 1 | 369 | |
| 7556 | 15607 | A | 8199 | 1 | 416 | |
| 7557 | 15608 | A | 82 | 999 | 1523 | WEMVEIWSYSSSEQEHQLIKLSYQRIKPL PHAHWWPFNPSPGLPPEASK*PPG*TLG FLGKKA*LQTFPLNYIRLENMQPRHGG CPVIPTLWKAEVGRSLELRSLRPAWATR RNPSTKNPKLAGGARHL*SPGTPEAEV GGSPPEP/GGRQGSSELRSRHCTPAWQHSE TPIS |
| 7558 | 15609 | A | 820 | 1362 | 1647 | |
| 7559 | 15610 | A | 8200 | 2 | 396 | |
| 7560 | 15611 | B | 8201 | 1 | 555 | MESTYMPINSGLDKENVESECKAYNPRP FCKTYTMDKQPLNTGEQKDMTEFFDLI TKIEEMSPESLRCEELHLHAENLSRRV WELLMLLPTCPNMLMAFQNISDEQGSYS DLYPDSDDSSSEDQVENSKNWSCKISSN FTSSSKTIWYFSAVWEQLRYTLDNNVL KKS VIIQKDSSEYED* |
| 7561 | 15612 | A | 8202 | 1 | 901 | |
| 7562 | 15613 | A | 8203 | 1 | 407 | |

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|------|-------|---|------|-------|-------|---|
| 7563 | 15614 | A | 8204 | 2 | 1149 | PDLELP RARPQLVNSPGADKMETNSSLP TNISGGTPAVSAGYLFDDIITYLVFAVTF VLGVLGNGLVIWVAGFRMTHVTITISYL NLAVADFCFTSTLPFFMVRKAMGGHWP FGWFLCKFVFTIVDINLFGSVFLIALIALD RCVCVLHPVWTQNHRTVSLAKKVIIGP WVMALLLTLPVIIRVTTVPKGTGTVACT FNFSPWTNDPKERINVAVAMLTVRGIIRF IIGFSAPMSIRVAVSYGLIATKIHKQGLIKV QVRP*GALSFVAKKAFFLCWSPYQVVA P**PTSQESREVNCKGMYQRKLGIAVDV NKVPLAFFNS/CAFNPMLVFMG/QDFR ERLIHALPAKSGRGLPTEDFNPKVPVQLT NSTLPSAEVALQAK |
| 7564 | 15615 | A | 8205 | 2 | 386 | |
| 7565 | 15616 | A | 8206 | 2 | 294 | |
| 7566 | 15617 | A | 8207 | 541 | 711 | SEVSAMVFLFFFF/CFFEMESRSAAQAGV QWCNLGSLQALPPRFTPFCSLSPSSWD Y |
| 7567 | 15618 | A | 8208 | 2 | 1730 | |
| 7568 | 15619 | A | 8209 | 1 | 183 | |
| 7569 | 15620 | A | 821 | 10289 | 10708 | SQHFGLRQEDHLRSGVREQPQGHGKT PYLLKIQKLARRSGACL*SQLLRRLRQEN RLNPGGVGCSEPRLLHHCTTAWTLQ*DPV SKKLKKKYIERQRYHQHMKHPWSTKIQ YVCMG*HRSVEKQIIQTLCMFVFTHTY |
| 7570 | 15621 | A | 8210 | 3 | 320 | |
| 7571 | 15622 | A | 8211 | 2 | 198 | |
| 7572 | 15623 | A | 8212 | 110 | 363 | |
| 7573 | 15624 | A | 8213 | 1 | 849 | |
| 7574 | 15625 | A | 8214 | 1 | 993 | |
| 7575 | 15626 | A | 8215 | 23 | 627 | |
| 7576 | 15627 | C | 8216 | 79 | 171 | MDISGTKCDFTVQVQLRFCLSETKATQP TN* |
| 7577 | 15628 | A | 8217 | 3 | 630 | |
| 7578 | 15629 | A | 8218 | 1 | 188 | |
| 7579 | 15630 | A | 8219 | 1 | 2295 | |
| 7580 | 15631 | A | 822 | 662 | 766 | |
| 7581 | 15632 | A | 8220 | 143 | 5972 | |
| 7582 | 15633 | A | 8221 | 3 | 753 | |
| 7583 | 15634 | A | 8222 | 57 | 272 | |
| 7584 | 15635 | A | 8223 | 1 | 218 | |
| 7585 | 15636 | A | 8224 | 180 | 293 | |
| 7586 | 15637 | A | 8226 | 3 | 145 | |
| 7587 | 15638 | A | 8227 | 16 | 546 | QLNGRSIRHEVMShrkFSAPRHGSLGFL PRKRSSRHGKVKSPKDDPSKPVHLTA FLGYKAGMTHIVREVDRPGSKVNKKEV VEAVTIVETPPMVVVGIVGYVETPRGLR TFKTVFAEHISDE/CRLPLRQKKAHLME IHVNGGTVAEKLDWARERLEQQVPVNP VFGQDEMIDVI |
| 7588 | 15639 | A | 8228 | 3 | 348 | TRHIVREVDRPGSKVNKKEVVEAVTIVE NTPMVVVGIVGYV/ETPR/GLRTFKTVFA EHISDECKRRFYKNWNKSKKIDLKFDIT SKLCHGRLQTMEEKKAFMGPLKKDRIA KEEGA |

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|------|-------|---|------|------|------|--|
| 7589 | 15640 | A | 8229 | 1 | 956 | VNHAPAHASDGVMSHRKFSAPRHC\SLG FLPRKRSSVRHKGKVSFPMDDPSKVPVH LTAFLGYKAGMTHIVRE\VDVPGSKVN KK\EVVEAVTIV*DTTHWCLLGIVGYVG NPSEGLRD\TFKTCLLLEHISY*MPRRRFL *RIWALKS*EGRPLPKYCKEIGKDED\GK KPAWKDFQQH*KKLLAQVHPCSIAQT QMRLPL\ROK\KAHLMEIQVNGGTVA RESWDWAREKLE\QQVPVNVQVFGQDEM NDV\GVTKGK\GFKGVTRSWPTN*LPFK A\HLGLSRVACFGAWH\PARAHWHVAR AGQKGYQPYTLLVHSDL |
| 7590 | 15641 | A | 823 | 749 | 853 | |
| 7591 | 15642 | A | 8230 | 1 | 375 | |
| 7592 | 15643 | A | 8231 | 1 | 399 | |
| 7593 | 15644 | A | 8232 | 2441 | 2706 | FCFGLSCSLPFFFFFFFEMESRSVAQAG VQWCDLSSLHPLPPG\SSNAPASASRVAG TTGAYHQCLANFGFVFLVETGVSLCWL GWS |
| 7594 | 15645 | A | 8233 | 1275 | 1749 | ILFWIIQLNLECSEFSWRLRQGRGIMLFFF PFLFFETESHVAQTGVQWCDLGLSLQP PPGLSDSPALASSVSITDVRHHLWLIF VFLVETGFRHVGOASLKLPTSGDLPTLA SQSAGITGVSHYAWLIFVFLVETEFHHV GQAGLELLAPSDPPA |
| 7595 | 15646 | A | 8234 | 3 | 200 | DALAFVIKVFAAEEVDGCSVTIGS/HNH SVASGSNHRTRFCFTVYLSSIVSWRY*SC RCRECRGRAF |
| 7596 | 15647 | A | 8235 | 1 | 1214 | |
| 7597 | 15648 | A | 8236 | 24 | 183 | |
| 7598 | 15649 | A | 8237 | 256 | 491 | |
| 7599 | 15650 | A | 8238 | 243 | 385 | |
| 7600 | 15651 | A | 8239 | 3 | 403 | SCYGFNVRGQVSDGGQLRSINGELYAP LQH\NHVNVEGATHKQVVDLIRAREKEL ILT\LSVPPHEADNLYPSDDSLGQSFYDY TEKQAVPISVPRYKHVEQNGEKFVVYN VYMAGRQLCSKRYRQFAILHQN |
| 7601 | 15652 | B | 824 | 1 | 855 | MDVVDPDIFNRDPRDHYDLLQRLGGGT YGEVFKLFAKCYTCIHTYDAMRVLFLM TKSGSQLPRLKEKGK\WYERTGGRSAN VHYIIVCESVHFLPILLPTLSTKPLSPEL NAAASYVPFPIIHIDTAASMCYLFHMY VGVRAGGGIGDEIEDPAGDEYELRVVF DITFFFFVIVILLAIHQGLIIDAFGELRDQ EQVKEDMETKCFICGIGSDYFDTTPHGFE THTLEEHNLANYMFFLMYLINKDETEHT GQSRALCRAFRGMRETGDLVRALKELA V* |
| 7602 | 15653 | A | 8240 | 1 | 706 | |
| 7603 | 15654 | A | 8241 | 323 | 496 | |
| 7604 | 15655 | A | 8242 | 1 | 483 | |
| 7605 | 15656 | A | 8243 | 2 | 740 | |
| 7606 | 15657 | A | 8244 | 249 | 390 | |
| 7607 | 15658 | A | 8245 | 24 | 426 | |
| 7608 | 15659 | A | 8246 | 1 | 240 | |
| 7609 | 15660 | A | 8247 | 935 | 1150 | |
| 7610 | 15661 | A | 8248 | 190 | 584 | |
| 7611 | 15662 | A | 8249 | 201 | 364 | |
| 7612 | 15663 | A | 825 | 65 | 290 | HLVSSLAKGLAVRQAPFARVPPQHP*V KVKNWDPLLQPPPCRGLALKVTGCRVL GTEGLPHLKDFPIRAATQPL |
| 7613 | 15664 | A | 8250 | 1 | 1122 | |

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|------|-------|---|------|------|------|--|
| 7614 | 15665 | A | 8251 | 1 | 1197 | MHKDWVVFVDSGEHKEALLHELQLCDS TLKPAAHGQTRLVDLSLSEHKAQGTGA HVYEERHQVSVSRDDVGCVPVSECLAR ACGAEVGCSNIAYPKLVMEMLPI/GFSG AGDFPGPPLSNPLFLEAFDPSGLRGLMIA VMLAALMSSLTSIFNSSSTLTMDIWRRL RPRSGERELLVGRGTGIPSTPPAPQSRLSF LLPETPPLERYLLGLVVM DLWL VIVALIG VSVAWIPVLQDSNSGQLFIYMQSVTSSL APPVTA VFLGVFWRRANEQGAFWGLI AGLVVGATRLVLEFLNPAPPCGEPDTRP AVLGSIHYLHFGVALFALSGAVVVAGSL LTPPPQSVQIENLTWWTLAQDVPLGTKA GDGQTPQKHAFWARVCGFNAILLMCVN IFFYAYFA |
| 7615 | 15666 | A | 8252 | 1 | 624 | |
| 7616 | 15667 | A | 8253 | 88 | 627 | |
| 7617 | 15668 | A | 8254 | 3 | 437 | |
| 7618 | 15669 | A | 8256 | 220 | 415 | |
| 7619 | 15670 | A | 8257 | 2 | 359 | |
| 7620 | 15671 | A | 8258 | 1 | 1270 | RTRGRTRGELVLESGEWRWLLERCRPG GAVALILLA AVVSICAVSQHAPPWTEDC RKSTYPPSRPTYRGAVP WDTI/HVLDLPP YKRWDELM LDMAPV/LSKVIVNSLKNMI NTFVPSGKIMQV VDEKLPGLLG NFP GP FEEEMKGIAAV/SLDIPLGEIISFNIFYELF TICTSIV AEDKKGHLIHGRNMGF/GVFLV WNINNDTWVITEQLKPLTVNLDFQRNN KTVFKASSFAGYVGMLTGFKPGLFSLTL NERFSINGGYLGILEWILGKKDAMWIGF LTRTVLENSTSYEEAKNLLTKTKILAPAY FILGGNQSGEGCVITRDRKESLDVYELD AKQGRWYVVQTN YDRWKHPFFLDDRR TPAKMCLNRTSQENISFETMYDVLSTKP VLNKLTVYTTLIDVTKGQFETYLRDCPD PCIGW |
| 7621 | 15672 | A | 8259 | 108 | 988 | TARGSKARSGGTRWSLGPPSSSGRRSW QPLVISRAV*H*GKSSRHQPLYSGHPLHG PVSHRGGPGPVRQPAAT*RPACASKLVQ PWH*WGP*LGSPALAGHL CRTGCEES HHTCFPGYVKP*RL*ALPGGRPV*VGER ARARPDEPREAAGFCGTEEQPHTDPAHP RLKRDCL/PSVSQAAVSTTASAGFPPAW AASAGFPPTWTPNLSPATLGMQRSSCAL TFRICRFLSDNKWMQRSITSM AIWICN GSGGSTSGRVSFSSSTLGGTDCSSSSLSKS ETFPSATSFSLR |
| 7622 | 15673 | A | 826 | 230 | 652 | GLSAPVAADPSLEPTALHASIRPEADLQ P*PRTPLRSWGS/PGVRSPTGDPSGVT RLHRAIHQ/PITISSSTWVTCTGPLCSVLIS PSQGESAPKRTVLEEHLRPPGAHADA HSGQLRAWPGQQREHGQEASQWEQHP |
| 7623 | 15674 | A | 8260 | 1 | 319 | |
| 7624 | 15675 | A | 8261 | 19 | 373 | AVFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFSSSSSSFFFFSFFLFFFFKLKELRLVI *PLNPEN*ESCPLFSPVNLDMPTFKDKR WKVNWARSTSRQQLLESARTKSWAERE GGTRWRAW |
| 7625 | 15676 | A | 8262 | 227 | 420 | KNFLPNCSAKELFFFFFFFFFLLLLLLL LYFKF/MI*WFKHLAFLLAFILSPTAL* RGVFHH |
| 7626 | 15677 | A | 8263 | 400 | 582 | |
| 7627 | 15678 | A | 8264 | 1205 | 1681 | |
| 7628 | 15679 | A | 8265 | 1 | 403 | |
| 7629 | 15680 | A | 8266 | 3 | 397 | |
| 7630 | 15681 | A | 8267 | 36 | 446 | |

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|------|-------|---|------|-----|------|---|
| 7631 | 15682 | A | 8268 | 1 | 453 | RHERHERHEELMTEGEDQFDVGSAAAR KEIIRNKIRAIGKMARVFSVLREESESFLT LKGLTPTGMLPSGVLAGGRQTLQSATVE AIEAEKAIRGFSPPHRCISFEEAKGLDRIN ERMPPRKDAVQQDGFNSLNTAHATENH GTGNHTAQ |
| 7632 | 15683 | A | 8269 | 644 | 809 | |
| 7633 | 15684 | A | 827 | 108 | 1102 | RMTQCLSECLICKFLSGKVTLGQAQWLT HVIPALWEAEAGRSPEVGRSRPSLAGMV KSRL/VLKIQKKKKKKISRAWWHMPV VPATWEAEAGELLEPGKA EVAARRDRA TALPAWGSQADGK*G*GLSAPVAADPSL EPTPALHASRRPEADLQ*PRPPPLRSWG SQVCEVPLGTTPPGSPASQSHPTSPYL PLPGSPARVPCARCSSRPASKRARQSAPC GRAPTPAARGSRRTQRAAQLARSAA RTRTEASAVGTAPAAGRTGRGGPDQOE FVHGLVPLKQDNGRLQCTAQERAPRAR TLRHTARPAAFGVLDLGGNHVLPQC |
| 7634 | 15685 | A | 8270 | 37 | 235 | |
| 7635 | 15686 | A | 8271 | 2 | 230 | |
| 7636 | 15687 | A | 8272 | 516 | 693 | |
| 7637 | 15688 | A | 8273 | 2 | 434 | |
| 7638 | 15689 | A | 8274 | 3 | 417 | RQAWHKAGLHAADWAGRARSLLGDSDH TSWSAGSIPGKHYQAVGLHLWKVEKRR VNLPRVLSMPPVAGTVCHAYDREVHLR CELSPGYLA V PSTFLKDAPGEVLLRVFS TGRVLSAIRAVAKNTTPGAALPAVERG T |
| 7639 | 15690 | A | 8275 | 308 | 614 | HGSHGIALRPRQSQAQPLVHKVCCFQEE QMGAPGKGPCEGSRICLLAQGLGFHL VCLDRV*HLAPHCSLSHGCGPHDVPFL VAKRSFLGLEGPLSSSP |
| 7640 | 15691 | A | 8276 | 11 | 161 | |
| 7641 | 15692 | A | 8277 | 163 | 437 | |
| 7642 | 15693 | A | 8278 | 1 | 660 | |
| 7643 | 15694 | A | 8279 | 2 | 1246 | SCSAPEELCSLRPTLGARRGNCEAKVTG DRAFQICSVDLGAPPM LAARLVCLRTL PSRVFHPAFTKASPVVKN SITKNQWLLT P/SREYAT*T*/RLGIRAWGELGQELKEGS IGNHSMGKNILKFDSGEEWLVA/GGA/ VVGLGSICAYLLALGL/GLN*DLGAI*KR L*FGPQYVK/DRNHSTYMYLAGGVLGLT A/LSAIAIQNRLLFFMELP*WRLLGWIT GVDLWQPWLGAGMLVRSIPYDQSPGPK HLAWLLHSGVMGAVVAPLTILGGPLLR AAWYVTAGIVGGLSVTVA/MCAPSEKFLN MGAPLGSGAGVSFVSSIGI*CFPPPTD/T VAGATLIYSVVA MYGGISSFLSMFLYDT PESKSSRAEVSPMYGVQKYDPINSM LIS IYMDTLNIFMRVATMLATGGNRKK |
| 7644 | 15695 | A | 828 | 241 | 1104 | |
| 7645 | 15696 | A | 8280 | 325 | 432 | |
| 7646 | 15697 | A | 8281 | 1 | 293 | |
| 7647 | 15698 | A | 8282 | 1 | 366 | |
| 7648 | 15699 | A | 8283 | 780 | 891 | |
| 7649 | 15700 | A | 8284 | 44 | 155 | |
| 7650 | 15701 | A | 8285 | 336 | 414 | |
| 7651 | 15702 | A | 8286 | 1 | 294 | KLDTVVEFPPIRGLNMSEFVCNMSARPYV YDLIAVSNHYGAMGVGHYKAAYVLFY QRRDDEFYKTPSLSSSGSSDGGTRPSSSQ QGFGDDEACSM D TN |
| 7652 | 15703 | A | 8287 | 302 | 486 | |
| 7653 | 15704 | A | 8288 | 1 | 620 | |
| 7654 | 15705 | A | 8289 | 1 | 804 | |
| 7655 | 15706 | A | 829 | 95 | 462 | |

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|------|-------|---|------|-----|------|---|
| 7656 | 15707 | A | 8290 | 164 | 399 | |
| 7657 | 15708 | A | 8291 | 1 | 2226 | |
| 7658 | 15709 | A | 8292 | 876 | 1102 | |
| 7659 | 15710 | A | 8293 | 2 | 426 | |
| 7660 | 15711 | A | 8294 | 1 | 128 | |
| 7661 | 15712 | A | 8295 | 33 | 279 | |
| 7662 | 15713 | A | 8296 | 198 | 779 | |
| 7663 | 15714 | A | 8297 | 1 | 441 | |
| 7664 | 15715 | A | 8298 | 132 | 700 | |
| 7665 | 15716 | A | 8299 | 303 | 617 | AKPSSGFECRSRFAFLSKECGKQLGPSSSS ALSLSGSFFHLGAPS*PRTPRKSDGARCR PHPPSSMIGVQLLLGGCLAQHPHRAQL LDADVPTTISIKHVKGQP |
| 7666 | 15717 | A | 83 | 2 | 448 | LHCCPLQLKMVACRAIGILSRFFAFRFLR SRGYICRNFTGSSALLTRTHINYGKGD VAGARVNSTNSKVNTLITELQSQFSQVM NEILSSYQIRRAVLISSEKPGCFIASSDINIL TACMTL*EVSHRSSEAQIIVQKLEMTTLS IVA |
| 7667 | 15718 | A | 830 | 2 | 648 | |
| 7668 | 15719 | A | 8300 | 50 | 257 | |
| 7669 | 15720 | A | 8301 | 110 | 179 | |
| 7670 | 15721 | A | 8302 | 187 | 571 | |
| 7671 | 15722 | A | 8303 | 2 | 150 | |
| 7672 | 15723 | A | 8304 | 227 | 857 | GDSRSRVTRRQDTA WNAWSASHCRRLS ASSRSPLTGPASVGGMAATGANA EKAES HNDPCVRLNPNIAKMKEDILYHFNLT SRH/NFPQALFGDVAKFVCVGGSPSRNEK PSSGCRLGA/ELGLDCPGRDYPNICAGTD RYAMYKVGVPVLSVSHGMGIPSISIMLHE LIKLLYYARCSNVTIIRIGTSGGIGLEPGT VVITEQAVDTCFK |
| 7673 | 15724 | A | 8306 | 1 | 714 | |
| 7674 | 15725 | A | 8307 | 225 | 382 | |
| 7675 | 15726 | A | 8308 | 2 | 862 | FLSVLPHSRALLTPKRAPKKKMAISGVP VLGFFHIAVLMSAQESWAIKEEHVHQAEP YLNPDQSGEFMFDFDGD EIFHVDMAKK ETVWRLEEFGRFASFEAQ GALANIAVDK ANLEJMTKRSNYTPITNVPEVTVLNSP VELREPNVICFIDKFTPPVVNVTLWRNG KPVTTGVSETVFLPRIEDHFFRK FHYLP FALPSTEDVYDCR/VEHWGLDEPLLKH EFDAPSPLAPETTENVV CALGLAVGLVGI IIGTIFHHSRELKSNCRQKRKGGLCKAQ WR |
| 7676 | 15727 | A | 8309 | 2 | 223 | |
| 7677 | 15728 | A | 831 | 90 | 401 | |
| 7678 | 15729 | A | 8310 | 1 | 3252 | MELSVTLVSRAPRGLPVFRQLNTAIAVS QMSSGQCRLAPLIQVIQDCSHLYHYTVK LLFKLHSCLPADTLQGHDRDFHEQFHS RNFFRRASDMLYFKRLIQIPRLPEGPPNF LRASALAEHIKPVVVIPEEAP EDEEPENLI EISTGPPAGEPVVADLFDQTFGPPNGSV KDDRDLQIESLKREVEMLRSELEKIKLEA ORYIAQLKSQVNALEGELEEQRKQKQK ALVDNEQLRHELAQLRAAQLEGERSQ |
| 7679 | 15730 | A | 8311 | 3 | 3253 | |
| 7680 | 15731 | A | 8312 | 1 | 673 | |
| 7681 | 15732 | A | 8313 | 177 | 393 | |
| 7682 | 15733 | A | 8314 | 177 | 400 | |
| 7683 | 15734 | A | 8316 | 1 | 473 | |

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|------|-------|---|------|-----|------|--|
| 7684 | 15735 | B | 8317 | 549 | 602 | MWWNSLDGIRNIVLSNPKKRNTLSLAM LKSLQSDILHDADSNDLKVIIIISAEQPVFS SGHDLKELTEEQGRDYHAEVFQTCISKV MMHIRNHPVPVIAMVNLATAAGCQLV ASCDICRGERQDLFCHSWVPRKVALEM LLTGEPISAEALLHGLLNKGGPEAELOE ETMRJARKIASLSRPGVSLGKATFYKQLP QDLGTDYYLTSQAMVDNLALRDRQEGI TAFLHKRKPVWSHEPV* |
| 7685 | 15736 | A | 8319 | 272 | 364 | |
| 7686 | 15737 | A | 832 | 276 | 488 | |
| 7687 | 15738 | A | 8320 | 1 | 322 | |
| 7688 | 15739 | A | 8321 | 37 | 344 | |
| 7689 | 15740 | A | 8322 | 3 | 412 | |
| 7690 | 15741 | A | 8323 | 37 | 438 | |
| 7691 | 15742 | A | 8324 | 2 | 424 | |
| 7692 | 15743 | A | 8325 | 543 | 848 | |
| 7693 | 15744 | A | 8326 | 2 | 242 | |
| 7694 | 15745 | A | 8327 | 2 | 246 | |
| 7695 | 15746 | A | 8328 | 294 | 402 | |
| 7696 | 15747 | A | 8329 | 259 | 350 | |
| 7697 | 15748 | A | 833 | 186 | 537 | IWFPLRRRKARQEEKSGLGAPRSPSHNY PPGYLGCLGKTINTS*TYILDQSNIGKRV VAILN*ILGGRKLRLEKSLSCQPKVEELYE RVAW/IP*KPGCLLLSVKVRNVFDWCT WVY |
| 7698 | 15749 | A | 8330 | 2 | 409 | RPPPPVSSVPGPRDQLGVTPLSGRHSLL CCWVRIVFPESDGAP*MASFPPRVNEKEI GKLLNLVDHTEVVRDLTFAPDGSLLV SASRDKTLRVWDLKDDGNMMKVLRGH QKLVYSCAFSPDSSMLCSVGASKA |
| 7699 | 15750 | A | 8331 | 453 | 684 | SLRFVLVFCQSLLLGAESSKYDTRETP KAWKESAAPELLGWAHSSGLTCDIKCC RARDLPWSPGPKIHTSVMCPSS |
| 7700 | 15751 | A | 8332 | 1 | 92 | |
| 7701 | 15752 | A | 8333 | 67 | 301 | |
| 7702 | 15753 | A | 8334 | 3 | 276 | |
| 7703 | 15754 | A | 8335 | 1 | 564 | |
| 7704 | 15755 | A | 8336 | 1 | 364 | |
| 7705 | 15756 | A | 8337 | 3 | 103 | |
| 7706 | 15757 | A | 8338 | 1 | 744 | |
| 7707 | 15758 | A | 8339 | 3 | 266 | |
| 7708 | 15759 | C | 834 | 79 | 405 | MIGGTPQMFFISGAKQWSPSLQPPRA HRSSPWAPSSKSTSGGTAALGSLGSKDY FPRTGDGVVELRRSDQRRALPGCPTVL RTLLPQQRGDRDLQQLRHHELRL* |
| 7709 | 15760 | A | 8340 | 481 | 637 | |
| 7710 | 15761 | A | 8341 | 1 | 3335 | LNLFIEIVLCKNLALDINELKPGNLLKD KDRLKNLDEQLSAPKKDVQPEELPPITT TTTSTTPATNTTCTATVPPQPQYSYHDIN VYSLAGLAPHITLNPITPLFQAHPQLKQC VRQAIERAVQELVHPVVDRSIKIAMTTC EQIVRKDFALDSEESRMRIAHHMMRN LTAGMAMITCREPLLSISITNLKNSFAS ALRTASPQREMMDQAAQLAQDNCE LACCFIQKTAVEKAGPEMDKRLATEFEL RK |
| 7711 | 15762 | A | 8342 | 1 | 520 | KMDSTEPPYSQKRYEEIVKEVSTYIKKIG YNPDTVAFVPISGWNGDNMLEPSANMP WFKGWKVTRKDGNASGTTLEALDCIL/ PPTRPTDKPLRLPLQDVYKIGGIGTVPG RVETGVLKPGMVVMHHEALSEALPGD NVGFNVKNVDVKDVRRGNGAGDSTNE PTMEANGFT |
| 7712 | 15763 | A | 8343 | 1 | 443 | |

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|------|-------|---|------|-----|------|---|
| 7713 | 15764 | A | 8344 | 41 | 665 | |
| 7714 | 15765 | A | 8345 | 2 | 394 | ADIERLRMRVMAAAATHASISGWNGD NMLEPSANMPWFKGWKVKTRKDNASG TTLLEALNCGIGTVPVGRVETGVLKPG MEVTFAPGNVTTEVKSVEKHHEALSEAL SGDNAGFNVKNVSVKDVRRGNV |
| 7715 | 15766 | A | 8346 | 1 | 461 | MLLEALDCILPPTRPDKPLHLPLQDVY KIGGIGSVPGVGRVETGVLKPGMVVTFAP VNVTEVKSVEMHHEALSEALPGDNVG FNVKNVSVKDVRRGNVAGDSKNDPPM EAAGRFAVRDMRQTVAVGVIAVDKK AAGAGKVTKSAQKAQKAK |
| 7716 | 15767 | A | 8347 | 1 | 743 | |
| 7717 | 15768 | A | 8348 | 208 | 945 | NWFKGWKVKTRKDNASGTTLLEALDCI LPPTRPDKPLRLPLQDVYKIGGIGTVPV GRLETGVLKPGMVVTFATVNVTEVKS VENHLVAPLDCPRTPFGRTPSTYIKKIG YYPDTLAFEPISGWNGDDMLEPSANMP WFKGWKVKTRKDNASGTTLLEALDCIL PPTRPDKPLRLTIQDVYKIGGIGTVPV RVETGVLKPGMVVTFAPVNGTT*VKS AMHHEALSEAHSVNDVGNVKNV |
| 7718 | 15769 | A | 8349 | 1 | 1434 | RGTIDISLWKFETSKYYVTIAPGHRDF JKNMITGTSQADCAVLIVAAGVGEFEAGI SKNGQTREHALLAYTLGVKQLVGVNK MDSTEPYSQKRYEEIVKEVSTYIKKIGY NPDTVAFVPISGWNGDNMLEPSANMPW FKGWKVKTRKDNASGTTLLEALDCILP TRPTDKPLRLPLQDVYKIGGIGTVPVGR VETGV/LFVPISGWNGDNMLEPRANMP WFKGWKVKTRKDNASGTTLLEALDCILP PTRPTDKPLRLPLQDVYKIGGIGTGPVGR LETGVLKPGMVVTFAPGNVTTEVKS VETLHEALSEAFPGDNVGNVKNVSVKDV RHNAGDSKNDPPMEAGFTAQVILNH PGQISTGYAPVLDCHTAHACKFAELKE KIDHRSGKKLEDGPKFLKSVDAAIVDMV PGKPMCYESFSDYPSLGCFAVRDMRQIV TVGVIAVDKKTAGAGKVTKSAQKAQK AK |
| 7719 | 15770 | A | 835 | 1 | 321 | |
| 7720 | 15771 | A | 8350 | 1 | 1254 | |
| 7721 | 15772 | A | 8351 | 1 | 1195 | |
| 7722 | 15773 | A | 8352 | 1 | 2471 | MGKEKTHINIVVIGHVDSGKSTTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFKYA WVLDKKAERERGITIDISLWKFETSKY YVTIAPGHRDFIKNMITGTSQADCAVL IVAAGVGEFEAGISKNGQTREHALLAYT LGVKQLVGVNKMDSTEPYSQKRYEE MWLREVSTYIKKIGYNPDTVAFVPISGW NGDNMLEPSANMPWFKGWKVKTRKDG NASATTLEALDCILPPTRPDKPLRLPL QDVYKIGGIGTDPAGRVKTGVLKPGMV/ VAPFAPVNGTTEVKSVEMHHEALSE/AL LLGDKGAFNVKNVSVKDVRRGNVAGD SKNDPPMEASGFTAQVILNHPQSQKNAR HMPLELDCHTAHACKFAELKEIDRRS GKKLEDGPKFLKSGDAAIVDMVPGKPM CVESFSDYPPGRFAVRDMRQTVAVGVI KAVDKKAAGAGKVTKSAQKAQKAK |
| 7723 | 15774 | A | 8353 | 184 | 819 | ETEIKMASRGKTETSKLKNLEEQLDRL MQQLQDLEECREELDTDEYEETKETLE QLSEFNDLKKIMSGNMTLVDELSGMQL AIQAASQAFKTPKVIRLCGKK/HHPVQL RPR*AEMDRDLMVGKLERDLYTQKVE ILTALRKLGEKLTADDEAFSANAGAILS QFEKVSTDLGRPPSYMNYLLDSHPSKNI DVPSKISFLKIQDL |

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| 7724 | 15775 | A | 8354 | 1 | 387 | |
| 7725 | 15776 | A | 8355 | 3 | 1022 | FLASLQWVQTSSFSSEKFVITDLLKPTSV NLSKSFVQLCSIAAGSLRPTPEIQEVKTP EELETFMLKHGENIIDTLGAEVDRLKEL KSGSLVPCIPAAVTKRGQGTAPAIASV GGSPKPWQLPRGVGPVGAQKSRTEVWK SLPRFQRMYGKHLDAQNDRSTDLSHSAP GKATDTQCQPLKAAKSGLYPAELKRWS CPWLWEPTFCISVTWSDLEQLRKIRRRSP HEDTESFTVYLRSDVEAKSLEVWGSPEA LAREKKLRKEAEIEYREKGSINSATLI/EF SRYLSDTRY/RTRSCAWCLKCICKIIPSTM ANSCSPNTCSLCLLYSSPALPWLKFA |
| 7726 | 15777 | A | 8356 | 4 | 516 | |
| 7727 | 15778 | A | 8357 | 1 | 248 | |
| 7728 | 15779 | A | 8358 | 3 | 4135 | |
| 7729 | 15780 | A | 8359 | 2 | 417 | |
| 7730 | 15781 | A | 836 | 101 | 290 | |
| 7731 | 15782 | A | 8360 | 43 | 239 | |
| 7732 | 15783 | C | 8361 | 141 | 356 | MSFDCGFGTLP LLLSPICCLGSYSNKVISP GLXXXXXXXXXXGGALLKDPWGGPIFP GGGKKFFFLFGGGF* |
| 7733 | 15784 | C | 8362 | 22 | 159 | MRGVFPLFPLKXXXXPKGLKIXXXGPI MSPPQKKVPFQKSQGGF* |
| 7734 | 15785 | A | 8363 | 64 | 240 | TLKFWKEGGPPISPQKKGPFKIPRGGL *GPPKKKKNFSPPPVKLGPPKGIFKRAP P |
| 7735 | 15786 | A | 8364 | 19 | 471 | |
| 7736 | 15787 | A | 8365 | 3 | 399 | |
| 7737 | 15788 | A | 8366 | 186 | 840 | |
| 7738 | 15789 | A | 8367 | 7 | 633 | PTITNVWSETSQELADGLRRGSQGDSDVQ QNGPPRKHIVERYTEFYHVPTHSDASKK RLIEDTEDWRPRTGTTQSRFRILAQITGT EHLKESEADNTEKANNSQEPSQLASSV ASTRSMPELSDSPTSGRPVTSLTAAAF KPVGSTGVKSPSWQRPNQGVSTGRISN SAAYSGSVAPANSALGQTQPSDQDTLVQ R*PTITNVWSETSQELADGLRRGSQGDS VQQNGPPRKHIVERYTEFYHVPTHSDAS KKRLIEDTEDWRPRTGTTQSRFRILAQI TGTEHLKESEADNTEKANNSQEPSQLA SSVASTRSMPELSDSPTSGRPVTSLTAA AAFKPVGSTGVKSPSWQRPNQGVSTG RISNSAAYSGSVAPANSALGQTQPSDQD TLVQRAEHIPAGN |
| 7739 | 15790 | C | 8368 | 78 | 386 | MTHLEAQNKIKGCTGSLNMTLQRASAA PKPEPGSCSKAHSHQVRDFSGASRG REEDPRVTNTQNGKIPPKRPPKPHCG ALYRVLSCTHFTVMPARRD* |
| 7740 | 15791 | A | 8369 | 20 | 442 | |
| 7741 | 15792 | A | 837 | 21 | 215 | |
| 7742 | 15793 | A | 8370 | 49 | 354 | |
| 7743 | 15794 | A | 8371 | 239 | 401 | |
| 7744 | 15795 | A | 8372 | 141 | 351 | |
| 7745 | 15796 | A | 8373 | 239 | 474 | MRMVTWWRGVFLATSPSPPRPSQLEKQ YTALYRKATSPN*FAPNCYPDPQPHLG* LAPVAHVPL*QRRKAESPSSN |
| 7746 | 15797 | A | 8374 | 1 | 740 | MVSDIRKEDGMNVLPLKYPNVGVNFSF AGVYLASETLPGSAHPEATSRGAVATG TTHLASAVEPNGDSWCKQSRPRSVHYI RINITGWVCTCCDIERNIMLSPLNIRNNI TARLRPKTGTQMPLREQRYTGIDENAHV VERRVF/RVPALHLRRPSQLEKQYIALYR KATSPN*FAPNCYPDPQPHLDRLAPVAH FPL*Q*RKAESPPSSN*VARGTCTS*LSKP RTVWKDPVARNRPPVGPT |

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| 7747 | 15798 | A | 8375 | 803 | 985 | |
| 7748 | 15799 | A | 8376 | 1 | 319 | |
| 7749 | 15800 | A | 8377 | 339 | 808 | GSQSQGGNRGWFSVPASRGVPPPAVMG VLRARGGRGAGSQSPPPGCLPPMRWG SGATRSGLWWETSDGLEPTPSRRWWG SS*TL/GGSPVQVY*LVTPDSGSSH*KANS FCLSGDNLIGKKASFRSKQVNLSSAGS KPNNVDDLGTGCKVSVSA |
| 7750 | 15801 | A | 8378 | 588 | 2278 | GWAHGGEACFCVPALHLCRPSOLEKQY PVLY*KATSSN*FAPNYYPDP*PHLG*LP PW |
| 7751 | 15802 | A | 8379 | 779 | 986 | ELQLYWLCKKPPIDIRSHWKSC*AGISTS RLCQLPKR*GSGVLPADSMMRGKVS SAWHRSLWSSPL |
| 7752 | 15803 | A | 838 | 158 | 955 | KMTSSSEQEEDEKNNQSATPRQTGPATT MNSKGQYPTQPTYPVQPPGNPVYPTLH LPQAPPYTDAPPAYSELYRPSFVHPGAA TVPTMSAAFPVASLYLPMASVAVGPL VSTIPMAYYPVGPIYPPGSTVLGGKGG YDAGARFGAGATAGNIPPPPG\CPNAA QLAVMQGANVLVTQIRKGNFFMGGSDG GYTHLVRNQGHLCAREKTSHTLQHSQ CNCFSHINLKLQFRHMLLGLSGAQTFR HFSNLIRNHVMVAVPP |
| 7753 | 15804 | A | 8380 | 179 | 795 | PAFFLIPGCAPPVG**IPSNVPAVGRSDFF SWTPYTHSPPDAGVEHPPWRTRLPWG VPAKGHQRGTGATRS LGFWWDTSGGLEP TPPRRWGSS*TLLEARSKCTE**HLTPD LPTERQTASGSQGRIC*RKHLS/WSKQV KQLSSAGSNPSNVYGLG/DCWM*SHCSL LNQAQILSRPVVGLRLGNRQEGSVPW LTRNYHSKGS |
| 7754 | 15805 | A | 8381 | 1 | 1029 | |
| 7755 | 15806 | A | 8382 | 989 | 2798 | |
| 7756 | 15807 | A | 8383 | 2 | 396 | |
| 7757 | 15808 | A | 8384 | 3 | 1773 | PGGRQQQAEGIMVQYELWAALPGASGV ALACCFVAAAVALRWSGRRRTARGAVV RARQKQRAGLENMDRAAQRFRQNPDL DSEALLALPLPQLVQKLHSRELAPEAVL FTYVGKAWEVNKGTCNVTSYLADCETQ LSQAPRQGLLYGVPVSLKECFTYKQDS TLGLSLNEGVPACDSVVVHVLKQGA VPFVHTNVPQSMFSDCSNPLFGQTVNP WKSSKSPGGSSGEGALIGSGGSPLGLG TDIGGSIRFPSSFCGICGLKPTGNRLSKSG LKGCYVQGEAVRLSVGPMARDVESLAL CLRALLCEDMFRLDPTVPPLPFREEVYTS SQPLRVGYETDNYTMPSPAMRRVLE TKQSLEAAGHTLVFPLPSNIPHALETST GGLFSDGGHTFLQNFKGDFVDPCLGDLV SILKLPQWLKGLLAFLVKPLLPRLSAFLS NMKSRSAGKLWELQHEIEVYRKTIVIAQ WRALDLDVVLTPMLAPALDINAPGRAT GAVSYTMLYNCLDFPAGVVPVTVTAE DEAQMEHYRGYFGDIWDKMLQKGMKK SVGLPVAVQCVALPWQEEVCLRFMREV ERLMTPEKQSS |
| 7758 | 15809 | A | 8385 | 660 | 772 | |
| 7759 | 15810 | A | 8386 | 27 | 372 | |
| 7760 | 15811 | A | 8387 | 685 | 769 | |
| 7761 | 15812 | A | 8388 | 305 | 425 | |
| 7762 | 15813 | A | 8389 | 308 | 410 | |
| 7763 | 15814 | A | 839 | 217 | 491 | |
| 7764 | 15815 | A | 8390 | 3 | 501 | |
| 7765 | 15816 | A | 8391 | 4 | 318 | |
| 7766 | 15817 | C | 8392 | 340 | 474 | |

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|------|-------|---|------|------|-------|---|
| 7767 | 15818 | B | 8393 | 317 | 702 | LAEWRPREPMQRKLVKVTSLPGTVVITE QAVDTCFKAEFEQIVLGKRVIRKTDLNK KLVQELLCSAELSEFTTVVGNMCTLD FYEQGGRLDGALCSYTEKDKQAYLEAA YAAGVRNIEMESSVFAAJ* |
| 7768 | 15819 | A | 8394 | 209 | 581 | |
| 7769 | 15820 | A | 8395 | 227 | 1302 | GDSRSRVTRRQDTAWNAWSASHCRRLS ASSRSPLTGPASVGGMAATGANAES HNDCPVRLNPNIAKMKEDILYHFNLT SRHNFTLFWFKFGLFGGNPSRMKPF RCLGPEIGLDCPVRDYPNICAGTDYAM YKVGTVLSVSHGMGIPSIIMLHELKLL YYARCSNVTHIRIGTSGGIGLEPGTVVITE QAVDTCFKAEFKQIVLGKRVIRKTDL NKKLVQELLVSAELSEFT/TTVVGNM CTLDFYEGQGRLDGALCSYTEKDKQA YLEAAVAAARVPQLFEMESSVFAAMCS ACGLQAAVVCVTLNRLEGDQISSPARN VLSEYQQRQPQLVSYFIKKLSKA |
| 7770 | 15821 | A | 8396 | 3 | 337 | |
| 7771 | 15822 | A | 8397 | 2 | 375 | NHEKDDNSLKIIISNASCTTNWLTPLAKGI HDNFGIVEGLMTTVHAITATQKTGDGPS GNWGVMAAGLSKTSSLPLLG/LGKAGG KVIPELNGKLTGMAFRVPTGNVAGVDLT CRLKKPGKYDDIK |
| 7772 | 15823 | A | 8398 | 3 | 1141 | IRHEVRQSAASSFASPAEHRSDTMGKV KVGTVNGFRIGRLVTRAAFNSGKVDIVA INDPFIDLNYMVYMFQYDSTHGKFGT VKAENGKLVNNGNPITIFQEPKIPSKIV GGDAGRLKYVVEFHAVFTTMEKGLG ASFRCGGAKRVNQSLPPSG*CPFCFHHG V*TIKDYDNSLKIIISNASCTTNCLTPLA KVIHDNFGVVEGLMTTVHAITATQKT GWALPGNCGVMGPRGSSRTSSLPLAA AKAVGKVNPLSLNGEAHLGMGFRVFN ANVSVDLTCRLEKPAKYDDIKVVK QASEGPLKILGYTEHQVSSDFNSDTH SSTFDAGAGIALNDHF/VSRLISWYDNEF GYSNRVVDLMAHMASKE |
| 7773 | 15824 | A | 8399 | 1 | 374 | |
| 7774 | 15825 | A | 84 | 247 | 287 | KRGFVLPPGLECGGPIWVNGR/LRLGLP PFSGLSFGSWDYGGPPGRVKIWHFLE KRGFRGVARVGSTLLTGEPPVLGF*KPPF F |
| 7775 | 15826 | A | 840 | 1789 | 2411 | KTYWRKKVEKVVVSNRLVTSPCCIVTS TYGWTANMGENH*KLQALKETTSTMG/ YYMASQRKHRGIKPLTSLIIEYLKAKRPE GLIRTDKSIVKDLVILLYETALLSSGFQS WKIPRHA*QVSYRMIKLAGLIDEDGPY LLDDTSAAVNLKELPPLEGDDDTFTHG KEVGLILLGLRGWTLPVSVLYNSSDNIF QGCFPLFLVNI |
| 7776 | 15827 | A | 8400 | 127 | 420 | |
| 7777 | 15828 | A | 8401 | 3 | 509 | KNRIKKISNLENLKSOLDVLDLHGNQITKI ENINHLCELRLVNLARNFLSHVDNLNGL DSLTELNLRHQITFVRDNDLPCLOHL FLSFNNISSFDSVCLADSSSLSDITFDGN PIAQESWYKHTVLQNMMLRH*DMEGE FTGRRKGVWHLF*PKKGKRKEPGKS |
| 7778 | 15829 | A | 8402 | 2 | 384 | |
| 7779 | 15830 | A | 8403 | 1 | 430 | ERVGNVCSLEISNIQKGEGGEYMCHAVN IIEGAKSFANVDIMPOEERVVALPPPEFC RSKYGFKGGRRQRTKN*FRUFEMPPRFI MPICDFKIPENSDAVFKCSVIGIPTPEVK WYKEYMCIEPDNIKYVISEEKGSHTLIIR |
| 7780 | 15831 | A | 8404 | 1 | 12064 | |
| 7781 | 15832 | A | 8405 | 2 | 383 | |
| 7782 | 15833 | A | 8406 | 1 | 1677 | |

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|------|-------|---|------|-----|------|---|
| 7783 | 15834 | A | 8407 | 2 | 2580 | GQKKLVILNKSDLVPKENLESWLNLYLK KELPTVVFRATKPKDKGKITKRVKAKK NAAPFRSEVCFGKEGLWKLLGGFQETCS KAIRVGVI GFNPVVGKSSINSLKQEQMC NVGVHGGGLQGSQVVPDLKQITIDISP SFIVSPLNSSALALRSPASNEVVKPMEA ASAILFOADVRQVVLYKTVPLQGLW EFFTMLAQRKEVWHQKGGUPKCLEGA AKLLWSEWTGASLAYYCHPPTSWTPPP YFNESIVVDMKSGFNLEELEKNNAQSIR GENCVSLLSSADRPVELLPVYMGLLSFP AIKGPHLANSILFQSSGLTNGIEEKDIHE ELPKRKERKQEEREDDKSDHETVDEEV DKKLD SMGSKRRRATSPSSVSGDFDDG HHSVSTPGPSRKRRLSNLPTVDPIAVCH ELYNTIRDYKDEQGRLLCELFIRAPKRRT DSEIYEDAVELQQFFIKIRDELCKNGEILL SPALSYTTKHLHNDVEKERKEKLPKEIEE DKLKREEEKRVEGHIQLHYCTNPDSKPK YPAQRTPOIHLQGEVLFYESKFRTLEEVT VVLDTIISINQPDYEVVSQPIDLMKIQ QKLKMEYDDVNLTTADFQLLFNNAKS YYKPDSPEYKAACKLWDLYLRTRNEFV QKGEADDEDDDEDGQDNQGTVTEGLLK ISITQKIRPVVILFHYGESWNLRLADQRLI FAKSWPRASRYQQGHQDLFILRSDLP SQ VFIRDKLMERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAADGVTFSPVPTP HTFRHSYAMHMLYAGIPLKVLQSLMGH KSSISTEVYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS |
| 7784 | 15835 | A | 8408 | 2 | 259 | |
| 7785 | 15836 | A | 8409 | 1 | 257 | |
| 7786 | 15837 | A | 841 | 225 | 336 | |
| 7787 | 15838 | A | 8410 | 3 | 365 | |
| 7788 | 15839 | A | 8411 | 2 | 243 | |
| 7789 | 15840 | A | 8412 | 2 | 339 | |
| 7790 | 15841 | A | 8413 | 2 | 182 | |
| 7791 | 15842 | A | 8414 | 2 | 381 | |
| 7792 | 15843 | A | 8415 | 59 | 572 | SGRPFFFFFSATGACLFPPGPGR LGAEY RQRHWGTWVWHGLELGR LGSNREGCA RACRDW SHPPRTERGPSGHGITSARLG TGTGERLRSGCVQGLVGMGRPVDRA C* SVLEPGGTPGRANWALDVEKLG NKY*E NKSLWVSRP/RQRCDRCRDPWERPRLQ VTPIARQ |
| 7793 | 15844 | A | 8416 | 3 | 1735 | |
| 7794 | 15845 | A | 8417 | 2 | 441 | |
| 7795 | 15846 | A | 8418 | 412 | 569 | |
| 7796 | 15847 | A | 8419 | 2 | 2812 | RGLAVFISDIRNCKSKEAEIKRINKELANI RSKFKGDKALDGYSKKKYVCKLLFIFLL GHDIDFGHMEAVNLLSSNRYTEKQIGYL FISVLVNSNSELIRLNNNAIKNDLASRNPT FMGLALHCIA SVGSREMAEAFAGEIPKV LVAGDTMDSVKQSAALCLRLYRTSPD LVPMGDWTSRVVHLLNDQHLGVVTA A TSLITTLAQKNPEEFKTSVSLAVSRLSRIV TSASTDLQDYTYFVPAPWLSVKLLRL L |
| 7797 | 15848 | A | 842 | 610 | 834 | |
| 7798 | 15849 | A | 8420 | 2 | 397 | |
| 7799 | 15850 | A | 8421 | 3 | 438 | |
| 7800 | 15851 | A | 8422 | 3 | 354 | |
| 7801 | 15852 | A | 8423 | 3 | 339 | |
| 7802 | 15853 | A | 8424 | 1 | 338 | |
| 7803 | 15854 | A | 8425 | 1 | 70 | |
| 7804 | 15855 | A | 8426 | 62 | 374 | |

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|------|-------|---|------|-----|------|---|
| 7805 | 15856 | A | 8427 | 2 | 374 | |
| 7806 | 15857 | A | 8429 | 1 | 342 | |
| 7807 | 15858 | A | 843 | 36 | 351 | |
| 7808 | 15859 | B | 8430 | 212 | 587 | MGKGSFKYAWVLDKLIKADRERGITIDIS LGKFETSKYYVTIIDAPGHRDFIKNMITG TSQADCAVLIVAAGVGEFEAGISKNGQT REHALLAYTLGVKQLIGGVTKMDSTEPP FRRKRYEEIVKGX* |
| 7809 | 15860 | A | 8431 | 1 | 1386 | |
| 7810 | 15861 | A | 8432 | 66 | 1574 | KLTPKPKWESVKTHINLAVIGHVDSG KS\TTTGHLYKCGGIDTKNHLKNLTKEA AEMGKGSFKYAWVLDKLIKAEERERGITI DISLWKFETSKYYVTIIDAPGHRDFIKN MITGTSQA*PGLGGFLFGG/CSPLIVAAG VGEFEAGISKNGQVREHALLAYTLGVK QLIVGC*QKWDSTPTPTAQKKILKEIV K/EKVSTFH*RKFGYNPDTVAFVVPNLV WN\GDNMLGAQVPNMPWFQGDGKVTR KD\GNASGTTLLWRALDCILPPTPTDQ APLR\LPFQ\DVLPKIGGYLGTWFLVWPE WETGVL/RNPGMGVTFAPVNVTTVEVKS VEMHHEALSEALPGDNVGFNVKNVSV KDVRGNAVAGDSKNDPPMEAAGFTAQ VIILNHPGQISAGYAPVLDCHTAHIACKF AELKEIDRRSGKKLEDGPKFLKSGDAA IVDMVPGKPMCVESFSDYPPLGRFAVRD MRQTVAVGVKAVDKKAAGAGKVTKS AQKAQKAK |
| 7811 | 15862 | A | 8433 | 2 | 265 | |
| 7812 | 15863 | A | 8434 | 3 | 318 | |
| 7813 | 15864 | A | 8435 | 2 | 896 | VGPRGMWRAGSMSAELGVGCALRAVN ERVQQA\VARRP/RGDLPAIQPRLVA\AVSK TKPADMVIEAYGHGQRTFGENYVQEL LEKAS\NPKILSLCPEIKWHF\IGHLQKQN VNKLMAV\PNLFML\ETV\DSVKL\ADKV NSSWQQRK\GSPERLKVMGPGFNTSREEI YLFVS\SLLEGKHGLPPSETIAIVEHINAK CP\NLAEFVGL\MTLGSFGHDL\SQGPND FQLLS\SLPEETVVKS*RIPADQVELSMGL SADMQHAVEVRSTDVWIRSTVFGEPTY SKKPTPDKCAADV\KAPLEVAQEH |
| 7814 | 15865 | A | 8436 | 202 | 349 | |
| 7815 | 15866 | A | 8437 | 1 | 129 | |
| 7816 | 15867 | A | 8438 | 3 | 387 | |
| 7817 | 15868 | A | 8439 | 505 | 693 | |
| 7818 | 15869 | A | 844 | 3 | 259 | |
| 7819 | 15870 | A | 8440 | 46 | 3454 | AGESIMDTDLYDEFGNYIGPELDSDEDD DELGRETKDLDEMDDDDDDDDVDGHD DDHPGMEVVLHEDKKYPTAEVYGP VETIVQEEDTQPLTEPIIKPVKTKKFTLME QTLPTVYEMDFLADLMDNSELIRNVTL CGHLHHGKTCFVDCLIEQTHPEIRKRYD QDLCYTDILFTEQERGVIKSTPVTVVLP DTKGKSYLFNIMDTPGHVNFSDVETAGL RISDGVVLFIDAAEGVMLNTERLIKHAV QER |
| 7820 | 15871 | A | 8441 | 2 | 639 | |
| 7821 | 15872 | A | 8442 | 60 | 345 | |
| 7822 | 15873 | B | 8443 | 26 | 384 | MHHEALSEALPGDNVGFNVKNVSVKDV RRGNVAGDSKNDPPMEAAGFTAQVIILN HPGQISAGYALYWIAIVDMVPGKPMCV ESFSDYPPLGRFAVRDMRQTVAVGVKA VDKKAAGLAS* |

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| 7823 | 15874 | A | 8444 | 33 | 99 | KLPLKAKMGKEKTHINIVVIGHVDSGKS TTTGHLYKCGGIDKRTIEKFEKEAAEMG KGSFKYAWVLDKLKAERERGITIDISLW KFETSKYYVTIIDAPGHRDFIKNMITGTS QADCAVLIVAAGVGEFEAGISKNGQTR EHALLAYTLGVKQLIVGVNKMDSPEPPY SQKRYEEIVKEVSTYIKKIGYNPDVAFV PISGWNGDNMLELACSNMPWFKGMKIV TRKDGNASGTTLLLEALDCILPPTPTDK PLRLPLQDVYKIGGIGTVPVGRVETGVL KPGMVVTFAPVNVTEVKSVEMHHEA LSEALPGDNVGFNVKKCVVSRMFRRGN VAGDSKNDPPMEAAGFTAQVILNHPAS QKNARHMPLELDCHTAHIACKFA*A*RK RFDRRSGKKLIEDGP*NSLKSG*CWPLV DMVPWASPMCV*EASQDYPPLGRFWPF RYMRQTALRLGVNQQLDKKIAAGVAG KVHQSLAQKA*KPKWERKRLISTLSSLD T |
| 7824 | 15875 | A | 8445 | 2 | 442 | |
| 7825 | 15876 | A | 8446 | 76 | 413 | |
| 7826 | 15877 | A | 8447 | 524 | 954 | |
| 7827 | 15878 | A | 8448 | 3 | 206 | |
| 7828 | 15879 | A | 8449 | 3 | 206 | |
| 7829 | 15880 | A | 845 | 3 | 661 | |
| 7830 | 15881 | A | 8450 | 3 | 327 | |
| 7831 | 15882 | A | 8451 | 56 | 324 | |
| 7832 | 15883 | A | 8452 | 33 | 159 | |
| 7833 | 15884 | A | 8453 | 2 | 494 | |
| 7834 | 15885 | A | 8454 | 130 | 716 | LFARLPEAIPWRQKKESSAQIRLEPPSRA QGETGFSWLGPDTTHSRFWWWLGL/CG EGWAGIPLCFFSPRKYNTPITRDFLGPPL TGQGNKKTNRSSQTLPIEKPLSL*KL PSLRERE*LFIGLGVRAPSGSLISGLGA QACPQ/GLPCLCLYPCLRGPGQDFPNQPR POHPPSPQKPPSSFPHGYSVESLF |
| 7835 | 15886 | A | 8455 | 1 | 578 | GGRSVLPVDPVRVSRHFMTHGNTGLSAG LDASAQTTSHELTIPNDLIGCIIGRQGAKI NEIRQMSGAIKIANPVEGSTDRQVTTIG SAASISLAQYLINVLENAPSSQAASVTI PDHLSINLSQPSTPSSSFSTTTPLATAG TSDAPSSLPNPSSDRPLCLQSAWHETHPF PGSPPPRLLLPATPPL |
| 7836 | 15887 | A | 8456 | 2 | 875 | IITLAGPTNAIFKAFAMIIDKLEEDISSM TNSTAASRPPVTLRLVVPASQICGSLIGK GGCKIKEYTREYRGFRSKVAGDMLPNLT ERAVTIAGIPQSIIECVKQICVVMLETLSQ SPPKGVTPYRKPVSPPVILQGGQPYTI QGQYAIQPDCLKHLQAMQQSHFPM HGNTGIQWHLNPASPRGSKAYWAGLAD ASAQTSSWNSPFPNGFDWAGIIGAFKG AKIWEIRQMSGAIKIANPVEGSTDRQ VTITGSAASISPGVNIHNVRLSSETGGM GSS |
| 7837 | 15888 | A | 8457 | 3 | 376 | HSSGLGGGVMLVHDIRRNESHLDIFRE SAPGALREETLQRSWETKPGLLVGVP MVKGLHEAHQLYGRLPWSQVLAFAAA VAQDGFNVTHDLARALAEQLPPNMSE FRETFLPFGVRPLPGS |
| 7838 | 15889 | A | 8458 | 1 | 1965 | |
| 7839 | 15890 | A | 8459 | 4 | 267 | |
| 7840 | 15891 | A | 846 | 33 | 382 | |
| 7841 | 15892 | A | 8460 | 10 | 464 | TGPVAMGRVIRGQRKGAGSVFRAHVKH RKGAARLRAVDFAERHGYIKGIVKDIH DPGRGAPLAKVVFRDPYRFRKRTFLIA AEGIHTGQFVYCGKKAQLNIGNVLPVGT MPEGTIVCAPVISKKVISSANRAVVGVA GCGRIRKRVK |

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| | | | | | | GGGRIDKPILKA |
| 7842 | 15893 | A | 8461 | 5 | 807 | TGPVAMGRVIRGQRKGAGSVFRAHVKH RKGAARLRAVDFAERHGYIKGIVKDIH DPGRGAPLAKVVFRDPYRFFKRTELFIA AEGIHGTQGFVYCGKKAQLNIGNVLPVGT MPEGTIVCCLGGEAWKTRGKLARASGN YATVISHNPETKKTRVKLPSGSKKVISS ANRAVVGVVAGGWPELTNP SLKAGRA YHKYKAK/RQRNCWP/RIRGIVAMNPVE HTFGGGQ/HPQHASPPTIRRDAP/AGRKV GLIAARRTGRLRGTKTVQEKEN |
| 7843 | 15894 | A | 8462 | 11 | 349 | |
| 7844 | 15895 | A | 8463 | 305 | 676 | RSKSDSAADLPSRRARLSGTGEKASENK GDPVHL*ADGGFVPLEDSL CM*FPAWAS SPSAALSIGLTVQVAGLQGLPWAPWVVP LGSTGRRSSGELEESEAGYLSTSTDGLL GSFKEGCSSC |
| 7845 | 15896 | A | 8464 | 352 | 784 | |
| 7846 | 15897 | A | 8465 | 3 | 381 | |
| 7847 | 15898 | A | 8466 | 1 | 233 | |
| 7848 | 15899 | A | 8467 | 3 | 356 | |
| 7849 | 15900 | A | 8468 | 2 | 374 | |
| 7850 | 15901 | A | 8469 | 2 | 482 | KFQNALLVRYTKKVPQVSTPTLVEVSRN LGKVGSKCKKHPEAKRMPCAEDYLSVV LNQLCVLHEKTPVSDRVTKCTESLVNR RPCFSALEVDETYVPKEFNAETFTFHVK HKPKATKEQLKAVMDDFAAFVEKCKKA DDKETCFAEEGKKLVAASQAAL |
| 7851 | 15902 | A | 847 | 21 | 371 | APSPDAMGHFTEEDKATITSLWGKVNVE DAGGETLGRLLVVYPWTQRFDSFGNLS SASAIMGNPKVKA/HPENFKLLGNVLVT VLAHFGKEFTPEVQASWQKMTGVAS ALSSRYH |
| 7852 | 15903 | A | 8470 | 2 | 435 | |
| 7853 | 15904 | B | 8471 | 73 | 384 | MFLYEYARRHPDYSVVLRLAKTYETT LEKCCAAADPHECYAKVFDEFKLLVEEP QNLIKQAWRVQIPECAISSLHQESTPSVN SNSCRGLKKPRKSGQQML* |
| 7854 | 15905 | C | 8472 | 11 | 475 | |
| 7855 | 15906 | A | 8473 | 1 | 608 | |
| 7856 | 15907 | A | 8474 | 1 | 593 | AKYICENQDISSKLKECCEKPLEKSHC IAEVENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDYSVV LLRLAKTYETTLEKCCAAADPHECYAK VFDEFKPLVEEPQNLIKQNCLEFEQLGEY KFQNALLVRYTKKVPQVSTPTLVEVSRN LGKVGSKCKKHPEAKRMPCAEDYLSRG PRTSRMFAKTMLRQRMSSWAC/CLYEY ARRHPDYSVVLRLAKTYETTLEKCCA AADPHECYAKVFDEFKPLVEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKKVPQ VSTPTLVEVSRNLGKVGSKCKKHPEAKR MPCAEDYLSRGP |

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| 7857 | 15908 | A | 8475 | 1 | 1428 | MKWVTFISLLFLFSSAYSRGVFRDRAHK SEVAHRFKDLGEENFKALVLIFAQYLQ QCPFEDHVKL VNEVTEFAKTCVADES NCDKSLHTLFGDKLCTVATLRETYGEM ADCCAKQEPERNECFLQHKDDNPNLRL VRPEVDVMCTAFHDNEETFLKKYLYEIA RRHPYFYAPELLFAKRYKAAFTECCQA ADKAACLLPKLDELDEGKASSAKQRL KCSLQKFGERAFAWAVARLSQRFPK AEFAEVSKLVTDLT KVHTECCHGDLLEC ADDRADLAKYICENQDSISSKLKECCEK PLEKSHCIAE/HRNLGKVGSKCKHPEA KRMPCAEDYLSVVLNQLCVLHEKTPVS DRVTCKCTESLVNRRPCFSALEVDETYV PKEFNAETFTFHADICTLSEKERQIKKQT ALVELVKHKPKATKEQLKAVMDDFAAF VEKCKADDKETCFAEKGKLVAAASQA ALGL |
| 7858 | 15909 | A | 8476 | 1 | 748 | |
| 7859 | 15910 | A | 8477 | 1 | 1515 | |
| 7860 | 15911 | A | 8478 | 1 | 2931 | MKWVTFISLLFLFSSAYSRGVFRTPGLP ASSLPQSFLKCLEQVRKIQGDGAALQE KLCATYKLCHEPELVLLGHSLGIPWAPL SSCPSQALQLAGCLSQLHSGFLYQGLL QALEGISPELGPTLDTLQLDVADFATTIW QQMEELGMAPALQPTQGAMPAFASAFQ RRAGGVLVASHLQSFLEVSYRVLRLHA QPGGGGDAHKSEVAHRFKDLGEENFKA LVLIFAQYLQ QCPFEDHVKL VNEVTEF AKTC |
| 7861 | 15912 | B | 8479 | 1 | 6124 | MKWVTFISLLFLFSSAYSRGVFRDRAHK SEVAHRFKDLGEENFKALVLIFAQYLQ QCPFEDHVKL VNEVTEFAKTCVADES NCDKSLHTLFGDKLCTVATLRETYGEM ADCCAKQEPGRNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNEETFLKKYLYEIA ARRHPYFYAPELLFAKRYKAAFTECCQ AADKAACLLPKLDELDEGKASSAKQRL LKCSLQKFGERAFAWAVARLSQRFP KAEFAEV |
| 7862 | 15913 | A | 848 | 24 | 474 | |
| 7863 | 15914 | A | 8480 | 241 | 348 | |
| 7864 | 15915 | A | 8481 | 2 | 191 | |
| 7865 | 15916 | A | 8482 | 3 | 370 | |
| 7866 | 15917 | A | 8483 | 1 | 351 | |
| 7867 | 15918 | A | 8484 | 44 | 454 | |
| 7868 | 15919 | A | 8485 | 200 | 408 | |
| 7869 | 15920 | A | 8486 | 1 | 110 | |
| 7870 | 15921 | A | 8487 | 48 | 462 | |
| 7871 | 15922 | A | 8488 | 1 | 721 | MHWGVGFASSRPCVVDLSWNQSIFFG WWAGSEEPFSFYGDIIAFPLQDYGGIMA GLGSDPWWKTLTYLTGGALLAAAAAYLL HELLVIRKQEQEIDSKDAIHLHQFARPNNG VPSLSPFCLKMETYLRLMADLPYQNYFGG KLSAQGKMPWIEYNHEKVSGTEFIIDFLE EKLGVNLNKNLGPHERAISRAVTKMVEE HFYALSWRWYHPVPTCLQKFLQFVRQ LMLFMRTSPSALPGH |
| 7872 | 15923 | A | 8489 | 3 | 785 | |
| 7873 | 15924 | A | 849 | 24 | 415 | |
| 7874 | 15925 | A | 8490 | 5 | 302 | |
| 7875 | 15926 | A | 8491 | 1 | 2086 | |
| 7876 | 15927 | A | 8492 | 3 | 2011 | |
| 7877 | 15928 | A | 8493 | 305 | 505 | |

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| 7878 | 15929 | A | 8494 | 3 | 1588 | EEEDYDVYKSEFPTEADLEDFTEAAVDE DDEDEEEGEEVVEDRDYYYDTFKGDDY NEENPTEPGSDGTMSDKEITHDVKAVCS QEAMTGPCRAVMPRWYFDLSKGKCVRF IYGGCGGNRRNFESEDYCMVCKAMIP PTPLPTNDVDVYFETSADDNEHARFQKA KEQLEIRHRNRMDRVKKEWEEAELQAK NLPKAERQTLIQHFQAMVKALEKEAASE KQQLVETHLARVEAMLNDRRRMALEN YLAALQSDPPRPHRILQALRRYVRAENK DRLHTIRHYQHVLAVDPEKAAQMKISQ VMTHLHVIEERRNQSLSLLYKVPYVAQ ENIQEEIDELLQEQRADMDQFTASISETPV DVRVSSDESEIIPFHPFHPFALPENEG SGVGEQDGGGIGAEKVINSKNKVDEK HGPLNETLDVKEMIFNAERVGGLEEEERE SVGPLREDFSLSSSALIGLLVIAVAIATV IVISLVMRLKRQYGTISHGIVE/VVDPML TPEERHLNKMQRNHGYENPTYKYLEQMQ I |
| 7879 | 15930 | B | 8495 | 73 | 1845 | MAATGTAAAAATGRLLLLLVGLTAPA LALAGYIEALANAGTGFAVAEPQIAMF CGKLNMHVNIQTGKWEPTGTGKSCFET KEEVLQYCQEMYPELQITNVMEANQRV SIDNWCRRDKKQCKSRFVTPFKCLVGEF VSDVLLVPEKCQFFHKERMEVCENHQB WHTVVKEACLQGMTLYSYGMLLPCG VDQFHGTEYVCCPQTKIIGSVSKEEEED EEEEEEDEEEDYDVYKSEFPTEADLEDF TEAAVDEDEDEEEGEEVVEDRDYYYD TFKGDDYNEENPTEPGSDGTMSDKEITH DVKAVCSQEAMTGPCRAVMPRWYFDL SKGKCVRFIYGGCGGNRRNFESEDYCM AVCKAMIPPTPLPTNDVDVYFETSADDN EHARFQKAKEQLEIRHRNRMDRVKKEW EEAELQAKNLPKAERQTLIQHFQAMVK ALEKEAASEKQQLVETHLARVEAMLND RRRMALENYLAALQSDPPRPHRILQALR RYVRAENKDRLHTIRHYQHVLAVDPEK AAQMKSQVMTHLHVIEERRNQILSLLYK VPYVAQEIQEEIDELLQEQRADMDQFTA SISEHPCGRPGEL* |
| 7880 | 15931 | B | 8496 | 55 | 274 | MADANKAEVPGATGGDSPHLQPAEPPG EPRREHPAAEKQQPQHSSSSNGVKME NDESAKEEKSDLKEKSTGX* |
| 7881 | 15932 | A | 8497 | 3 | 754 | FLFEHPAEARKQQPQHSSSSNGVKME NDESAKEEKSDLKEKSTGSKKANRFHPY SKDKNSGTGEKKGPNNRVFISNIPYDM KWQAIKDLMREKVGEVTVYELFKDAEG KSRGCGVVEFKDEEFVKKALETMNKYD LSGRRVNIKEDPDGENARRALQRTGTSTF QGSHASDVGSGLVNLPPSILNNPNIPPEVI SNLQAGRLGSTIFVANLDFKVGWKKLKE VFSIAGTVKAGRYKEDKDGQSRGMGT |
| 7882 | 15933 | A | 8498 | 2 | 346 | |
| 7883 | 15934 | A | 8499 | 1 | 414 | AWHEETHKVDLGLPEKKKNKKVVKEPE TRYSVLNNDYFADVSPLRATSPSKSVA HGQAPEMPLVKKKKKKKKIVSAALGKE VKRSQSKLRLRNTSP*VMTLRPPQKRK*S PKRR*SSQSSRSQ*KGKRRRGKRG |
| 7884 | 15935 | A | 85 | 2 | 526 | RGGCDRDGPFSSPLAMASLTVKAYLL GKEDAVAREIRFSLCCSTEPEAQAEVAA GPGPCERLLIRVAALFPAVRPGGFQAHY RDEDGDLVAFSSDEELTMAMSYVKDDIF RIYIKETNECLA\DHRRPPDAHERA/PRNM VHLNEICDG*NGPVAGTLYMCSFCPYYY LCTPFNV |

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| 7885 | 15936 | A | 850 | 24 | 432 | APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGTF AQLSELHCDKLHVDPENFKLLGNVHFG KEFTPEVQASWQKMTGVASALSSRYH |
| 7886 | 15937 | A | 8500 | 1 | 1977 | MEVDFKIRKVGQWTITLQEHVPSVLLFIE ETHPENKPTSTAVEESHISRDVTMVNFQ CQLDWSKGYLEAYLTKINSICSHRFLD GSVTCHDETGSSRDARDTVGTGVRVND ESVEQLGLRRTMWLGICRGAAMAAVST VTAFAGRPRPGRSRNPRGWAGDSK WTS GSRRSWLSRGGGEISPTGMITKTHFVYL GLPEK KKKR VVKEPETRYSVLNDDY FADV SPLRATSPS*DV AHGQAPEMPLVK K K K K K K G V S T L C E E H V E P E T T L P A R R T E K S P S L R K Q V F G H L E F L R G K R K N K S P L A M S H A S G V K T S Q D P R Q G E E T R V G K K S K K H K K E K K G G P G P H S L A P V Q D P W F C E A R E A R D V G D T C S V G K K D E E Q A A L G Q K R K R K S P R E H N G K V K K K K I H Q E G D A L P G H S K P S R M E S S P R K G S K K K P V K V E A P E Y I P I S D D P K A S A K K K M K S K K K V E Q P V I E E P A L K R K K K K R K E S G V A G D P W K E V V F P S E M D F A V G E L R E T D T D L E V V L E K K G N M D E A H I D Q V R R K A L Q E E I D R E S G K T E A S E T R K W T G T Q F G Q W D T A G F E N E D Q K L F L R L M G G F K N L S P S F S R P A S T I A R P N M A L G K K A A D S L Q Q N L Q R D Y D R A M S W K Y S R G A G L G F S T A P N K I F Y I D R N A S K S V K L E D |
| 7887 | 15938 | A | 8501 | 2 | 376 | TAGFLLPQGLPCKYHLMYGSHLMPNVW RRTTTREPKPLGDAEPNTRSLMWEVKRS SSGPWVFKSNIACHIPFRITSTSSAYD/W PFTHSF**FSGIIPPCPHGCHQFSDQDMVT FPLCQLPAHLH |
| 7888 | 15939 | A | 8502 | 2 | 956 | |
| 7889 | 15940 | A | 851 | 323 | 737 | |
| 7890 | 15941 | A | 852 | 24 | 589 | |
| 7891 | 15942 | A | 853 | 100 | 684 | |
| 7892 | 15943 | A | 854 | 135 | 851 | APSPDAMGHFTEEDKATITSLWCKVNV EDAGGETLGRLLVVYPWTQRFFDSFGNL SSASAIMGNPKVKAYGKKVLTSLGDAI KHLDDLKGTFQAQA*SELHCDKLHVD ENFKLLGKAGDPFLAIPFSAKEFTPGG CRLPGQKDG*LGVGQCPGPPDTTEAQLP MNAELFKDMALFLQAITNNKSISAKRSN FKLLGNVLVTVLAIHFGKEFTPEVQASW QKMTGVASALSSRYH |
| 7893 | 15944 | A | 855 | 40 | 505 | QPQTVSILHLTPEEKSAVTALWGKVNLD EVDVEALGRLLVVYPWTQRLLSFGNL STPDVAVMGNPKVKAHGKKVLGAFSDG LAHLNLLKGTFATLSELHCDKLHVDPEN FRLGQRAWV/LAGPITFGKEFTPPVAG LPIRKLVAIVANALAHK |
| 7894 | 15945 | A | 856 | 41 | 536 | APSPRRPWGHFTEEDKATITSLWGKVN VEDAGGETLGRLLVVYPWTQRFFD\SF GNLSSASAIMGNPKVKAHGKKVLTSL GDA\TKHLDDLKGTFQAQA*SELHCDKL HVDPENFKLLGNVLVTVLAIIPFSAKEF TPEGCRASWAERWVTWSWPVPCSSRYH |
| 7895 | 15946 | A | 857 | 241 | 435 | |
| 7896 | 15947 | A | 858 | 243 | 449 | |
| 7897 | 15948 | C | 859 | 275 | 397 | MLCWKLGVHHYSGNNIELGTAMRENT YRVLHTGLFIDPG* |
| 7898 | 15949 | A | 86 | 285 | 326 | NLPKILGHTQKRLQSTRSWKRMMLSLIN LQHIIYNPVIPIFVGITPDHLDVFS*IVRRGP VSSDANYIQYDL*NPNKSLSV |
| 7899 | 15950 | A | 860 | 2 | 424 | |

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| 7900 | 15951 | A | 861 | 73 | 608 | SVMTPVAPTLKAASKSDSSGPHRLREN PWCLSPADKTNVKAAGWKVGAHAGEY GAEAL\ERMFLSFPTTKTYFPHDLSHGVS AQV*GATGKKVADAL\TNAVAHVGR LPNALSGPEATLHAHKLRGGPGSTFKLL \SHLPCLGEPWAAHLPGRVSPLGCKAS LGTNFLGFLKQPC |
| 7901 | 15952 | A | 862 | 7 | 330 | |
| 7902 | 15953 | A | 863 | 2 | 379 | |
| 7903 | 15954 | A | 864 | 3 | 722 | HERGSVSCFNSGWTDHIRGHLPQPTAL RFPLRLQPPGPSSRPSPASGTCQHQLWL APSCQPTMSSQIRQNYSTDVEAAVNSLV NLYLQASYTYLSLGFYFDRDDVALEGVS HFFRELAEEKREGYERLLRMQTRGGR ALFQDIKKPAEDEWGTKTPDAMKAAMAL EKKLNLQALLDLHALGSARTDPHLCDFLE THFLDEEVKLIKMGDHLTNLHRLGGPE AGLGEYLFERLTCLKHD |
| 7904 | 15955 | A | 865 | 40 | 264 | |
| 7905 | 15956 | A | 866 | 3 | 1231 | |
| 7906 | 15957 | A | 867 | 3 | 496 | |
| 7907 | 15958 | A | 868 | 1121 | 1442 | |
| 7908 | 15959 | A | 869 | 2380 | 2714 | EETEGQARWLTPVIPTLWEAEAGGSPEV GSSRPA*PPLSAFLYPAFFLRSARFL |
| 7909 | 15960 | A | 87 | 133 | 392 | LITIYYIPENCQPGQHSETSSL/KKKKLA GCGGTHL*SQLLGRLRREDYLSPPGQICS EP*SYHCTPAWVTGQDPASKKKKKKKK R |
| 7910 | 15961 | A | 870 | 3260 | 3533 | |
| 7911 | 15962 | A | 871 | 6330 | 6802 | RSKGRAKIKSRRAGQVQWLMPVIPALW EAKAGGSPEARSL*PAWPIW*NPALHSSL /V**SKALSQKQKKQKKNHGDGQHDETV SLLKIQKSAG AHL*SQLLREAEAGELLEP RRQTLQ*AEILPLHSLGLDGSKTPSQKKK KKRSQGVGVREPOGP |
| 7912 | 15963 | A | 872 | 1 | 500 | |
| 7913 | 15964 | A | 873 | 63 | 375 | |
| 7914 | 15965 | A | 874 | 27 | 374 | |
| 7915 | 15966 | A | 875 | 1 | 801 | |
| 7916 | 15967 | A | 876 | 1286 | 1388 | |
| 7917 | 15968 | A | 877 | 1 | 1056 | |
| 7918 | 15969 | A | 878 | 651 | 1467 | |
| 7919 | 15970 | A | 879 | 3 | 414 | |
| 7920 | 15971 | A | 88 | 2 | 359 | EVLRMAGTGLVAVEVVVDALPDFEEGY EGPGGREAAAALVEDETRRYRPTMNYL SYLTSPDYSAFETDILNNDSERLAARQPA I*LLTMKLYLSSPSCGHYFVLLHVYNC LSLYFPSP |
| 7921 | 15972 | A | 880 | 164 | 412 | |
| 7922 | 15973 | A | 881 | 29 | 489 | |
| 7923 | 15974 | A | 882 | 44 | 847 | IKENSIWIRASTITYLKGETIGTEPEGK EGECASGLVNPFRDFPSKIVSFPKIPV*T SLHITPLAIVCPFQNIWSLHGKQGRGK QNINKRETKNNTTLFREPKQNPQIPFF* TTQGHVEVKSLSVPL*ITGRKAISTQSL* QEFSTLEASEHAEDG/ALLRVPLPSWARA PSGVGVKSRFSH/VPRDHQPTTHWWP WWSMAGRQRPSTLSHFLSWMTSCLGP SHFRRELAFWKPTFPIHHRTRQSAHILVP LVFKGHFQOTL |
| 7924 | 15975 | A | 883 | 40 | 431 | |
| 7925 | 15976 | A | 884 | 122 | 341 | |
| 7926 | 15977 | A | 885 | 23 | 419 | |

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| 7927 | 15978 | A | 886 | 1 | 598 | LARNPGSTHASGGILLGRQCWVLFMAP KKAKKRAGGANSNVFSMFEQTQIQEFK EAFITMDQNRDGFIDKNDLRDTFACPW RKLNVKNEEIDEMAKEAPGPINFVFLT MFWGRNLKGADPEGKPFNLNRISKVFDPE GKGVAEGLDYVREMLNNAARRGFRKE VDQMFAAFPPDVTGNLDYKNLVHIITH GEEKD |
| 7928 | 15979 | A | 887 | 174 | 452 | |
| 7929 | 15980 | C | 888 | 60 | 245 | |
| 7930 | 15981 | A | 889 | 1878 | 2295 | SFSPA WPSRWCASSSWCTDCLVPSTCAA LQHPVVFLDKGNHFLIFFYFFFFVILYTSS SHEVED*PCVMFSKIKWYLLE/VRYILVV AYRLSFCKERKKTIKLCQIILLCLAARTW LPCLSLSLPPFLSFLCMDFFFEKK |
| 7931 | 15982 | A | 89 | 69 | 342 | VGNMSGTNLDGNDEFDEQLRMLELYGD GKDGDTLTDAGGEPDSLGOYSTDTNPT WDLDI*AWFFMISEYFLFTYLVQFMAFL LYCGFMFL |
| 7932 | 15983 | A | 890 | 3218 | 3469 | |
| 7933 | 15984 | A | 891 | 618 | 1236 | |
| 7934 | 15985 | A | 892 | 12 | 138 | |
| 7935 | 15986 | A | 893 | 1 | 1002 | |
| 7936 | 15987 | A | 894 | 66 | 293 | RLFRFFCPTGCSLDVVLSLFS*GCGFL*S LHTGFMPSPEFWPGDSLVSQIVTNFSWR FSSAVAFSSASGSFPQGS |
| 7937 | 15988 | A | 895 | 2202 | 2335 | |
| 7938 | 15989 | A | 896 | 343 | 906 | |
| 7939 | 15990 | A | 897 | 1455 | 1604 | |
| 7940 | 15991 | A | 898 | 370 | 807 | |
| 7941 | 15992 | A | 899 | 1 | 1548 | |
| 7942 | 15993 | A | 9 | 1130 | 1377 | ASHLRSGVRDQPEQHGETPTLALKIQKSP GCGGRHL*SQLPGRRLQENHLNLGGGG CGELRSHHCIPAWVTETLTKKKKKKRR |
| 7943 | 15994 | A | 90 | 144 | 2205 | DRRERCHPFKRALMP/LRPAEPRPAFPIH HPLLQDANEAPG/CWAEAVQGCPT/AE DPPCVSRAAPGGSVPPFC/PGRL*GWGG PRGKGDPEGLADSGPPCELRFEESRPPR VVGESPAEKLAYPPGPLCFF*PFSEF/PE L*TKSPS*EMTNHMLHSGGGGSWPGSPT SPGPPPGSLPRAAALPPKTPGQTRAPAG AGCPHADLAMSPGTPGSPVAPTSLVA DCSSQNV*HPRVPEPTQAATPVQFPKNVI TSPGCQSPPKQ/APVPVPRMYN/MPRVT EPAQAATPESLGHVPELRSTQTVATASP GHLTPMKGTLGSAREIPEVGTGPPWCPV PPPSPLPCAPRGSAAGGLTLPLRASQTS GSTFLLISFPFCKLTSPFPLGVQGTAPAG RSVCTVVQGVVSEGGTSVGQLLHLPVP LCPPLSKQVMAPIAGL/PIQCSGPPVQW GDPRPTPP*CIQPGQVYCCD/VLPALLCR FPGAAQPRTPHEWACPALAECLPCALRQ VPRAGQPG*TMCGAGTGPGCWKGGQK EAGGRCEKLTPLNTTALPAPAGPCSQ PLSHGWPGLPSPH*DSRQGGPDP/ASPS QPWLRKPPNPTMGLRKPRK*LLPASPKR LRKPKAASLPVRHPKASLGCS*GLIWA LP*GWPCRWGPLGALGGTWQPPRHPGP VLISRA*GLQPQLTK |
| 7944 | 15995 | A | 900 | 3 | 127 | VLCQFSKGMLPVFAQSV*YWLWVRYVP SIPSLLRVFSMKGC |

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| 7945 | 15996 | B | 901 | 1 | 1926 | MFSDSLTPMHKERVITLLKREGHVVGFM GDGINAPALRAADIGISVDGAVDIARE AADIILLEKSLMVLEEGVIEGRRTFANML KYIKMTASSNFGNVFVSVLVAFLPFLP MLPLHLLIQNLLYDVSQVAIPFDNVDD QIQKPQRWNPADLGRFMIFFGPISSIFDIL TFCLMWWVFHANTPETQTLFQSGWFVV GLLSQTLIVHMIRTRRVPIQSCASWPLM IMTVIVMIVGIALPFSPLASYLQALPLS YFPWLVAIAGLATNSDRFDLNLHVFRQ TGNFNARTCREGGVVFGEFGFASGFDDR FYVIQRLTCLCSDVCRYFARFRIYRDLTG GDDHIAQINXLYVRPIAAGPAFGTFRWL HSRRAMLLTRADMEDRERFLNARDTLR ALLDNNIVPVINENDAVATAEIKVGDND NLSALAAIAGADKLLLLTDQKGLYTAD PRSNPQAEIKDVYGIDDALRAIAGDSVS GLGTGGMSTKLQAADVACRAGIDTIIAA GSKPGVIGDVMEGISVGTLFHAQATPLE NRKRWIFGAPPAGEITVDEGATAAILERG SSLLPKGIKSVTGNFSRGEVIRICNLEGRD IAHGVSRYNSDALRRIAGHHSQEIDAILG YEYGPVAVTMHMYR* |
| 7946 | 15997 | A | 902 | 1 | 1602 | |
| 7947 | 15998 | A | 903 | 1 | 972 | |
| 7948 | 15999 | A | 904 | 280 | 358 | |
| 7949 | 16000 | A | 905 | 141 | 152 | QCPPQPRPPGRCPTQSGHTGCSTGG*GL NPLYYNLCDRSGAWGIVLEAVAGAGIVT TFVLTHLVASLPFVQDTKKRSLLTQRLR GRCHHTAGTMGSC |
| 7950 | 16001 | A | 906 | 177 | 247 | |
| 7951 | 16002 | A | 907 | 574 | 737 | |
| 7952 | 16003 | A | 908 | 221 | 576 | GVGGDTHDTHPNTGREGGPPSRGAHVA GPARGRRSLESPLPGARSSGSPNPTASP SPPLTQSHT*GFPKRPESSCRLSRGVAAW WLWAEYIVFKPAGSSWHCPSPWLLAVA RGRMMS |
| 7953 | 16004 | A | 909 | 1 | 157 | TKTWTLKKHFVGYPTNSDFELKTAELPP LKN/GRVAAKRLKEGDTMMGQVAK |
| 7954 | 16005 | A | 91 | 122 | 874 | SPLLGGRLRQKIFFNWEAGGSIKPKLTSP PARQGQGGPFSSSSPSSSPES*LFPALRT PSRQGGSAIPASGLSTPACVPSGSTRNL FHAPHVGRVSLLLPAS*KAAGPSKKGPG QVNPA*FRKPGVGI*RSVGPRQLPLE*LH ARKNRAGPVPLPGLGKEGPSLQGPKRTO LASLLMEGPPTHPTIHDGTTAQPELWPC RGPQMOSWGSQPEHTFGPRQPHPPHPS RHRSDSESSLLQASAHGKA |
| 7955 | 16006 | A | 910 | 3 | 484 | VRLREDDRRGPSLGTCHKSDPGRPAAQS QPPSPGSGTFGLLSFRMVRTKTWTLKKH FVGYPNTSDFELKTAELPPLKNGEVLE ALFLTVDPYMRVVESKNVALPKGTIVLA SPGWTTSHISDGKDLEKLLTEWPDITPLS LALATVGMPGLTAYFGLLE |
| 7956 | 16007 | A | 911 | 1 | 1147 | MLLCQKAPSLKTTYNHPPAADSAGTAL NLETTVKQTRTQLEYNNVGTDLSPPEK SFNYPLLSSSGDQFEIQLNQQLWSLIPNN DVRRLVSHVIRTLKTDCTETHLQLACAK LISRTGLLMKLLSEQQELRTVSMATAWKP RMNRKSRMRQSHFASHAGRWVHNH STLQOSPKLQMAELSEARRRSFRMVRT KTWTLKKHFVGYPTNSDFELKTAELPPL KNGGLEFLIAYGMLYFVEVLLEALFLT DPYMRVAAKRLKEGDTMMGQVAKV VESKNVALPKGTIVLASPGWTTSHISDG KDLEKLLTEWPDITPLSLALGTVMGMPGL TAYFGLLEICGVKGETVMVNAAGAV GSVVGQIAKLKCKVVGAVGSDEK |

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|------|-------|---|-----|-----|------|---|
| 7957 | 16008 | A | 912 | 214 | 540 | |
| 7958 | 16009 | A | 913 | 495 | 684 | |
| 7959 | 16010 | A | 914 | 1 | 1911 | |
| 7960 | 16011 | A | 915 | 3 | 1381 | KTPFVGYQHQRPKVDKTTKMGRNQSRK AENSKNQSTSSPPKDRSSLPATEQSWTE NDFDELTEVGFRRSAITNFSELKEHVLTR RKEAKNLEKRLDEWLTRINSVEKTLNDL MELKTMAQELRDARTSFNS*FNQVEKRI SVIEDQIDEIKQDDKAAETCNWRWVSES LRQLRASVDAFHARASHYNAGECLHQL AALNSRLNCAQEMARRDSIGEVPVPW RTVVGSGIAGEAKLDHLRLVSLIGREVN KENSPAATRWLFSFQAGALAGGQIVLQA AKPNAHGQPVVATRNLNPAGIVAVLK QRPRLVAAAQAFYLRDPIDLRACRVFK TFLPETRIMTSYYAJEWSLWTLVDVLHA ENSESAHMSHNSYDPPSDVARHLTHLPM SPIPDYIARFRYRHSRVRLTARKLSPAF MRCSSSEIQRYSTMLERGFNGGYCRSTTV RVVTEATRMLSF |
| 7961 | 16012 | A | 916 | 1 | 1191 | |
| 7962 | 16013 | A | 917 | 1 | 227 | |
| 7963 | 16014 | A | 918 | 1 | 392 | |
| 7964 | 16015 | A | 919 | 157 | 388 | |
| 7965 | 16016 | A | 92 | 27 | 319 | IINTSISLWFLGLSSIIHHYQERFL*FN*FG SYMVFIEIFFGISSAFFVC*WPK/Y/LLYFR YCRCFLILLLSIFEF/DLCYLVL*IFMFFL FFYMFLCV |
| 7966 | 16017 | A | 920 | 451 | 593 | |
| 7967 | 16018 | A | 921 | 467 | 1038 | |
| 7968 | 16019 | A | 922 | 233 | 345 | |
| 7969 | 16020 | A | 923 | 1 | 1386 | |
| 7970 | 16021 | A | 924 | 1 | 1254 | |
| 7971 | 16022 | A | 925 | 36 | 695 | |
| 7972 | 16023 | B | 926 | 52 | 554 | MGKEKTHINIVVIGHVDGSGKSTTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFKYA WVLDKLLKAERERGITIDISLWKFETSKY YVTIIDAPGHRDFIKNMILNHPGQISAGY APVLDCHTAHIACKFAELKEKIDRRSGK KLEDGPKFLKSGDAAIVDMVPGKPI* |
| 7973 | 16024 | A | 927 | 63 | 1545 | PLKAKMGKEKTHINIVVIGHVDVTKGST TTGHLIYKCGGIDKRTIEKFEKEAAEM GKGSFKYA*VLDKLLKAERERGITIDISL WKFETSKYYVD*SLIAPGHRDFYSKT* FTGTISRLDLVWGAPFLGG/CLP*LFAAG VWWNLKAGISQEWGRTREHALLGLHTG VWKQTKLFGVNKNWIST*GHPTAQKKIL KEIVKGKSALTIRKIGYNPDTSSILCPISG WNGDNMLEPSAANMPWFQGDGKVTRK DGNASGTTLEALDCILPPTPTDKPLGL PLQDVYKIGGIGTVPVGRVETGVLPKM VVTFGPVNVTTEVKSVMHHEALGEAL PGDNVGFNVKNVSVKDVRRGNVAGDS KNDPPMEAAGFPAQVILNHPGQISAGY APVLDCHTAHIACKFAELKEKIDRRSGK KLEDGPKFLKSGDAAIVDMVPGKPMCV ESFSDYPPLGCFVVRDMRQTVAVGVVKA VDKKAAGAGKVTKSAQKAQKAK |
| 7974 | 16025 | A | 928 | 2 | 246 | |
| 7975 | 16026 | A | 929 | 318 | 420 | |
| 7976 | 16027 | A | 93 | 264 | 664 | IRLAFCGIFQAFSICNSNIWLLPEIPLLG IYP*E*NTKTCTQMFTAALFIIS*KVEISQ MPIINEKINKLWYIHMTCHTKNKVLIRDT T*MNLENIKLNERGQTKKKKKAIYCLSL FM*YVQNRQIHTDEK |
| 7977 | 16028 | A | 930 | 205 | 400 | |

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|------|-------|---|-----|------|------|--|
| 7978 | 16029 | A | 931 | 234 | 425 | ICKWILPCGLAGSYKIAKWVSGFTLLLT HMGAAWV*LSLFGYTILF*FPKMSSFL TMKKDIF |
| 7979 | 16030 | A | 932 | 405 | 862 | |
| 7980 | 16031 | A | 933 | 2 | 412 | |
| 7981 | 16032 | A | 934 | 110 | 431 | |
| 7982 | 16033 | B | 935 | 754 | 1544 | MREIVHIQAGQCGNQIGAKFWEPWKASS IELSQCRNSPSKVFRSKEHDGLPVTPTTR R* |
| 7983 | 16034 | A | 936 | 1 | 451 | |
| 7984 | 16035 | A | 937 | 1 | 258 | |
| 7985 | 16036 | A | 938 | 3 | 1906 | |
| 7986 | 16037 | A | 939 | 1 | 585 | ECLCVSTAVRIRHEKTMTELLRGGSF FKDMRVPSALVTLHMLLCSIPLSGRDLS DEQKIQNDIIDILLTFTQGVNEKLTISEET LANNTWSLMLKEVLSSILKVPEGFFSGLI LSELPLPLPMQTTQVSLPYNMHLINDC SNTF*KASDSVKKQKPPSPFLPKRHKITG *GGDKTETSWSLRKYGGKNFK |
| 7987 | 16038 | A | 94 | 2 | 605 | SHGTPGRPTRPVEFFSGGSAGSFPWFPK KAKKRAGGADSNVFSMFEQTQMQUEFK EAFSIMDQNRDGFIDKNLDLDTFAALGE VMNVKNEEIDEMIKAEAPGPLNFTVFLTN VWGENLREADPEETILNAFKVFDPRP KGCMKA/DYVSGKMLTHAGRFRFSKE EV\QMFAGLPPLT*LGNDYKNLVHIIT HGEEKD |
| 7988 | 16039 | A | 940 | 625 | 2115 | |
| 7989 | 16040 | A | 941 | 180 | 359 | GSLQRDRWPTSSWRTGRQGSSLLRPRWI SFLAQLWRV*RIAGTFVIRIEDGNGRRA FI |
| 7990 | 16041 | A | 942 | 1286 | 2188 | |
| 7991 | 16042 | A | 943 | 1 | 2537 | |
| 7992 | 16043 | A | 944 | 2 | 437 | |
| 7993 | 16044 | A | 945 | 298 | 581 | GARAEARAGSGQGAGLVSSPVRWRG WSDKGAERPGGPLSPLREVSRAGPSG/H AARGQQGRPRFPFPPGPRPRRCPCTRA RPGGAAGGGPCL |
| 7994 | 16045 | A | 946 | 377 | 639 | |
| 7995 | 16046 | A | 947 | 1279 | 2253 | |
| 7996 | 16047 | A | 948 | 268 | 369 | |
| 7997 | 16048 | A | 949 | 15 | 440 | |
| 7998 | 16049 | A | 95 | 1 | 1254 | |
| 7999 | 16050 | A | 950 | 118 | 375 | VAVVQIIFLPVFIAEKYKDLVPDNSKTAD NATKNAEPLINLDVNNPDFKAGVMALA NLLQIQRHDDYLVMLKVAIRILVQERLTQ D |
| 8000 | 16051 | A | 951 | 1 | 969 | AATVLTITIGEAPSRSDSAPARPLAASPV PAPPAPPRFFSPGRPGDQSEKRWTFMR RKLTSLDYHNPAGFNCKDETEFRNFIV WLEDQKIRHYKIEDRGWNLNIHSSDWPK VFEKYFKRC*TCPFKIQDRQESYLTGFFG LAVRLEYGDNAEKYKDLVPDNSKTA*Q LQLKIAEPLINLDVNNPDFKAGVVGFG* TWLQIQRH\GLPGQMLKANSGFVWQE RLDHQGCQFA*GQIKQKRGLPVA\LDKHI LGFD\TGDAVLNEAAQILRLHIEELRELQ TKINEAIVAVQAIADPKTDHRLGKSLED EHLRTSASHLL |
| 8001 | 16052 | A | 952 | 1258 | 1429 | |
| 8002 | 16053 | A | 953 | 189 | 403 | |

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|------|-------|---|-----|-----|------|--|
| 8003 | 16054 | A | 954 | 51 | 1702 | GLPRCASVQPVCEYQRRWKRWLWDIT WEKWKQMDTVQKSIYRNILAEKYRNLVL LDGKLAAGAKTSRVEQQDISKED*SQRL EMEELAKRKSVPEEIWKSRGQFKNQQLN KENNLGQEIATCTKIPTKRDIENEF/RE KFYCKINTCC/MNR*ILWKRIVINMVHVE RCSNKTQI*LYKESMMEKKKPKYSECG RTFRGHITLVQHQTICGERPCKCTEGRK GFNQSSHLRNNQRKTLSEKPYKCECG KAFSYCLVLNQHQRIHSGEKPYEGTECG KTFIQSSYLTQHQR/TSHTGEKPYTCLEC GRLFSQNTHTLTHQRIHTGEKPYECNEC GRSFSQTAHLTQHQRMYTGEKLYECNE CEKAFHDHSAHQHIVHTAEKPYDIT GKTFSYCSDLIQHQRMTGEKPYKCECG GNAFSDCSSLIQHQRTHTGEEPYECKQC GKAFSRSTYLTQHQRSHAGEKQYKCE CEKTFSLSSFLTQHMRVQTGEKPYKYNE YGKAFSDCSGHFQRTHTGEKPYCECND GKPFSCSALIQHKRIHTRKKP |
| 8004 | 16055 | A | 955 | 2 | 270 | REEKEWPPHTQPWYPEGCFKDGQHYEE GSVIKENCNS*WTAQNYSQFWGMTLED GFKFRLGTLPPSPMLLSMNEMTVSVPSD SRMCMYL |
| 8005 | 16056 | A | 956 | 1 | 999 | |
| 8006 | 16057 | A | 957 | 1 | 1518 | VHCSEFPGRPPRPRTRGRKVEAIPVFOR MWTGYKILIFSULTTEIWMEKQYLSQRE VDLEAYFTRNHTFLQTHFKRAIFQIGQ YCRNFGCCEDRDDGCVTEFYAANALCY CDKFCDRENSDCPDYKSFCEKEWPP HTQPWYPEGCFKDGQHYEEGVIKENC NSCTCSGQWKCQSHVCLVRPELIEQV NKGDYGWTAQNYSQFWGMTLEDGFKF RLGTLPPSLMLLSMNEMTASLPATDLP EFFVASYKWPGWTHGPLDQKNCAASW AFSTASVAADRIAQSKGRYTANLSPQNL ISCCAENRHCNSGSIDRAWWYLRKRG LVSHACYPLFKDQATNNGCAMASRSD GRGKRHATKPCPNVKEKSNRIYQCSPPY RVSSNETEIMKEIMQNGPVQAIMQVHED FFHYKTGIYRHVTSTNKESEKYRKLQTH AVKLTGWGTLRGAQGOKEKFWIAANS WGKSWGNGYFRILRGVNESDIEKLJIAA WGQLTSSDEP |
| 8007 | 16058 | A | 958 | 316 | 411 | |
| 8008 | 16059 | A | 959 | 314 | 390 | |
| 8009 | 16060 | B | 96 | 52 | 554 | MGKEKTHINIVVIGHVDSGKSTTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFKYA WVLDKLAERERGITIDISLWKFETSKY YVTIIDAPGHRDFIKNMILNHPGQISAGY APVLDCHTAHIAKFAELKEKIDRRSGK KLEDGPKFLKSGDAAIVDMVPGKPI* |
| 8010 | 16061 | A | 960 | 112 | 1154 | SCGLGHRKTFVSLPARNETQPKACRE QNMEGDFSVCRCNC*RHVVSANFTLHEA YCLRFLVLCPECEEPVPKETMEEHCKLE HQQVAGCTMCQQIMHKSSLEFHKANECQ ERPVECKFCCLDMQLSKLEHESYCGSR TELCQCGQFIMHRMLAQRRDVCSEQ AQLGKGERISAPEREIYCHYCNQMIPEN KYFHHMGKCCPDSEFKKHFPVGNPEILP SSLPSQAAENQTSTMEKDVRPKTRSINRF PLHSESSSKAPRSKNKTLDPMLMSEPKP RTSSPRGDKAAYDILRRCSQCIGILLPLIL NQHQEKCRWLASSKRKTSEKFLDLLEK ERYYKFKRFHF |
| 8011 | 16062 | A | 961 | 103 | 538 | |
| 8012 | 16063 | A | 962 | 1 | 405 | |
| 8013 | 16064 | C | 963 | 334 | 471 | |

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|------|-------|---|-----|------|------|--|
| 8014 | 16065 | A | 964 | 1 | 1137 | |
| 8015 | 16066 | A | 965 | 1 | 451 | GDRPFRV*DPRAGQAATFWTDPSLS*SL LLGVMFPAAPSPRTPGTGPRRGPLAGLG PGSTPRITASRMGLPLGSAVSSPVLFSPGG RRSSLISRGTPTRMLPHHSITESVNYDAK TIGSSLPVKVM EALTLAEVDDQLTNINE GGWACLV |
| 8016 | 16067 | A | 966 | 301 | 1867 | |
| 8017 | 16068 | A | 967 | 57 | 383 | GWLAHTANERPVRFCFPWLEGFLENIRA PTLNF*QIQQSLAIFVEPIKTILLPFCFFRIF STRVRICTYSSHSFPGPGAGLLHFCSSSL VRFKISFGDTVAVAPVPDF |
| 8018 | 16069 | A | 968 | 507 | 904 | GKRAGECWRRSLRPRGPRGETRAASPSS ARPSLALASAPRPKSGPRPROGPRRLW PRGLKGQVCARGPGRGGPGGVGRRSA SARAPRVPGDQPPPPAPSS*ED/WT*EIG RLSSHAPLAVLHTRSALLNS |
| 8019 | 16070 | A | 969 | 379 | 858 | |
| 8020 | 16071 | A | 97 | 1 | 1299 | |
| 8021 | 16072 | A | 970 | 259 | 483 | |
| 8022 | 16073 | A | 971 | 175 | 588 | |
| 8023 | 16074 | A | 972 | 1 | 383 | |
| 8024 | 16075 | A | 973 | 79 | 445 | |
| 8025 | 16076 | A | 974 | 1163 | 1401 | |
| 8026 | 16077 | A | 975 | 80 | 406 | |
| 8027 | 16078 | C | 976 | 70 | 240 | MITGTSQADCAVLIVAAGVGEFXAGISK NGQTRRDMRKXLRKSALTIRKLATTPT Q* |
| 8028 | 16079 | B | 977 | 68 | 490 | MGKEKTHINIVVIGHVDSGKSTTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFKYA WVLDKLKAERERGITIDISLWKFETSKY YVTIIDAPGHRDFIKNMITGTSQADCAVL IVAAGVGEFEAGISKNGQTREHALLA* |
| 8029 | 16080 | A | 978 | 261 | 406 | |
| 8030 | 16081 | A | 979 | 1 | 678 | |
| 8031 | 16082 | A | 98 | 36 | 697 | KLPLKAKMGKEKTHINIVVIGHVDSGKS TTTGHLYKCGGIDKRTIEKFEKEAAEMG KGSFKYAWVLDKLKAERERGITIDISLW KFETSKYYVTIIDAPGHRDFIKNMITGTS QADCAVLIVAAGVGEFEAGISKNGQTRE HALLAYTLGVKQLIIVGVNKM DSTGAIL TGDFPSLEPRHVSTWLQHVVTIPTNRNH KCYCVGVVANFLNVSADFLNNF |
| 8032 | 16083 | A | 980 | 181 | 340 | |
| 8033 | 16084 | A | 981 | 1 | 375 | |

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|------|-------|---|-----|------|------|---|
| 8034 | 16085 | A | 982 | 1 | 2583 | MVNFTVDQIRAIMDKKANIRNMSVIAHV DHGKSTLTDSLVCAGIASARAGETRFT DTRKDEQERCIPIKVNAISLFYELASEND LNFIQSKDGAGFLINLIDSPGWHVDFSSE VTAALRVMTMGALVVVDCVSGVCVQTET VLRQAIARIKPVLMNMKMDRALLELQ LEPEELYQTFQRIVENNVIIISTYGEGESG PMGNIMIDPVLGTGVFGSGLHGWAFTLK QFAEMYVAKFAAKGEGQLGPAERAKK VEDMMKKLWGDYFDPANGKFSKPAT SPEGKKLPRTFCQLILDPIFKVFDAMNF KKEETAKLIEKLDIKLDESKDEKPKLL KAVMRRWLPAGDALLQMITIHLPSVTA QKYRCELLYEGPPDDEAAMGIKSCDPKG PLMMYISKMVPTSDKGRFYAFGRVFSGL VSTGLKVRIMGPNYTPGKKEDLYLKPIQ RTILMMGRYVEPIEDVPCGNIVGLVGVD QFLVKTGTITTFEHAHNMRVMKFSVSPV VRVAVEAKNPADLPKLVEGLKRLAKSD PMVQCIIEESGEHIIAGAGELHLEICKDL EEDHACIPIKSDPVVSYRETVSEESNVL CLSKSPNKHNLRYMKARPPDGLAEDID KGEVSARQELKQRARYLAEKYEWDVAE ARKIWCFGPDGTGNILTDITKGVQYLN EIKDSVVAGFQWATKEGALCEENMRGV RFDVHDVTLHADAIHRGGGQIPTARRC LYASVLTAPRLMEPIYLVEIQCPQVVG GIYGVNLNRKRGHVFEESQVAGTPMFVV KAYLPVNESFGFTADLRNTGGQAFQPC VFDHWQILPGDPFDNSSRPSQVVAETRK RKGLKEGIPALDNFLDKL |
| 8035 | 16086 | A | 983 | 1326 | 1498 | |
| 8036 | 16087 | A | 984 | 60 | 966 | RRRNSDGNACQPATHLLLSARFITGHGQ KLKSELKKTQVIMLNIQKVRIPTRDGY NEKDILSTGKNVEKLELSNAGYPSNIEK KEYQEQSVLSCCSEKRDANPKSVVCSFF MQEQCTKGEKRFIPGTLSDRHLRYFG ILPTVSNAAVVKEVPTVSNAAVVTEAPT GSNAAVVTEAPTGSNAARVMEVPTGSN AAVVTEVPTGSNAAVVTEAPTGSNAAV VKEAPTGSNAARVMEVPTGSNAAVVKE APTGSNAARVMEVPTGSNAAVVKEVPT GSNAAVVKEVPTGVTLRWSRKRPRE |
| 8037 | 16088 | A | 985 | 1393 | 1625 | |
| 8038 | 16089 | A | 986 | 358 | 475 | |
| 8039 | 16090 | A | 987 | 232 | 329 | |
| 8040 | 16091 | A | 988 | 127 | 461 | |
| 8041 | 16092 | A | 989 | 562 | 897 | |
| 8042 | 16093 | A | 99 | 62 | 1548 | PLKAKMGKEKTHINIVVIGHVDSGKST TTGHLIYKC/GGNDKRTIEKFEKEAAEM GKGSFKYAWVLDKKAERIERGITIDISL WKFETSKYYVD*SLIAPGHQETFIQKH DLQGTSQGLAWFGGPPFWGGSPLIVAA GIVGEF*SLVSPKNGADPTKHALLGLHT GVWKQTKLFGVNKNWIST*/EPPYSPEED IEGNC*GKVSTYIKKIGYNPDTSILCPIS GWNGDNMLEPSPNMPWFQGDGKVTR KDGNASGTTLEALDCILPPTPTDKPLG LPLQDVYKIGIGITVPVGRVETGVLPKPG MVVTFGPVNVTEVKSVMHHEALGEA LPGDNVGFNVKNVSVKDVRRGNVAGDS KNDPPMEAAGFPAQVILLNHPGQISAGY APVLDCHTAHIACKFAELKEKIDRRSGK KLEDGPKFLKSGDAAIVDMVPGKPMCV ESFSDYPPLGCFVRDMRQTVAVGVVKA VDKKAAGAGKVTKSAQKAQKAK |
| 8043 | 16094 | A | 991 | 7 | 494 | |
| 8044 | 16095 | A | 992 | 206 | 357 | |

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|------|-------|---|-----|-----|------|--|
| 8045 | 16096 | A | 993 | 1 | 101 | |
| 8046 | 16097 | A | 994 | 256 | 407 | |
| 8047 | 16098 | A | 995 | 254 | 432 | |
| 8048 | 16099 | A | 996 | 249 | 400 | |
| 8049 | 16100 | A | 997 | 37 | 465 | |
| 8050 | 16101 | C | 998 | 127 | 216 | MRLRKQAEKNVEKKIDKYTEVLKTHGL LV* |
| 8051 | 16102 | A | 999 | 1 | 1258 | LFLPLLEPGERRGLLYRSRPGGAVALILL AAAVSICAVSQHAPPWTEDCRKSTYPPS RPTYRGAVPWDTIQCLTYHPYKRWHEL MLDKAPV/LQKVIVNSLKNMINTFVPSG KIMQVVDEKL\PGLLGNFP\GPFEEEMKG IGRCLLDIPLGEIISFNIFYELFTICTSIVA EDKKGHLIHGRNMDFGVFLVWNINND TWVITEQLKPLTVNLDFQRNNKTVFKAS SFAGYVGMLTGFKPGLFSLTLNERFSIN GGYLGILEWILGKKDAMWIGFLTRTVLE NSTSYEEAKNLLTKTKILAPAYFILGQNQ SGEGCVITRDRKESLDVYELDAKQGRW YVVQTNVDRWKHPFFLDDRTPAKMCL NRTSQENISFETMYDVLSTKPVLNKLTV YTTLIDVTKGQFETYLRDCPDPCIGW |

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-8051, a mature protein coding portion of SEQ ID NO: 1-8051, an active domain of SEQ ID NO: 1-8051, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-8051.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-8051, a mature protein coding portion of SEQ ID NO: 1-8051, an active domain of SEQ ID NO: 1-8051, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-8051, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 8052-16102, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-8051.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/14827

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70; C07K 14/00

US CL : 536/23.1; 435/320.1, 455, 468; 530/300

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/320.1, 455, 468; 530/300

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EST, GENESEQ, GENEEMBL, ISSUED_PATENTS, EAST**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------|
| X | Database SPTREMBL, ID No. Q9TS35, Bailey et al. 01 May 2000. See sequence alignment. | 1-9, 19, and 22-26 |
| X | Database Swiss-prot, ID No. P01922, Michelson et al. 21 July 1986. See sequence alignment. | 1-9, 19, and 22-26 |
| X | Database Swiss-prot, ID No. P01923, Zucherkanndl et al. 21 July, 1986. See sequence alignment. | 1-9, 19, and 22-26 |
| X | Database Swiss-prot, ID No. P01924, Matsuda et al. 21 July 1986. See sequence alignment. | 1-9, 19, and 22-26 |



Further documents are listed in the continuation of Box C.



See patent family annex.

| * Special categories of cited documents: | |
|---|--|
| "A" document defining the general state of the art which is not considered to be of particular relevance | "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| "E" earlier application or patent published on or after the international filing date | "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| "O" document referring to an oral disclosure, use, exhibition or other means | "&" document member of the same patent family |
| "P" document published prior to the international filing date but later than the priority date claimed | |

Date of the actual completion of the international search

01 November 2001 (01.11.2001)

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/14827

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9, 19, 22-26, and SEQ II NO:1

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.